

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 15:30:52 ; Search time 1652 seconds  
(without alignments)  
264.251 Million cell updates/sec

Title: US-09-750-609-10

Perfect score: 15

Sequence: 1 cctctcccccctgtt 15

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*  
2: gb\_hig.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*  
15: em\_ba.\*  
16: em\_fun.\*  
17: em\_hum.\*  
18: em\_in.\*  
19: em\_mu.\*  
20: em\_om.\*  
21: em\_or.\*  
22: em\_ov.\*  
23: em\_pat.\*  
24: em\_ph.\*  
25: em\_pl.\*  
26: em\_ro.\*  
27: em\_sts.\*  
28: em\_un.\*  
29: em\_vi.\*  
30: em\_htg\_hum.\*  
31: em\_htg\_inv.\*  
32: em\_htg\_other.\*  
33: em\_htg\_mus.\*  
34: em\_htg\_pln.\*  
35: em\_htg\_rod.\*  
36: em\_htg\_mam.\*  
37: em\_htg\_vrt.\*  
38: em\_sy.\*  
39: em\_htgo\_hum.\*  
40: em\_htgo\_mus.\*  
41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
C 1	15	100.0	190	9	HSA288489	AL288489 Homo sapi
C 2	15	100.0	600	5	AF506010	AF506010 Gallus ga
C 3	15	100.0	1689	9	AK021867	AK021867 Homo sapi
C 4	15	100.0	1721	4	AF232676	AF232676 Sus scro
C 5	15	100.0	3190	9	BC000776	BC000776 Homo sapi
C 6	15	100.0	3347	5	CHK7GFA	L01121 Gallus gall
C 7	15	100.0	3752	9	AF312211	AF312211 Homo sapi
C 8	15	100.0	4353	9	AB018279	AB018279 Homo sapi
C 9	15	100.0	11001	5	FR092H06	AF035357 Fugu rubr
C 10	15	100.0	11896	1	AE009810	AE009810 Pyrobacul
C 11	15	100.0	12602	14	AF144617	AF144617 Pestiviru
C 12	15	100.0	32802	1	BSSRFAP	X70356 B. subtilis
C 13	15	100.0	34578	9	AC107069	AC107069 Homo sapi
C 14	15	100.0	43347	9	AL138734	AL138734 Human DNA
C 15	15	100.0	56701	9	AL583852	AL583852 Human DNA
C 16	15	100.0	61720	2	AC131033	AC131033 Mus muscu
C 17	15	100.0	62755	2	AC097798	AC097798 Rattus no
C 18	15	100.0	64209	2	AC120156	AC120156 Mus muscu
C 19	15	100.0	65377	9	AL391356	AL391356 Human DNA
C 20	15	100.0	65421	2	AC129736	AC129736 Rattus no
C 21	15	100.0	66283	2	AC108314	AC108314 Rattus no
C 22	15	100.0	68171	9	AL158205	AL158205 Human DNA
C 23	15	100.0	71117	9	HSJ132F21	AL079335 Human DNA
C 24	15	100.0	88502	2	AC021967	AC021967 Homo sapi
C 25	15	100.0	99752	2	AC111526	AC111526 Rattus no
C 26	15	100.0	102853	2	AC116184	AC116184 Rattus no
C 27	15	100.0	106186	2	AC105876	AC105876 Rattus no
C 28	15	100.0	110000	2	AC103237_2	Continuation (3 of
C 29	15	100.0	110000	2	AC125066_2	Continuation (2 of
C 30	15	100.0	110000	2	AC125102_1	Continuation (2 of
C 31	15	100.0	113370	9	AL591493	AL591493 Human DNA
C 32	15	100.0	126392	2	AC018785	AC018785 Homo sapi
C 33	15	100.0	132526	2	AC120946	AC120946 Rattus no
C 34	15	100.0	141105	2	AC117134	AC117134 Rattus no
C 35	15	100.0	141289	9	AL449363	AL449363 Human DNA
C 36	15	100.0	142059	2	AC121163	AC121163 Rattus no
C 37	15	100.0	142662	2	AC118810	AC118810 Rattus no
C 38	15	100.0	142682	2	AC128133	AC128133 Rattus no
C 39	15	100.0	144201	9	HS230119	293942 Human DNA s
C 40	15	100.0	146191	1	D50453	D50453 Bacillus su
C 41	15	100.0	146427	2	AC124033	AC124033 Rattus no
C 42	15	100.0	148500	2	AC094249	AC094249 Rattus no
C 43	15	100.0	151514	2	AC113827	AC113827 Rattus no
C 44	15	100.0	154023	2	AC112466	AC112466 Rattus no
C 45	15	100.0	154888	2	AC114830	AC114830 Rattus no
C 46	15	100.0	155497	2	AC096300	AC096300 Rattus no
C 47	15	100.0	158374	2	AC120953	AC120953 Rattus no
C 48	15	100.0	159070	2	AL354939	AL354939 Homo sapi
C 49	15	100.0	161802	2	AC095162	AC095162 Rattus no
C 50	15	100.0	166475	2	AC130756	AC130756 Rattus no
C 51	15	100.0	166845	2	AC103006	AC103006 Rattus no
C 52	15	100.0	167098	5	AL590149	AL590149 zebrafish
C 53	15	100.0	167161	2	AL645945	AL645945 Mus muscu
C 54	15	100.0	167230	2	AC107010	AC107010 Rattus no
C 55	15	100.0	167264	2	AC095776	AC095776 Rattus no
C 56	15	100.0	167441	9	AC012084	AC012084 Homo sapi
C 57	15	100.0	167862	9	AC011966	AC011966 Homo sapi
C 58	15	100.0	167898	10	AL645630	AL645630 Mouse DNA
C 59	15	100.0	171864	2	AC016248	AC016248 Homo sapi
C 60	15	100.0	172803	2	AC130990	AC130990 Rattus no
C 61	15	100.0	176688	2	AC084696	AC084696 Mus muscu
C 62	15	100.0	177717	9	AC060788	AC060788 Homo sapi
C 63	15	100.0	179290	2	AC097041	AC097041 Rattus no
C 64	15	100.0	182301	9	AC012498	AC012498 Homo sapi
C 65	15	100.0	183783	2	AC109410	AC109410 Rattus no

c 66	15	100.0	184203	9	AC008249	AC008249 Homo sapi	139	14	93.3	90992	2	AC098357	AC098357 Rattus no
c 67	15	100.0	190687	2	AC094723	AC094723 Rattus no	140	14	93.3	93329	2	AC097393	AC097393 Rattus no
c 68	15	100.0	192428	10	AL672015	AL672015 Mouse DNA	141	14	93.3	93805	9	HS424E5	AL035468 Human DNA
c 69	15	100.0	194367	9	AC016820	AC016820 Homo sapi	142	14	93.3	93821	9	AC004254	AC004254 Homo sapi
c 70	15	100.0	195523	2	AC103103	AC103103 Rattus no	c 143	14	93.3	95747	9	AL358175	AL358175 Human DNA
c 71	15	100.0	195524	2	AC055756	AC055756 Homo sapi	c 144	14	93.3	98533	2	AP003828	AP003828 Oryza sat
c 72	15	100.0	195529	2	AC114417	AC114417 Mus muscu	c 145	14	93.3	98688	2	AC108245	AC108245 Rattus no
c 73	15	100.0	197706	2	AL772232	AL772232 Mus muscu	c 146	14	93.3	98713	9	AC002511	AC002511 Human DNA
c 74	15	100.0	198148	1	BSUB0003	BSUB0003 Mus muscu	c 147	14	93.3	99213	2	AC126466	AC126466 Rattus no
c 75	15	100.0	209100	1	AC124688	AC124688 Mus muscu	c 148	14	93.3	100000	9	AP000019	AP000019 Homo sapi
c 76	15	100.0	209404	2	AL845485	AL845485 Mus muscu	c 149	14	93.3	100000	9	AP000160	AP000160 Homo sapi
c 77	15	100.0	211397	10	AC098887	AC098887 Mus muscu	c 150	14	93.3	100516	2	HS171M_3	Continuation (4 of
c 78	15	100.0	212232	2	AL845485	AL845485 Mus muscu	c 151	14	93.3	100740	2	AC131216	AC131216 Rattus no
c 79	15	100.0	212237	2	AC079235	AC079235 Homo sapi	c 152	14	93.3	103184	2	AC111427	AC111427 Rattus no
c 80	15	100.0	212727	2	AC131110	AC131110 Mus muscu	c 153	14	93.3	103184	2	AC1119740	AC1119740 Homo sapi
c 81	15	100.0	214186	2	AC078933	AC078933 Mus muscu	c 154	14	93.3	104418	2	AC126312	AC126312 Rattus no
c 82	15	100.0	214186	1	BSUB0002	BSUB0002 Mus muscu	c 155	14	93.3	106684	2	AC126312	AC126312 Rattus no
c 83	15	100.0	21160	1	AC126130	AC126130 Rattus no	c 156	14	93.3	106747	2	AC095126	AC095126 Rattus no
c 84	15	100.0	221203	2	AL732510	AL732510 Danio rer	c 157	14	93.3	107372	2	AC098415	AC098415 Rattus no
c 85	15	100.0	228208	2	AC087420	AC087420 Mus muscu	c 158	14	93.3	107372	2	AC098415	AC098415 Rattus no
c 86	15	100.0	228856	2	AC073823	AC073823 Mus muscu	c 159	14	93.3	108660	10	AL671863	AL671863 Mouse DNA
c 87	15	100.0	261498	2	AC073823	AC073823 Mus muscu	c 160	14	93.3	110000	2	AC108692_2	Continuation (3 of
c 88	15	100.0	267982	2	AC124422	AC124422 Homo sapi	c 161	14	93.3	110004	2	AC106477	AC106477 Rattus no
c 89	14	93.3	316	9	HSU13613	U13613 Human aggre	c 162	14	93.3	110220	2	AL591415	AL591415 Human DNA
c 90	14	93.3	389	6	AX334095	AX334095 Sequence	c 163	14	93.3	110758	2	AC108534	AC108534 Rattus no
c 91	14	93.3	389	6	AX410588	AX410588 Sequence	c 164	14	93.3	112059	2	AC130641	AC130641 Rattus no
c 92	14	93.3	720	8	CNS105D5	AL115377 Botrytis	c 165	14	93.3	113248	2	AC094145	AC094145 Rattus no
c 93	14	93.3	1014	14	NVS5964	AC005964 faba bean	c 166	14	93.3	113530	9	AC073216	AC073216 Homo sapi
c 94	14	93.3	1015	14	FBEL132185	AL132185 faba bean	c 167	14	93.3	115604	2	AC123175	AC123175 Rattus no
c 95	14	93.3	1805	9	HUMDBPG	MI7156 Human vitam	c 168	14	93.3	116172	2	AC103371	AC103371 Mus muscu
c 96	14	93.3	1998	10	BC021386	BC021386 Mus muscu	c 169	14	93.3	116177	2	HS265A22	HS265A22 Homo sapi
c 97	14	93.3	2601	9	AF222345	AF222345 Homo sapi	c 170	14	93.3	117928	9	AC024722	AC024722 Homo sapi
c 98	14	93.3	2775	9	AB002110	AB002110 Homo sapi	c 171	14	93.3	119721	9	AC034655	AC034655 Homo sapi
c 99	14	93.3	5842	9	AF090893	AF090893 Homo sapi	c 172	14	93.3	120835	2	AC110644	AC110644 Rattus no
c 100	14	93.3	6905	9	AB071605	AB071605 Homo sapi	c 173	14	93.3	121046	8	OSJN00203	AL663003 Oryza sat
c 101	14	93.3	10348	9	AF321003	AF321003 Homo sapi	c 174	14	93.3	125196	2	AC027389	AC027389 Homo sapi
c 102	14	93.3	12016	1	AE009851	AE009851 Pyrobacul	c 175	14	93.3	125528	8	AP004912	AP004912 Lotus jap
c 103	14	93.3	12920	9	AC131186	AC131186 Mus muscu	c 176	14	93.3	134264	2	AC094055	AC094055 Rattus no
c 104	14	93.3	18890	9	HS115K14	AL134450 Human DNA	c 177	14	93.3	134346	9	HS127B20	HS127B20 Mus muscu
c 105	14	93.3	31613	3	CSEF5468	Z19155 Caenorhabdi	c 178	14	93.3	135259	2	AC068279	AC068279 Homo sapi
c 106	14	93.3	35281	9	HS196A2	Z68165 Human DNA s	c 179	14	93.3	135351	9	AL596089	AL596089 Human DNA
c 107	14	93.3	38876	9	AC005945	AC005945 Homo sapi	c 180	14	93.3	135751	9	AC090974	AC090974 Oryza sat
c 108	14	93.3	39876	10	AL731802	AL731802 Mouse DNA	c 181	14	93.3	137054	2	AC011920	AC011920 Homo sapi
c 109	14	93.3	43346	9	AC005787	AC005787 Homo sapi	c 182	14	93.3	139043	2	AC104925	AC104925 Mus muscu
c 110	14	93.3	46478	10	AL713912	AL713912 Mouse DNA	c 183	14	93.3	140369	2	AP005618	AP005618 Oryza sat
c 111	14	93.3	49738	2	AC015752	AC015752 Homo sapi	c 184	14	93.3	140736	2	AC083769	AC083769 Homo sapi
c 112	14	93.3	55136	9	HUMVITDBP	IL0641 Human vitam	c 185	14	93.3	140899	2	AP004304	AP004304 Pan trogl
c 113	14	93.3	56099	2	AC118706	AC118706 Mus muscu	c 186	14	93.3	141287	2	AC093404	AC093404 Oryza sat
c 114	14	93.3	56475	9	AL353658	AL353658 Human DNA	c 187	14	93.3	141293	2	AP004337	AP004337 Oryza sat
c 115	14	93.3	56475	9	AL353658	AL353658 Human DNA	c 188	14	93.3	142559	2	AC112559	AC112559 Rattus no
c 116	14	93.3	56475	9	AL353658	AL353658 Human DNA	c 189	14	93.3	142559	2	AC123281	AC123281 Rattus no
c 117	14	93.3	57423	9	AL1133473	AL1133473 Human DNA	c 190	14	93.3	144555	2	AC119116	AC119116 Rattus no
c 118	14	93.3	59828	2	AC117755	AC117755 Mus muscu	c 191	14	93.3	144963	2	AC008521	AC008521 Homo sapi
c 119	14	93.3	60855	2	AC113482	AC113482 Mus muscu	c 192	14	93.3	147514	9	AC085867	AC085867 Human DNA
c 120	14	93.3	62309	2	AC083935	AC083935 Homo sapi	c 193	14	93.3	147803	9	AL356867	AL356867 Rattus no
c 121	14	93.3	62309	2	AC083935	AC083935 Homo sapi	c 194	14	93.3	148678	2	AC113169	AC113169 Rattus no
c 122	14	93.3	67605	2	AC096816	AC096816 Rattus no	c 195	14	93.3	148900	2	AC113769	AC113769 Rattus no
c 123	14	93.3	69660	9	HS407F17	HS407F17 Human DNA s	c 196	14	93.3	150014	2	AC113067	AC113067 Oryza sat
c 124	14	93.3	71157	2	AC073029	AC073029 Homo sapi	c 197	14	93.3	150151	2	AC116339	AC116339 Rattus no
c 125	14	93.3	74002	2	AC124990	AC124990 Mus muscu	c 198	14	93.3	151008	2	AP004261	AP004261 Oryza sat
c 126	14	93.3	74912	2	AC034115	AC034115 Homo sapi	c 199	14	93.3	151091	9	AC026720	AC026720 Homo sapi
c 127	14	93.3	76276	9	AF314199S7	AF314199S7 Rattus no	c 200	14	93.3	151091	2	AC125871	AC125871 Rattus no
c 128	14	93.3	78359	9	HS454G6	HS454G6 Human DNA s	c 201	14	93.3	151207	2	AP001031	AP001031 Homo sapi
c 129	14	93.3	78533	9	HS454G6	HS454G6 Human DNA s	c 202	14	93.3	151438	2	AC103516	AC103516 Rattus no
c 130	14	93.3	79376	9	AC111937	AC111937 Rattus no	c 203	14	93.3	152150	2	AC116247	AC116247 Rattus no
c 131	14	93.3	80135	2	AC016354	AC016354 Homo sapi	c 204	14	93.3	153097	2	AC125750	AC125750 Rattus no
c 132	14	93.3	81675	2	AC016354	AC016354 Homo sapi	c 205	14	93.3	153097	2	AC051632	AC051632 Oryza sat
c 133	14	93.3	86196	9	AL592046	AL592046 Human DNA	c 206	14	93.3	153182	8	AC127736	AC127736 Rattus no
c 134	14	93.3	86428	9	AL390776	AL390776 Human DNA	c 207	14	93.3	153258	2	AC104160	AC104160 Canis fam
c 135	14	93.3	87187	9	AL161744	AL161744 Human DNA	c 208	14	93.3	153344	2	AC119778	AC119778 Rattus no
c 136	14	93.3	89723	9	AP001417	AP001417 Homo sapi	c 209	14	93.3	153710	2	AC023953	AC023953 Homo sapi
c 137	14	93.3	90049	2	AC095836	AC095836 Rattus no	c 210	14	93.3	153937	2	HSAC002087	HSAC002087 Human BAC
c 138	14	93.3	90575	2	AC117060	AC117060 Rattus no	c 211	14	93.3	154028	9		



c 212	14	93.3 154120	2	AP002472	AP002472 Homo sapi	c 285	14	93.3 180895	2	AC110552	AC110552 Mus muscu
c 213	14	93.3 154260	2	AC123292	AC123292 Rattus no	286	14	93.3 181204	2	AC119576	AC119576 Rattus no
c 214	14	93.3 155843	2	AC106772	AC106772 Homo sapi	c 287	14	93.3 181343	10	AL671882	AL671882 Mouse DNA
c 215	14	93.3 156602	9	AC012487	AC012487 Homo sapi	c 288	14	93.3 181507	2	AC015907	AC015907 Homo sapi
c 216	14	93.3 157227	2	AC118442	AC118442 Rattus no	c 289	14	93.3 181808	9	AL356267	AL356267 Human DNA
c 217	14	93.3 157430	2	AC108975	AC108975 Rattus no	290	14	93.3 182017	2	AL824710	AL824710 Mus muscu
c 218	14	93.3 157979	9	CNS0501D4	AL355922 Human chr	291	14	93.3 182166	2	AC098066	AC098066 Rattus no
c 219	14	93.3 158016	2	AC026570	AC026570 Homo sapi	292	14	93.3 182441	2	AC121709	AC121709 Rattus no
c 220	14	93.3 158179	2	OSJN00106	AL606669 Oryza sat	293	14	93.3 182659	2	AC120130	AC120130 Mus muscu
c 221	14	93.3 159295	2	AC096444	AC096444 Rattus no	294	14	93.3 182806	2	AC098902	AC098902 Rattus no
c 222	14	93.3 159983	2	AC128001	AC128001 Rattus no	c 295	14	93.3 182898	2	AC079122	AC079122 Homo sapi
c 223	14	93.3 160008	2	AC022823	AC022823 Homo sapi	296	14	93.3 183036	2	AC074174	AC074174 Mus muscu
c 224	14	93.3 160331	2	AC129612	AC129612 Rattus no	297	14	93.3 183580	8	AP003561	AP003561 Oryza sat
c 225	14	93.3 160385	2	AC120080	AC120080 Rattus no	c 298	14	93.3 183714	2	AC103508	AC103508 Rattus no
c 226	14	93.3 161363	10	AL645535	AL645535 Mouse DNA	c 299	14	93.3 184245	2	AC120488	AC120488 Rattus no
c 227	14	93.3 161546	2	AC108270	AC108270 Rattus no	c 300	14	93.3 184245	2	AC127355	AC127355 Mus muscu
c 228	14	93.3 161840	9	AC023430	AC023430 Homo sapi	301	14	93.3 184427	14	EHV020824	U20824 Equine herp
c 229	14	93.3 162518	2	AC094485	AC094485 Rattus no	c 302	14	93.3 185181	2	AP005620	AP005620 Oryza sat
c 230	14	93.3 162900	2	AC123889	AC123889 Rattus no	303	14	93.3 186449	2	AC111954	AC111954 Rattus no
c 231	14	93.3 163121	2	AC114255	AC114255 Rattus no	c 304	14	93.3 187495	9	AC026887	AC026887 Homo sapi
c 232	14	93.3 163258	2	AP003514	AP003514 Oryza sat	305	14	93.3 188158	9	AC092465	AC092465 Homo sapi
c 233	14	93.3 163475	9	AC092619	AC092619 Homo sapi	306	14	93.3 189188	9	AC040965	AC040965 Homo sapi
c 234	14	93.3 163537	2	AC102348	AC102348 Mus muscu	c 307	14	93.3 189385	9	CNS06C7Y	AL391152 Human chr
c 235	14	93.3 163623	9	AP005203	AP005203 Homo sapi	c 308	14	93.3 189665	2	AC113066	AC113066 Mus muscu
c 236	14	93.3 163657	2	AC120645	AC120645 Rattus no	309	14	93.3 189904	2	AL845451	AL845451 Mus muscu
c 237	14	93.3 164518	2	OSJN00128	AL607001 Oryza sat	310	14	93.3 189939	2	AL831715	AL831715 Mus muscu
c 238	14	93.3 165318	2	AC126747	AC126747 Rattus no	311	14	93.3 190105	2	AC111599	AC111599 Rattus no
c 239	14	93.3 165330	2	AC121372	AC121372 Rattus no	312	14	93.3 191052	10	AL683814	AL683814 Mouse DNA
c 240	14	93.3 165491	2	AP004273	AP004273 Oryza sat	c 313	14	93.3 192192	2	AC129342	AC129342 Rattus no
c 241	14	93.3 165997	2	AC109706	AC109706 Rattus no	314	14	93.3 192309	2	AC115642	AC115642 Rattus no
c 242	14	93.3 166294	2	AC122113	AC122113 Atelerix	315	14	93.3 193136	2	AC125683	AC125683 Rattus no
c 243	14	93.3 166486	9	CNS01DWC	AL137100 Human chr	316	14	93.3 193389	2	AL645531	AL645531 Mus muscu
c 244	14	93.3 166595	9	AC108215	AC108215 Homo sapi	317	14	93.3 194197	9	AC064871	AC064871 Homo sapi
c 245	14	93.3 166601	2	AC097684	AC097684 Rattus no	318	14	93.3 196283	10	AL672215	AL672215 Mouse DNA
c 246	14	93.3 167123	2	AP001495	AP001495 Homo sapi	319	14	93.3 196437	2	AC131036	AC131036 Mus muscu
c 247	14	93.3 167428	2	AC114343	AC114343 Rattus no	c 320	14	93.3 196715	2	AC094874	AC094874 Rattus no
c 248	14	93.3 167694	2	AC103113	AC103113 Rattus no	c 321	14	93.3 196744	2	AC120667	AC120667 Rattus no
c 249	14	93.3 167651	2	AC068969	AC068969 Homo sapi	c 322	14	93.3 196938	10	AL672218	AL672218 Mouse DNA
c 250	14	93.3 168751	2	AC109716	AC109716 Rattus no	c 323	14	93.3 197063	2	AC129280	AC129280 Rattus no
c 251	14	93.3 169410	2	AC031980	AC031980 Homo sapi	c 324	14	93.3 197423	2	AC107448	AC107448 Rattus no
c 252	14	93.3 169913	2	AC129774	AC129774 Mus muscu	c 325	14	93.3 200021	2	AC117635	AC117635 Mus muscu
c 253	14	93.3 170082	2	AB026295	AB026295 Oryza sat	c 326	14	93.3 200146	2	AC073774	AC073774 Mus muscu
c 254	14	93.3 170371	8	AB026295	AB026295 Oryza sat	c 327	14	93.3 200257	2	AC124472	AC124472 Mus muscu
c 255	14	93.3 170425	2	AC024490	AC024490 Homo sapi	c 328	14	93.3 200843	2	AC102311	AC102311 Mus muscu
c 256	14	93.3 170491	2	AC114199	AC114199 Rattus no	329	14	93.3 201050	2	AC128356	AC128356 Rattus no
c 257	14	93.3 170883	9	AC067805	AC067805 Homo sapi	330	14	93.3 201390	2	AC098182	AC098182 Rattus no
c 258	14	93.3 170928	9	AL356740	AL356740 Human DNA	331	14	93.3 201465	2	AC122424	AC122424 Mus muscu
c 259	14	93.3 171363	2	AC084863	AC084863 Papio cyn	c 332	14	93.3 201990	9	AC002385	AC002385 Human BAC
c 260	14	93.3 172524	2	AC097314	AC097314 Homo sapi	333	14	93.3 203363	9	CNS01RHB	AL161668 Human chr
c 261	14	93.3 172664	2	AC119609	AC119609 Rattus no	334	14	93.3 203568	9	AC008693	AC008693 Homo sapi
c 262	14	93.3 172738	9	AC091953	AC091953 Homo sapi	335	14	93.3 203756	2	AL772132	AL772132 Danio rer
c 263	14	93.3 173185	9	AP004606	AP004606 Homo sapi	336	14	93.3 205662	9	AC017002	AC017002 Homo sapi
c 264	14	93.3 173331	2	AC083903	AC083903 Homo sapi	337	14	93.3 205688	2	AC107344	AC107344 Rattus no
c 265	14	93.3 173346	2	AL773561	AL773561 Mus muscu	338	14	93.3 207245	2	AC123552	AC123552 Mus muscu
c 266	14	93.3 174534	9	AL672138	AL672138 Human DNA	c 339	14	93.3 209693	2	AC113363	AC113363 Homo sapi
c 267	14	93.3 174631	2	AC069059	AC069059 Homo sapi	c 340	14	93.3 209882	2	AC103554	AC103554 Rattus no
c 268	14	93.3 174693	2	AL732588	AL732588 Mus muscu	c 341	14	93.3 211308	2	AC094850	AC094850 Rattus no
c 269	14	93.3 175439	8	AP001111	AP001111 Oryza sat	342	14	93.3 213097	2	AL672180	AL672180 Mus muscu
c 270	14	93.3 175694	9	AC016753	AC016753 Homo sapi	343	14	93.3 213473	2	AC094371	AC094371 Rattus no
c 271	14	93.3 176975	2	AC098753	AC098753 Rattus no	344	14	93.3 215528	2	AC099105	AC099105 Rattus no
c 272	14	93.3 177293	2	AC069525	AC069525 Homo sapi	345	14	93.3 217141	2	AC073998	AC073998 Homo sapi
c 273	14	93.3 177433	9	AL691476	AL691476 Mus muscu	c 346	14	93.3 217421	9	AC006211	AC006211 Homo sapi
c 274	14	93.3 177829	9	AC026392	AC026392 Homo sapi	347	14	93.3 219175	9	AC092641	AC092641 Homo sapi
c 275	14	93.3 178049	2	AL672146	AL672146 Mus muscu	348	14	93.3 220809	2	AC123955	AC123955 Mus muscu
c 276	14	93.3 178892	2	AC096931	AC096931 Rattus no	349	14	93.3 220820	2	AC126962	AC126962 Rattus no
c 277	14	93.3 178975	2	AP001500	AP001500 Homo sapi	350	14	93.3 221941	2	AC099391	AC099391 Rattus no
c 278	14	93.3 179198	2	AC130729	AC130729 Oryza sat	c 351	14	93.3 223977	2	AC124199	AC124199 Mus muscu
c 279	14	93.3 179324	2	AC101874	AC101874 Mus muscu	c 352	14	93.3 224560	2	AC115725	AC115725 Mus muscu
c 280	14	93.3 179430	2	AC103238	AC103238 Rattus no	353	14	93.3 226191	2	AC115665	AC115665 Rattus no
c 281	14	93.3 180538	2	AC073514	AC073514 Homo sapi	354	14	93.3 226608	2	AC105612	AC105612 Rattus no
c 282	14	93.3 180722	9	AC021619	AC021619 Homo sapi	c 355	14	93.3 227364	2	AC105604	AC105604 Rattus no
c 283	14	93.3 180744	2	AC094049	AC094049 Rattus no	c 356	14	93.3 228878	2	AC090652	AC090652 Mus muscu
c 284	14	93.3 180819	2	AC126857	AC126857 Rattus no	357	14	93.3 230571	2	AC026911	AC026911 Mus muscu

C 358	14	93.3	232089	2	AC130222	AC130222 Mus muscu	C 431	13	86.7	867	9	AB079246S6	AB079251 Homo sapi
C 359	14	93.3	232860	2	AL808123	AL808123 Mus muscu	C 432	13	86.7	884	11	CNS06K3X	AL402403 T7 end of
C 360	14	93.3	235559	2	AC105824	AC105824 Rattus no	C 433	13	86.7	957	6	AX226440	AX226440 Sequence
C 361	14	93.3	237896	2	AC096317	AC096317 Rattus no	C 434	13	86.7	966	6	AX241571	AX241571 Sequence
C 362	14	93.3	238551	2	AC095726	AC095726 Rattus no	C 435	13	86.7	1014	5	HSILGFS2	U13801 Human insul
C 363	14	93.3	239685	2	AC096310	AC096310 Rattus no	C 436	13	86.7	1041	5	CP091420	U91420 Carharinu
C 364	14	93.3	247462	3	LMFLCHR4B	LMFLCHR4B Leishmani	C 437	13	86.7	1047	5	AB018982	AB018982 Rhinogobi
C 365	14	93.3	248160	3	AC122000	AC122000 Mus muscu	C 438	13	86.7	1047	5	AF412173	AF412173 Poeciliop
C 366	14	93.3	249243	2	AC114544	AC114544 Mus muscu	C 439	13	86.7	1077	6	AX226363	AX226363 Sequence
C 367	14	93.3	270516	2	AC096350	AC096350 Rattus no	C 440	13	86.7	1085	1	ECNHSNGE	X89444 E.chrysanth
C 368	14	93.3	270852	2	AC125346	AC125346 Mus muscu	C 441	13	86.7	1094	8	BNCHITIN	X61488 B.napus mRN
C 369	14	93.3	283765	2	AL672224	AL672224 Mus muscu	C 442	13	86.7	1194	8	AF072009	AF072009 Arabidops
C 370	14	93.3	300189	2	AC121683	AC121683 Rattus no	C 443	13	86.7	1284	4	AF509590	AF509590 Bos tauru
C 371	14	93.3	309662	2	AC004469	AC004469 Homo sapi	C 444	13	86.7	1356	6	AX194096	AX194096 Sequence
C 372	14	93.3	339681	1	AP003009	AP003009 Mesorhizo	C 445	13	86.7	1369	9	AB065758	AB065758 Homo sapi
C 373	14	93.3	340000	9	AP001730	AP001730 Homo sapi	C 446	13	86.7	1380	6	AX194318	AX194318 Sequence
C 374	14	93.3	340000	9	HS21C009	HS21C009 Homo sapi	C 447	13	86.7	1419	6	AR051312	AR051312 Sequence
C 375	14	93.3	340000	9	HS21C102	HS21C102 Homo sapi	C 448	13	86.7	1419	6	HUMCH13GEN	HUMCH13GEN Human genom
C 376	14	93.3	347750	1	AP002998	AP002998 Mesorhizo	C 449	13	86.7	1458	8	AF223358	AF223358 Mesembrya
C 377	14	93.3	349116	1	AP003003	AP003003 Mesorhizo	C 450	13	86.7	1458	8	AF223358	AF223358 Mesembrya
C 378	14	93.3	349116	1	AP003003	AP003003 Mesorhizo	C 451	13	86.7	1506	5	CHMKARKS	CHMKARKS Homo sapi
C 379	13	86.7	92	10	MMV51NM26	Z12520 M.musculus	C 452	13	86.7	1595	10	BC022727	BC022727 Chicken myr
C 380	13	86.7	119	1	AF503927	AF503927 Geobacter	C 453	13	86.7	1632	10	BC001578	BC001578 Lentinus
C 381	13	86.7	189	8	AF164378	AF164378 Oryza sat	C 454	13	86.7	1634	10	BC011067	BC011067 Mus muscu
C 382	13	86.7	201	11	AF098957	AF098957 Ovis arie	C 455	13	86.7	1670	9	BC008030	BC008030 Homo sapi
C 383	13	86.7	210	6	AX193049	AX193049 Sequence	C 456	13	86.7	1769	9	BC025749	BC025749 Homo sapi
C 384	13	86.7	231	9	HS190G11R	Z55080 H.sapiens C	C 457	13	86.7	1905	6	AR198640	AR198640 Sequence
C 385	13	86.7	239	11	G45463	G45463 Z23659_1 Ze	C 458	13	86.7	1937	8	RICOCs	M29259 Rice oryzac
C 386	13	86.7	260	9	HSU35893	HSU35893 Human throm	C 459	13	86.7	1974	10	BC027376	BC027376 Mus muscu
C 387	13	86.7	306	6	AX186927	AX186927 Sequence	C 460	13	86.7	1975	9	AK054700	AK054700 Homo sapi
C 388	13	86.7	308	8	HVU234775	AJ234775 Hordeum v	C 461	13	86.7	2007	6	AX431590	AX431590 Sequence
C 389	13	86.7	341	11	G47380	G47380 Z24275_1 Ze	C 462	13	86.7	2007	9	HSU19111	HSU19111 Human HOXB6
C 390	13	86.7	383	6	AX333410	AX333410 Sequence	C 463	13	86.7	2017	9	HSN802377	HSN802377 Sequence
C 391	13	86.7	383	6	AX408430	AX408430 Sequence	C 464	13	86.7	2040	6	AX460885	AX460885 Sequence
C 392	13	86.7	396	11	G64359	G64359 B47614/T7	C 465	13	86.7	2041	8	THA243799	AJ243799 Trichoder
C 393	13	86.7	430	3	LPY422074	LPY422074 Limatula	C 466	13	86.7	2050	3	AF234189	AF234189 Trypanoso
C 394	13	86.7	435	9	AF009305	AF009305 Homo sapi	C 467	13	86.7	2050	8	AB007849	AB007849 Lentinula
C 395	13	86.7	447	14	G45806	G45806 Z4452_1 Zeb	C 468	13	86.7	2088	9	HS420478	HS420478 Homo sapi
C 396	13	86.7	447	14	AF233147	AF233147 Human pol	C 469	13	86.7	2090	9	AK092728	AK092728 Homo sapi
C 397	13	86.7	480	9	HS4309474	AJ309474 Homo sapi	C 470	13	86.7	2103	9	AK092728	AK092728 Homo sapi
C 398	13	86.7	500	11	G34590	G34590 human SRS S	C 471	13	86.7	2135	9	AF279649S6	AF279649 Homo sapi
C 399	13	86.7	529	6	AX194651	AX194651 Sequence	C 472	13	86.7	2141	8	AF105110	AF105110 Nymphaea
C 400	13	86.7	530	9	HS4327382	AJ327382 Homo sapi	C 473	13	86.7	2141	9	AK056318	AK056318 Homo sapi
C 401	13	86.7	561	11	G54558	G54558 SHGC-100153	C 474	13	86.7	2164	10	AB03719S08	AB03719S08 Mus muscu
C 402	13	86.7	564	11	G54961	G54961 SHGC-100157	C 475	13	86.7	2219	3	AF144214	AF144214 Leptodora
C 403	13	86.7	594	6	AX320062	AX320062 Sequence	C 476	13	86.7	2307	3	AF144214	AF144214 Leptodora
C 404	13	86.7	597	6	A51316	A51316 Sequence 1	C 477	13	86.7	2325	9	AK093602	AK093602 Homo sapi
C 405	13	86.7	598	8	RICCP1	J03469 Rice cystei	C 478	13	86.7	2364	9	AK022631	AK022631 Homo sapi
C 406	13	86.7	643	8	S49967	S49967 oryzacystat	C 479	13	86.7	2451	14	AF357218S1	AF357218 Deer tick
C 407	13	86.7	647	9	AF395965	AF395965 Homo sapi	C 480	13	86.7	2486	9	BC018702	BC018702 Homo sapi
C 408	13	86.7	685	9	HUM4S12S2	M62750 Homo sapien	C 481	13	86.7	2496	9	HUMTASIO2	M83228 Human trans
C 409	13	86.7	695	11	G34888	G34888 STS SHGC-95	C 482	13	86.7	2539	10	BC027155	BC027155 Mus muscu
C 410	13	86.7	705	6	AX437493	AX437493 Sequence	C 483	13	86.7	2616	14	AF383234	AF383234 HIV-1 98C
C 411	13	86.7	705	6	AX437494	AX437494 Sequence	C 484	13	86.7	2630	9	AK027086	AK027086 Homo sapi
C 412	13	86.7	745	9	HS4337047	AJ337047 Homo sapi	C 485	13	86.7	2675	9	AK054809	AK054809 Homo sapi
C 413	13	86.7	776	11	G75117	G75117 MARC 13236-	C 486	13	86.7	2683	10	BC003260	BC003260 Mus muscu
C 414	13	86.7	778	8	AF435976	AF435976 Oryza sat	C 487	13	86.7	2687	6	I24726	I24726 Sequence 8
C 415	13	86.7	792	8	AX3424918	AJ324918 Homo sapi	C 488	13	86.7	2708	10	HUM4M11AA	U33842 Mus musculu
C 416	13	86.7	831	11	PM12F10G	PM12F10G Penicilli	C 489	13	86.7	2722	9	AK056158	AK056158 Homo sapi
C 417	13	86.7	832	9	GGU19115	GGU19115 Gorilla gor	C 490	13	86.7	2759	9	AK056158	AK056158 Homo sapi
C 418	13	86.7	846	3	AB050862	AB050862 Carabus h	C 491	13	86.7	2773	9	BC010628	BC010628 Homo sapi
C 419	13	86.7	846	3	AB050863	AB050863 Carabus i	C 492	13	86.7	2809	8	MTHAHE	X74126 H.annuus m1
C 420	13	86.7	846	3	AB050864	AB050864 Carabus r	C 493	13	86.7	2830	10	MMGIRK115	AF040050 Mus muscu
C 421	13	86.7	846	3	AB050865	AB050865 Carabus p	C 494	13	86.7	2863	10	BC024859	BC024859 Mus muscu
C 422	13	86.7	846	3	AB050866	AB050866 Carabus q	C 495	13	86.7	2873	6	I11774	I11774 Sequence 1
C 423	13	86.7	846	3	AB050867	AB050867 Carabus g	C 496	13	86.7	2873	6	I24719	I24719 Sequence 1
C 424	13	86.7	848	3	AB031400	AB031400 Leptocara	C 497	13	86.7	2877	6	E03372	E03372 gDNA encodi
C 425	13	86.7	848	3	AB031401	AB031401 Leptocara	C 498	13	86.7	2900	9	AF277094	AF277094 Homo sapi
C 426	13	86.7	851	3	AB031399	AB031399 Leptocara	C 499	13	86.7	2902	9	HSU81262	HSU81262 Homo sapien
C 427	13	86.7	858	9	HKU19112	U19112 Hylobates k	C 500	13	86.7	2941	1	AB026631	AB026631 Streptomy
C 428	13	86.7	858	9	HLU19117	U19117 Hylobates l	C 501	13	86.7	2944	9	AF312028	AF312028 Homo sapi
C 429	13	86.7	858	9	SSU19113	U19113 Hylobates s	C 502	13	86.7	2982	1	ATLEUCD	X84647 A.leichomyc
C 430	13	86.7	860	8	OSU54702	U54702 Oryza sativ	C 503	13	86.7				

504	13	86.7	2992	9	AY037298	Homo sapi	13	86.7	10801	1	AE009925	AE009925	Pyrobacul
505	13	86.7	3072	9	AB063100	Macaca fa	13	86.7	11021	9	AL645724	AL645724	Human DNA
506	13	86.7	3210	9	HSB803041	Homo sapi	13	86.7	11375	9	AY043013	AY043013	Homo sapi
507	13	86.7	3225	9	XSAMLJM	H.sapiens A	13	86.7	11416	2	AC015061	AC015061	Drosophila
508	13	86.7	3383	6	AX3430266	Sequence	13	86.7	11451	2	AF025841	AF025841	Homo sapi
509	13	86.7	3403	1	TFPOLDNA	Sequence	13	86.7	11503	9	AF518727	AF518727	Homo sapi
510	13	86.7	3415	6	AX402493	Sequence	13	86.7	13456	9	AF509589	AF509589	Bos taurus
511	13	86.7	3419	6	E26630	Sequence	13	86.7	14026	4	HMTGMA1A	HMTGMA1A	Human trans
512	13	86.7	3478	9	AK092046	Homo sapi	13	86.7	14230	1	AE013209	AE013209	Thermoana
513	13	86.7	3517	5	AF154052	Polypterus	13	86.7	14451	1	AX335609	AX335609	Sequence
514	13	86.7	3511	9	AK023742	Homo sapi	13	86.7	14537	6	AK023742	AK023742	Sequence
515	13	86.7	3616	9	AF110763	Homo sapi	13	86.7	14537	6	AK023742	AK023742	Sequence
516	13	86.7	3706	6	A91749	Sequence 5	13	86.7	14687	2	AC126800	AC126800	Mus muscu
517	13	86.7	3773	10	RNP2X3	X60651 R.norvegicu	13	86.7	14725	10	AF410425S4	AF410425S4	Mus muscu
518	13	86.7	3788	8	ZMPCALAC	X66692 Z.mays gene	13	86.7	14980	1	AE001059	AE001059	Archaeogl
519	13	86.7	4117	8	AF021318	Filobasid	13	86.7	16387	5	AP002935	AP002935	Poromitra
520	13	86.7	4187	8	AF098963	AF098963 Arabidops	13	86.7	16866	2	AC087249	AC087249	Mus muscu
521	13	86.7	4272	9	HUMAMFP	DI3979 Homo sapien	13	86.7	17048	5	D21070	D21070	Rana catesb
522	13	86.7	4287	6	E07332	E07332 DNA fragmen	13	86.7	17243	9	HSL241B9C	HSL241B9C	Human DNA s
523	13	86.7	4287	6	I30202	Sequence 1	13	86.7	17255	1	AE007089	AE007089	Mycobacte
524	13	86.7	4287	6	I96216	Sequence 53	13	86.7	18078	9	HSY15155	HSY15155	Homo sapien
525	13	86.7	4406	1	EC4410309	Erwinia c	13	86.7	19994	9	HSTI1INX5	HSTI1INX5	H.sapiens t
526	13	86.7	4475	8	ZMEEMAGEN	X91882 Z.mays ZEMA	13	86.7	20439	2	AC014002	AC014002	Drosophila
527	13	86.7	4502	9	HSB801483	AL133662 Homo sapi	13	86.7	21156	3	CEP31B9	CEP31B9	Caenorhabdi
528	13	86.7	4503	6	AR072702	Sequence	13	86.7	21373	2	AC094556	AC094556	Rattus no
529	13	86.7	4503	6	E15695	E15695 Human mRNA	13	86.7	23008	9	AB016194	AB016194	Homo sapi
530	13	86.7	4503	9	HSU65785	U65785 Human 150 k	13	86.7	23449	8	AF072725	AF072725	Zea mays
531	13	86.7	4515	8	AY036881	AY036881 Phaneroch	13	86.7	26914	1	MTCY428	MTCY428	Mycobacteri
532	13	86.7	4884	6	A91755	A91755 Sequence 11	13	86.7	30509	9	AC119501	AC119501	Homo sapi
533	13	86.7	4945	9	AB051544	AB051544 Homo sapi	13	86.7	31204	9	AP000690	AP000690	Homo sapi
534	13	86.7	5180	9	AF274875	AF274875 Homo sapi	13	86.7	32816	3	U41536	U41536	Caenorhabdi
535	13	86.7	5194	9	AB062934	AB062934 Macaca fa	13	86.7	34820	2	AC131521	AC131521	Rattus no
536	13	86.7	5337	8	ZMAUX311	X56737 Maize Aux31	13	86.7	35197	9	AC005782	AC005782	Homo sapi
537	13	86.7	5405	9	AB033039	AB033039 Homo sapi	13	86.7	36007	9	HSAC002084	HSAC002084	Human Cos
538	13	86.7	5418	3	AY058703	AY058703 Drosophila	13	86.7	36598	2	AC095907	AC095907	Rattus no
539	13	86.7	5455	3	DROGPRNA	M74104 Drosophila	13	86.7	37322	2	CEK10D11	CEK10D11	Caenorhabdi
540	13	86.7	5574	8	M2EABP1X	L08425 Zea mays au	13	86.7	37633	9	AB065685	AB065685	Homo sapi
541	13	86.7	5642	1	AE006825	AE006825 Sulfolobu	13	86.7	38601	5	AL731564	AL731564	Zebrafish
542	13	86.7	5728	6	AX400803	AX400803 Sequence	13	86.7	39744	9	AC068296	AC068296	Homo sapi
543	13	86.7	5728	10	AB010466	AB010466 Rattus no	13	86.7	39769	9	AC005174	AC005174	Homo sapi
544	13	86.7	5775	10	RNU73038	U73038 Rattus norv	13	86.7	39841	9	AC113353	AC113353	Homo sapi
545	13	86.7	5828	6	E26936	E26936 Method for	13	86.7	40157	2	AC068281	AC068281	Mus muscu
546	13	86.7	5833	6	AX009310	AX009310 Sequence	13	86.7	40162	9	DB7017	DB7017	Homo sapi
547	13	86.7	5938	6	AX334125	AX334125 Sequence	13	86.7	40451	9	AL139802	AL139802	Human DNA
548	13	86.7	5938	6	AX335861	AX335861 Sequence	13	86.7	40775	9	HSICK721Q	HSICK721Q	Homo sapi
549	13	86.7	5938	6	S69002	S69002 AML1-EV1-1-	13	86.7	41621	9	AC091705	AC091705	Homo sapi
550	13	86.7	5980	6	AX009311	AX009311 Sequence	13	86.7	42749	9	HSU42H12	HSU42H12	Human DNA s
551	13	86.7	5995	6	AX009312	AX009312 Sequence	13	86.7	43178	10	AC004405	AC004405	Mus muscu
552	13	86.7	6013	6	A91747	A91747 Sequence 3	13	86.7	43576	10	AC003994	AC003994	Mouse cos
553	13	86.7	6032	6	AR198650	AR198650 Sequence	13	86.7	43982	2	AC095768	AC095768	Rattus no
554	13	86.7	6032	12	AF214480	AF214480 Cloning v	13	86.7	44912	2	AC105045	AC105045	Homo sapi
555	13	86.7	6056	6	E26937	E26937 Method for	13	86.7	45786	9	AL391829	AL391829	Human DNA
556	13	86.7	6129	9	HSAX314835	AX314835 Homo sapi	13	86.7	46708	9	AL359434	AL359434	Human DNA
557	13	86.7	6349	1	AB083655	AB083655 Bacillus	13	86.7	46797	9	AC004204	AC004204	Homo sapi
558	13	86.7	6768	6	AX034571	AX034571 Sequence	13	86.7	49023	2	AC110582	AC110582	Homo sapi
559	13	86.7	6916	10	AB061741	AB061741 Rattus no	13	86.7	49472	2	AC118722	AC118722	Mus muscu
560	13	86.7	7181	1	AE010334	AE010334 Methanopy	13	86.7	49600	8	AP004342	AP004342	Oryza sat
561	13	86.7	7265	9	HUMAML1BA	D43668 Homo sapien	13	86.7	50149	2	AC011955	AC011955	Homo sapi
562	13	86.7	7646	3	AF000634	AF000634 Lytechinu	13	86.7	50308	2	AC099858	AC099858	Mus muscu
563	13	86.7	7800	9	DB7019	DB7019 Homo sapien	13	86.7	51536	2	AC116774	AC116774	Mus muscu
564	13	86.7	7984	3	DMU59923	DMU59923 Drosophila	13	86.7	51626	5	AL662878	AL662878	Zebrafish
565	13	86.7	8278	6	A91750	A91750 Sequence 6	13	86.7	51820	2	AC099967	AC099967	Mus muscu
566	13	86.7	8379	1	AE008196	AE008196 Agrobacte	13	86.7	52521	2	AC106629	AC106629	Rattus no
567	13	86.7	9449	8	ZMU041000	ZMU041000 Zea mays co	13	86.7	52703	2	AC111411	AC111411	Rattus no
568	13	86.7	9800	1	AE010670	AE010670 Methanosa	13	86.7	53646	2	AC107689	AC107689	Mus muscu
569	13	86.7	10070	6	A91751	A91751 Sequence 7	13	86.7	53752	2	AC118739	AC118739	Mus muscu
570	13	86.7	10265	1	AE010160	AE010160 Pyrococcu	13	86.7	53784	2	AC116670	AC116670	Mus muscu
571	13	86.7	10364	1	AE008452	AE008452 Streptoco	13	86.7	53874	2	AC124053	AC124053	Mus muscu
572	13	86.7	10364	1	AE005957	AE005957 Caulobact	13	86.7	54536	2	AC084132	AC084132	Homo sapi
573	13	86.7	10394	1	AE011048	AE011048 Methanosa	13	86.7	54819	9	AC079454	AC079454	Homo sapi
574	13	86.7	10581	1	AE008975	AE008975 Agrobacte	13	86.7	56222	10	AL671978	AL671978	Mouse DNA
575	13	86.7	10674	4	SSBATIC	Z34846 S.scrofa BA	13	86.7	56404	4	AY044827	AY044827	Sus scrofa
576	13	86.7	10800	14	AF311056	AF311056 Deer tick	13	86.7	57014	10	AL691494	AL691494	Mouse DNA

650	13	86.7	57103	2	AC087467	AC087467 Homo sapi	c 723	13	86.7	71699	2	AC027378	Homo sapi
651	13	86.7	57353	2	AC124318	Homo sapi	c 724	13	86.7	72038	2	AC023768	Homo sapi
652	13	86.7	57969	2	AC100083	Mus muscu	c 725	13	86.7	72591	2	AC080137	Homo sapi
653	13	86.7	58097	9	AL157758	Human DNA	c 726	13	86.7	72788	8	NCB2A19	Neurospor
654	13	86.7	58132	2	AC101310	Mus muscu	c 727	13	86.7	72969	2	AC027724	Homo sapi
655	13	86.7	58190	2	AC124329	Mus muscu	c 728	13	86.7	73048	2	AC103741	Homo sapi
656	13	86.7	58182	2	AC102832	Mus muscu	c 729	13	86.7	73052	2	AC013538	Homo sapi
657	13	86.7	59084	2	AC131506	Lytechinu	c 730	13	86.7	73141	2	AC120902	Rattus no
658	13	86.7	59320	3	AC024746	Caenorhab	c 731	13	86.7	73148	2	AC123731	Mus muscu
659	13	86.7	59339	9	AF287967	Homo sapi	c 732	13	86.7	73228	2	AC111529	Rattus no
660	13	86.7	59499	2	AC115550	Rattus no	c 733	13	86.7	73322	2	AC069380	Homo sapi
661	13	86.7	59942	2	AC130768	AC130768 Rattus no	c 734	13	86.7	73605	9	AL136309	Human DNA
662	13	86.7	60016	2	AC126381	Homo sapi	c 735	13	86.7	73666	2	AC130343	Homo sapi
663	13	86.7	60042	2	AC100484	Mus muscu	c 736	13	86.7	73782	2	AC123702	Mus muscu
664	13	86.7	60163	9	AC012018	Homo sapi	c 737	13	86.7	73852	2	AC123702	Mus muscu
665	13	86.7	60609	2	AC023519	Homo sapi	c 738	13	86.7	74510	2	AC101524	Mus muscu
666	13	86.7	60661	2	AC120009	AC120009 Mus muscu	c 739	13	86.7	74521	9	AC101683	Mus muscu
667	13	86.7	61212	9	AL391812	Human DNA	c 740	13	86.7	74905	9	AP000275	Homo sapi
668	13	86.7	61245	2	AC069449	Mus muscu	c 741	13	86.7	74905	2	AC097836	Rattus no
669	13	86.7	61309	2	AC090748	AC090748 Homo sapi	c 742	13	86.7	75106	8	ATFL6M2	Arabidops
670	13	86.7	61412	2	AC021493	AC021493 Homo sapi	c 743	13	86.7	75254	2	AC016176	Homo sapi
671	13	86.7	61588	10	AL611970	AL611970 Mouse DNA	c 744	13	86.7	75306	2	AC100494	Mus muscu
672	13	86.7	61958	2	AC121467	AC121467 Rattus no	c 745	13	86.7	75939	9	AL606519	Human DNA
673	13	86.7	61977	2	AC100640	AC100640 Mus muscu	c 746	13	86.7	76556	2	AL691517_3	Continuation (4 of
674	13	86.7	62076	2	AC091416	AC091416 Rattus no	c 747	13	86.7	76730	9	AC114105	Rattus no
675	13	86.7	62078	2	AC013711	AC013711 Homo sapi	c 748	13	86.7	77730	2	AC105760	Homo sapi
676	13	86.7	62499	2	AC091183	AC091183 Homo sapi	c 749	13	86.7	77830	10	AL672057	Mouse DNA
677	13	86.7	62649	2	AC022552	AC022552 Homo sapi	c 750	13	86.7	78423	10	AL671896	Mouse DNA
678	13	86.7	62791	2	AC026350	AC026350 Homo sapi	c 751	13	86.7	78843	2	AC094380	Rattus no
679	13	86.7	63170	10	AL645799	AL645799 Mouse DNA	c 752	13	86.7	78843	2	AC015455	Homo sapi
680	13	86.7	63403	10	AL611923	AL611923 Mouse DNA	c 753	13	86.7	79202	8	AP005165	Oryza sat
681	13	86.7	63427	2	AC130366	AC130366 Homo sapi	c 754	13	86.7	79277	2	AC131495	Lytechinu
682	13	86.7	63528	2	AC091196	AC091196 Homo sapi	c 755	13	86.7	79899	2	AC109972	Rattus no
683	13	86.7	63596	2	AC108913	AC108913 Mus muscu	c 756	13	86.7	80218	2	AC096336	Rattus no
684	13	86.7	63600	2	AC101405	AC101405 Mus muscu	c 757	13	86.7	80478	2	AC084700	Homo sapi
685	13	86.7	63668	2	AC116754	AC116754 Mus muscu	c 758	13	86.7	80609	9	AL589941	Human DNA
686	13	86.7	64260	2	AC112046	AC112046 Rattus no	c 759	13	86.7	80803	9	AL128424	Rattus no
687	13	86.7	64326	9	AP000331	AP000331 Homo sapi	c 760	13	86.7	81120	2	AC022851	Human DNA
688	13	86.7	64638	2	AC103116	AC103116 Rattus no	c 761	13	86.7	81374	9	HSJ300H18	Human DNA
689	13	86.7	64776	2	AC101127	AC101127 Mus muscu	c 762	13	86.7	81878	2	AC013647	Homo sapi
690	13	86.7	65147	2	AC101675	AC101675 Mus muscu	c 763	13	86.7	83001	2	AC015632	Homo sapi
691	13	86.7	65174	2	AC025214	AC025214 Homo sapi	c 764	13	86.7	83379	2	AC092113	Homo sapi
692	13	86.7	65356	2	AC108800	AC108800 Mus muscu	c 765	13	86.7	83453	2	AC111885	Rattus no
693	13	86.7	65612	2	AC087452	AC087452 Homo sapi	c 766	13	86.7	83783	2	AC016513	Rattus no
694	13	86.7	65612	2	AC087452	AC087452 Homo sapi	c 767	13	86.7	84003	2	AC110461	Homo sapi
695	13	86.7	65762	2	AC118238	AC118238 Mus muscu	c 768	13	86.7	84163	2	AC013510	Homo sapi
696	13	86.7	65762	2	AC118238	AC118238 Mus muscu	c 769	13	86.7	84906	2	AC019750	Drosophil
697	13	86.7	66206	10	AC093315	AC093315 Mus muscu	c 770	13	86.7	85022	2	AC121484	Rattus no
698	13	86.7	66505	2	AC102041	AC102041 Mus muscu	c 771	13	86.7	85454	9	HS83387	Human DNA
699	13	86.7	66624	2	AC101520	AC101520 Mus muscu	c 772	13	86.7	85454	9	HS83387	Human DNA
700	13	86.7	66666	2	AC123639	AC123639 Mus muscu	c 773	13	86.7	87065	9	AP002957	Homo sapi
701	13	86.7	67045	2	AC118213	AC118213 Mus muscu	c 774	13	86.7	87834	9	HSJ1174H9	Homo sapi
702	13	86.7	67346	10	AL732624	AL732624 Mouse DNA	c 775	13	86.7	88295	9	AC004612	Homo sapi
703	13	86.7	67645	10	AL645583	AL645583 Mouse DNA	c 776	13	86.7	88295	9	AC004612	Homo sapi
704	13	86.7	67808	2	AC114539	AC114539 Mus muscu	c 777	13	86.7	89937	2	AC096092	Rattus no
705	13	86.7	68419	2	AC016014	AC016014 Homo sapi	c 778	13	86.7	90378	2	AC097566	Rattus no
706	13	86.7	68543	9	AC115779	AC115779 Mus muscu	c 779	13	86.7	90513	9	AC107627	Homo sapi
707	13	86.7	68651	2	AC027343	AC027343 Homo sapi	c 780	13	86.7	90608	2	AC128541	Rattus no
708	13	86.7	68899	2	AC034301	AC034301 Homo sapi	c 781	13	86.7	90701	2	AC094040	Human DNA
709	13	86.7	68946	2	AC128842	AC128842 Rattus no	c 782	13	86.7	91025	9	AL359270	Rattus no
710	13	86.7	69314	2	AC108417	AC108417 Mus muscu	c 783	13	86.7	91025	9	AL359270	Rattus no
711	13	86.7	69734	2	AC010953	AC010953 Homo sapi	c 784	13	86.7	91098	2	AC111605	Rattus no
712	13	86.7	69894	2	AC123604	AC123604 Mus muscu	c 785	13	86.7	91202	2	AC007609	Homo sapi
713	13	86.7	70310	9	AC079839	AC079839 Homo sapi	c 786	13	86.7	91410	2	AC095538	Rattus no
714	13	86.7	70511	2	AC091083	AC091083 Homo sapi	c 787	13	86.7	91503	9	AL592488	Human DNA
715	13	86.7	70556	2	AC113141	AC113141 Homo sapi	c 788	13	86.7	91927	9	AC004771	Homo sapi
716	13	86.7	70866	2	AC114419	AC114419 Mus muscu	c 789	13	86.7	92276	2	AC023646	Homo sapi
717	13	86.7	70878	2	AC100628	AC100628 Mus muscu	c 790	13	86.7	92337	2	AC108839	Mus muscu
718	13	86.7	70982	2	AC107577	AC107577 Rattus no	c 791	13	86.7	93001	2	AC007286	Homo sapi
719	13	86.7	71166	2	AC023783	AC023783 Homo sapi	c 792	13	86.7	93329	2	AC097393	Rattus no
720	13	86.7	71464	2	AC124296	AC124296 Homo sapi	c 793	13	86.7				
721	13	86.7	71544	9	AC093792	AC093792 Homo sapi	c 794	13	86.7				
722	13	86.7	71605	2	AC119332	AC119332 Rattus no	c 795	13	86.7				

796	13	86.7	93423	2	AC120035	AC120035 Homo sapi	869	13	86.7	106604	9	HSXSRPX	AJ239329 Homo sapi
C 797	13	86.7	93526	2	AC128218	AC128218 Rattus no	870	13	86.7	106866	10	AL7332550	AL7332550 Mouse DNA
C 798	13	86.7	93610	2	AC127757	AC127757 Rattus no	871	13	86.7	107092	2	AC094284	AC094284 Rattus no
C 799	13	86.7	93701	8	AC006954	AC006954 Arabidops	C 872	13	86.7	107163	9	AL449105	AL449105 Human DNA
C 800	13	86.7	93721	2	AC122625	AC122625 Rattus no	C 873	13	86.7	107133	9	AL354702	AL354702 Human DNA
C 801	13	86.7	94533	2	AC058788_3	Continuation (4 of	C 874	13	86.7	107422	9	AL354681	AL354681 Human DNA
C 802	13	86.7	94625	9	AC011337	AL050332 Homo sapi	C 875	13	86.7	107689	9	AC008631	AC008631 Homo sapi
C 803	13	86.7	94770	9	HSJ570F3	AL050332 Human DNA	C 876	13	86.7	107857	9	AP000057	AP000057 Homo sapi
C 804	13	86.7	95092	2	AC129002	AC129002 Rattus no	C 877	13	86.7	107947	8	NCB7N14	AL668986 Neurospor
C 805	13	86.7	95594	2	AC122615	AC122615 Rattus no	C 878	13	86.7	108287	2	AP003814	AP003814 Oryza sat
C 806	13	86.7	96676	2	AC099305	AC099305 Rattus no	C 879	13	86.7	108315	9	HS41P2	AL049748 Human DNA
C 807	13	86.7	96741	2	AC109685	AC109685 Rattus no	C 880	13	86.7	108579	2	AC091566	AC091566 Homo sapi
C 808	13	86.7	96975	9	AC004975	AC004975 Homo sapi	881	13	86.7	108685	2	AL157383	AL157383 Homo sapi
C 809	13	86.7	97464	2	AC095194	AC095194 Rattus no	C 882	13	86.7	109043	5	CNS08CA7	AL808032 BAC 30B15
C 810	13	86.7	97468	2	AC111394	AC111394 Rattus no	C 883	13	86.7	109270	2	AC107541	AC107541 Rattus no
C 811	13	86.7	97792	2	AC097881	AC097881 Rattus no	884	13	86.7	109391	2	AL831758	AL831758 Datto rer
C 812	13	86.7	98031	2	AC105808	AC105808 Rattus no	C 885	13	86.7	109394	9	AC010979	AC010979 Homo sapi
C 813	13	86.7	98145	2	AC126313	AC126313 Rattus no	C 886	13	86.7	109626	9	AC010346	AC010346 Homo sapi
C 814	13	86.7	98340	2	HS344J2	AL449213 Homo sapi	C 887	13	86.7	109626	9	AC010346	AC010346 Homo sapi
C 815	13	86.7	98490	9	HS1018D12	AL031650 Human DNA	C 888	13	86.7	110000	2	AC112065_0	AC112065 Rattus no
C 816	13	86.7	98562	2	AC098628	AC098628 Rattus no	C 889	13	86.7	110000	2	AC112065_2	Continuation (3 of
C 817	13	86.7	98597	9	AC008416	AC008416 Homo sapi	C 890	13	86.7	110000	2	AC15817_1	Continuation (2 of
C 818	13	86.7	99141	8	AP003704	AP003704 Oryza sat	C 891	13	86.7	110000	2	AC122235_0	AC122235 Mus muscu
C 819	13	86.7	99156	8	AF466932	AF466932 Zea mays	C 892	13	86.7	110000	2	AC125228_0	AC125228 Mus muscu
C 820	13	86.7	99156	8	AF466932	AF466932 Zea mays	C 893	13	86.7	110000	2	AL772293_0	AL772293 Mus muscu
C 821	13	86.7	99657	2	AC106957	AC106957 Rattus no	C 894	13	86.7	110000	2	LMFLCHR18_03	Continuation (4 of
C 822	13	86.7	99876	9	HSJ901O8	AL078461 Human DNA	C 895	13	86.7	110000	2	LMFLCHR31_00	Continuation (5 of
C 823	13	86.7	99920	2	AC096218	AC096218 Rattus no	C 896	13	86.7	110000	2	LMFLCHR31_04	Continuation (5 of
C 824	13	86.7	100000	9	AP000037	AP000037 Homo sapi	C 897	13	86.7	110276	9	AC010169	AC010169 Homo sapi
C 825	13	86.7	100000	9	AP000105	AP000105 Homo sapi	C 900	13	86.7	110276	9	AC099129	AC099129 Rattus no
C 826	13	86.7	100000	9	AP000172	AP000172 Homo sapi	C 903	13	86.7	111016	2	AC098255	AC098255 Rattus no
C 827	13	86.7	100000	9	AP000181	AP000181 Homo sapi	C 904	13	86.7	111295	2	AC128720	AC128720 Rattus no
C 828	13	86.7	100000	9	AP000508	AP000508 Homo sapi	C 905	13	86.7	111659	2	AC128720	AC128720 Rattus no
C 829	13	86.7	100025	2	AC130913	AC130913 Rattus no	C 906	13	86.7	111723	9	HSJ101K10	AL080276 Human DNA
C 830	13	86.7	100079	9	AC108002	AC108002 Homo sapi	C 907	13	86.7	111855	8	AF267176	AF267176 Pyricular
C 831	13	86.7	100241	2	AC115168	AC115168 Rattus no	C 908	13	86.7	111948	2	AC094563	AC094563 Rattus no
C 832	13	86.7	100644	2	AC105511	AC105511 Rattus no	C 909	13	86.7	112311	9	AL358780	AL358780 Human DNA
C 833	13	86.7	100644	2	AC105511	AC105511 Rattus no	C 910	13	86.7	112428	2	AP003906	AP003906 Oryza sat
C 834	13	86.7	100644	2	AC105511	AC105511 Rattus no	C 911	13	86.7	112442	9	AL355340	AL355340 Human DNA
C 835	13	86.7	100674	2	AC126873	AC126873 Rattus no	C 912	13	86.7	112662	9	AC104453	AC104453 Homo sapi
C 836	13	86.7	101199	2	AC120605	AC120605 Rattus no	C 913	13	86.7	112686	9	AC002086	AC002086 Human PAC
C 837	13	86.7	101737	2	AC130446	AC130446 Rattus no	C 914	13	86.7	112813	2	AC102504	AC102504 Mus muscu
C 838	13	86.7	102057	2	AC122587	AC122587 Rattus no	C 915	13	86.7	112846	9	AC004991	AC004991 Homo sapi
C 839	13	86.7	102271	2	AC097693	AC097693 Rattus no	C 916	13	86.7	112876	9	AC122138	AC122138 Homo sapi
C 840	13	86.7	102316	9	AL159153	AL159153 Human DNA	C 917	13	86.7	112917	2	AC096013	AC096013 Rattus no
C 841	13	86.7	102326	9	AC087407	AC087407 Homo sapi	C 918	13	86.7	112968	9	AC093833	AC093833 Homo sapi
C 842	13	86.7	102377	2	AC004086	AC004086 Homo sapi	C 919	13	86.7	113164	10	AL731688	AL731688 Mouse DNA
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C 844	13	86.7	102422	2	AC129557	AC129557 Mus muscu	C 921	13	86.7	113468	2	AC113911	AC113911 Rattus no
C 845	13	86.7	102488	9	AP005231	AP005231 Homo sapi	C 922	13	86.7	113513	2	AC115368	AC115368 Rattus no
C 846	13	86.7	102515	2	AC112323	AC112323 Rattus no	C 923	13	86.7	113633	2	AC094512	AC094512 Rattus no
C 847	13	86.7	102555	2	AC099466	AC099466 Rattus no	C 924	13	86.7	113704	2	AC119345	AC119345 Rattus no
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C 849	13	86.7	103190	5	AF016020	AF016020 Gallus ga	C 926	13	86.7	114576	9	AC074397	AC074397 Homo sapi
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C 863	13	86.7	105565	2	AC104103	AC104103 Mus muscu	C 940	13	86.7	118247	2	AC109841	AC109841 Rattus no
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ALIGNMENTS
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LOCUS Homo sapiens partial COL4A3 type IV collagen, exon
DEFINITION
ACCESSION AJ288489
VERSION AJ288489.1 GI:135559182
KEYWORDS alpha3 type IV collagen; col4a3 gene.
SOURCE human.

RESULT 1
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LOCUS HSA288489 190 bp DNA linear PRI 04-APR-2001
DEFINITION Homo sapiens partial COL4A3 type IV collagen, exon
ACCESSION AJ288489
VERSION AJ288489.1 GI:135559182
KEYWORDS alpha3 type IV collagen; col4a3 gene.
SOURCE human.

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AC107284 Rattus no
AL713929 Roriza sat
AC120331 Rattus no
AC094827 Rattus no
AC110849 Rattus no
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AL096866 Human DNA
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 75 CCTTCTCCCTGTT 61

RESULT 3  
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LOCUS  
DEFINITION Homo sapiens cDNA FLJ11805 fis, clone HEMBA1006278, moderately similar to POLY(A) POLYMERASE (EC 2.7.7.19).  
ACCESSION AK021867  
VERSION 1  
KEYWORDS oligo capping; fis (full insert sequence).  
SOURCE Homo sapiens embryo, 10 weeks whole embryo, mainly head cDNA to mRNA, clone lib:HEMBA1006278.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.

1  
Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,K., Takeuchi,K., Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahara,K., Masuho,Y. and Oshima,A.  
NEDO human cDNA sequencing project  
Unpublished  
2 (bases 1 to 1689)  
Isogai,T. and Otsuki,T.  
Direct Submission  
Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)  
NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection; Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

FEATURES  
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Query Match 100.0%; Score 15; DB 5; Length 600;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGTT 15  
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Db 75 CCTTCTCCCTGTT 61

RESULT 3  
AK021867/c  
LOCUS  
DEFINITION Homo sapiens cDNA FLJ11805 fis, clone HEMBA1006278, moderately similar to POLY(A) POLYMERASE (EC 2.7.7.19).  
ACCESSION AK021867  
VERSION 1  
KEYWORDS oligo capping; fis (full insert sequence).  
SOURCE Homo sapiens embryo, 10 weeks whole embryo, mainly head cDNA to mRNA, clone lib:HEMBA1006278.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.

1  
Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,K., Takeuchi,K., Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahara,K., Masuho,Y. and Oshima,A.  
NEDO human cDNA sequencing project  
Unpublished  
2 (bases 1 to 1689)  
Isogai,T. and Otsuki,T.  
Direct Submission  
Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)  
NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection; Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 123 CCTTCTCCCTGTT 109

RESULT 4  
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LOCUS  
DEFINITION Sus scrofa prophet of pit-1 (prop-1) mRNA, complete cds.  
ACCESSION AF232676  
VERSION AF232676.1  
KEYWORDS GI:11275672  
SOURCE Sus scrofa.  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 1721)  
Sloop,K.W., McCutchan Schiller,A., Smith,T.P., Blanton,J.R. Jr., Rohrer,G.A., Meier,B.C. and Rhodes,S.J.  
Biochemical and genetic characterization of the porcine Prophet of pit-1 pituitary transcription factor  
Mol. Cell. Endocrinol. 168 (1-2), 77-87 (2000)  
JOURNAL  
MEDLINE 20519384  
PUBMED 11064154  
2 (bases 1 to 1721)  
McCutchan Schiller,A.L., Sloop,K.W., Blanton,J.R. Jr., Meier,B.C. and Rhodes,S.J.  
Direct Submission  
Submitted (07-FEB-2000) Biology, Indiana University Purdue University Indianapolis, 723 West Michigan Street, Indianapolis, IN 46202-5132, USA

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 236 CCTTCTCCCTGTT 222

RESULT 5  
BC000776



LOCUS BC000776 3190 bp mRNA linear PRI 12-JUL-2001  
DEFINITION Homo sapiens, Similar to KIAA0736 gene product, clone  
IMAGE:3509807, mRNA, partial cds.  
ACCESSION BC000776  
VERSION 1  
KEYWORDS BC000776.1 GI:12653962  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 3190)  
AUTHORS Strausberg,R.  
TITLE Direct Submission  
JOURNAL Submitted (15-NOV-2000) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov  
COMMENT Contact: MGC help desk  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Institute for Systems Biology  
http://www.systemsbio.org  
contact: amadan@systemsbio.org  
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia  
Greene, Mark Kettelman and Anuradha Madan  
Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
Series: IRAL Plate: 7 Row: 1 Column: 18  
This clone was selected for full length sequencing because it  
passed the following selection criteria: Hexamer frequency ORF  
analysis.  
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DEFINITION Homo sapiens neo-poly(A) polymerase mRNA, complete cds.  
ACCESSION AF312211  
VERSION AF312211.1  
KEYWORDS AF312211.1 GI:15080910  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CHKTGFB 3347 bp mRNA linear VRT 21-JUL-1994  
LOCUS Gallus gallus transforming growth factor-beta type III receptor  
DEFINITION mRNA, complete CDS.  
L01121  
ACCESSION L01121.1  
VERSION GI:511842  
KEYWORDS TGF-beta; betaglycan; plasma membrane; transforming growth  
factor-beta receptor; transforming growth factor-beta type III  
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SOURCE Gallus gallus (library: lambda zap) embryonic brain cDNA to mRNA.  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 3347)  
AUTHORS Barnett,J.V., Moustakas,A., Lin,W., Wang,X.F., Lin,H.Y.,  
Galper,J.B. and Maas,R.L.  
TITLE Cloning and developmental expression of the chick type II and type  
III TGF beta receptors  
JOURNAL Dev. Dyn. 199 (1), 12-27 (1994)  
MEDLINE 94220749  
PUBMED 8167376  
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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ACCESSION AF312211  
VERSION AF312211.1  
KEYWORDS AF312211.1 GI:15080910  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



**TITLE**  
JOURNAL  
Submitted (08-Oct-1998) Osamu Ohara, Kazusa DNA Research Institute,  
Laboratory of OCA Technology; Yana 1532-3, Kisarazu, Chiba  
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913;  
Fax:+81-438-52-3914)

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LQ"

**BASE COUNT**     914 a   1181 c   1192 g   1066 t

**ORIGIN**

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Best Local Similarity    100.0%; Pred. No. 39;  
Matches    15; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

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AL035357  
AL035357.1    GI:15723143  
topialpha gene; topoisomerase I.  
Takifugu rubripes  
Takifugu rubripes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;  
Tetraodontidae; Takifugu.  
1 (bases 1 to 11001)  
Smith,S.F., Metcalfe,J. and Elgar,G.  
Unpublished  
2 (bases 1 to 11001)  
Smith,S.F.  
Direct Submission  
Submitted (01-FEB-1999) Smith S.F., Fugu Group, UK HGMP Resource  
Centre, Wellcome Genome Campus, Hinxton Hall, Hinxton,  
Cambridgeshire, CB10 1SB, UNITED KINGDOM  
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VERSION	AE009810.1 GI:18159943									
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ORGANISM	Archaea; Crenarchaeota; Thermoprotei; Thermoproteales; Thermoproteaceae; Pyrobaculum.									
REFERENCE	1 (bases 1 to 11896) Fitz-Gibbon,S.T., Ladner,H., Kim,U.J., Stetter,K.O., Simon,M.I. and Miller,J.H. Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum Proc. Natl. Acad. Sci. U.S.A. 99 (2), 984-989 (2002) 11792869									
JOURNAL	2 (bases 1 to 11896) Fitz-Gibbon,S.T., Ladner,H., Kim,U.-J., Stetter,K.O., Simon,M.I. and Miller,J.H. Direct Submission Submitted (12-DEC-2001) Microbiology and Molecular Genetics, University of California, Los Angeles, 405 Hilgard Ave, Los Angeles, CA 90095-1489, USA Location/Qualifiers 1. .11896 /organism="Pyrobaculum aerophilum" /strain="IM2" /db_xref="taxon:13773" complement(129. .608) /gene="PAE1218" complement(129. .608) /gene="PAE1218" /note="Hypothetical; Conserved"									
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VERSION	AE009810.1 GI:18159943									
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SOURCE	Pyrobaculum aerophilum									
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VERSION
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Pestivirus.
REFERENCE 1 (bases 1 to 12602)
AUTHORS Becher,P., Orlich,M., Kosmidou,A., Konig,M., Baroth,M. and
Thiel,H.J.
TITLE Genetic diversity of pestiviruses: identification of novel groups
and implications for classification
MEDLINE 99420379
PUBMED 10489341
REFERENCE 2 (bases 1 to 12602)
AUTHORS Avalos-Ramirez,R., Orlich,M., Thiel,H.J. and Becher,P.
TITLE Evidence for the presence of two novel pestivirus species
MEDLINE 21378881
PUBMED 11485413
REFERENCE 3 (bases 1 to 12602)
AUTHORS Avalos-Ramirez,R., Orlich,M., Thiel,H.J. and Becher,P.
TITLE Complete genomic sequences of pestiviruses from giraffe and
reindeer: evidence for the presence of two novel species within the
genus pestivirus
JOURNAL Unpublished
REFERENCE 4 (bases 1 to 12602)
AUTHORS Becher,P. and Orlich,M.
TITLE Direct Submission
JOURNAL Submitted (21-APR-1999) Justus-Liebig-Universitaet Giessen,
Institut fuer Virologie (Fachbereich Veterinaermedizin),
Frankfurter Str. 107, Giessen D-35392, Germany
REFERENCE 5 (bases 1 to 12602)
AUTHORS Avalos-Ramirez,R., Orlich,M. and Becher,P.
TITLE Direct Submission
JOURNAL Submitted (26-MAR-2001) Justus-Liebig-Universitaet Giessen,
Institut fuer Virologie (Fachbereich Veterinaermedizin),
Frankfurter Str. 107, Giessen D-35392, Germany
REMARK Sequence update by submitter
COMMENT On Aug 23, 2001 this sequence version replaced gi:6049239.
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REFERENCE 1 (bases 1 to 32802)  
AUTHORS Grandi,G.  
TITLE Direct Submission  
JOURNAL Submitted (28-JAN-1993) G. Grandi, Enricerche, Via F Maritano 26,  
20097, S Donato Milanese (MI), ITALY  
REFERENCE 2 (bases 1 to 32802)  
AUTHORS Cosmina,P., Rodriguez,F., de Ferra,F., Grandi,G., Perego,M.,  
Venema,G. and van Sinderen,D.  
TITLE Sequence and analysis of the genetic locus responsible for  
surfactin synthesis in Bacillus subtilis  
JOURNAL Mol. Microbiol. 8 (5), 821-831 (1993)  
MEDLINE 93360813  
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## RESULT 13

AC107069/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

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Homo sapiens BAC clone RP11-249A8 from 2, complete sequence.

AC107069.5 GI:20146820

HTG.

Homo sapiens.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 34578)

Sulston, J.E. and Waterston, R.

Toward a complete human genome sequence

Genome Res. 8 (11), 1097-1108 (1998)

99063792

MEDLINE

PUBMED

2 (bases 1 to 34578)

Scott, K., Kozlowski, A., Spalding, L. and Trani, L.

The sequence of Homo sapiens BAC clone RP11-249A8

Unpublished (2001)

3 (bases 1 to 34578)

Waterston, R.H.

Direct Submission

Submitted (15-JAN-2002) Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

4 (bases 1 to 34578)

Waterston, R.H.

Direct Submission

Submitted (04-APR-2002) Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

5 (bases 1 to 34578)

Waterston, R.H.

Direct Submission

Submitted (13-APR-2002) Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

6 (bases 1 to 34578)

Waterston, R.

Direct Submission

Submitted (29-MAY-2002) Department of Genetics, Washington

University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

On Apr 13, 2002 this sequence version replaced gi:19924179.

----- Genome Center

Center: Washington University Genome Sequencing Center

Web site: http://genome.wustl.edu/gsc

Contact: sapiens@wustl.wustl.edu

----- Summary Statistics

----- Center project name: H\_NH0249A08

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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

## MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D.

McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

## SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osogawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tatenno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>  
VECTOR: pBACe3.6

## NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-495023, 2000 bp overlap; the clone sequenced to the right is RP11-563C6, 2000 bp overlap. Actual start of this clone is at base position 126621 of RP11-495023.

FEATURES	Location/Qualifiers
source	1..34578
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/chromosome="2"
	/map="2"
	/clone="RP11-249A8"
	/clone_lib="RPCI-11"
repeat_region	431..464
	/rpt_family="AT-rich"
repeat_region	565..616
	/rpt_family="L2"
repeat_region	804..1128
	/rpt_family="MER2_type"
repeat_region	2134..2757
	/rpt_family="L2"
repeat_region	3071..3357
	/rpt_family="Alu"
repeat_region	3430..3655
	/rpt_family="MIR"
repeat_region	3664..4328
	/rpt_family="ERV1"
repeat_region	4372..4459
	/rpt_family="ERV1"
repeat_region	5637..5789
	/rpt_family="MER1_type"
repeat_region	6117..6390
	/rpt_family="L1"
repeat_region	6872..6897
	/rpt_family="(ATAGG)n"
repeat_region	6917..7221
	/rpt_family="MER2_type"
repeat_region	7240..7267
	/rpt_family="(ATAGG)n"
repeat_region	7699..7750
	/rpt_family="L2"
repeat_region	8517..9128
	/rpt_family="L2"
repeat_region	9623..9916
	/rpt_family="Alu"
repeat_region	10230..10311
	/rpt_family="CT-rich"
repeat_region	10910..11214
	/rpt_family="Alu"
repeat_region	11616..11700
	/rpt_family="L2"
repeat_region	11711..11996
	/rpt_family="Alu"
repeat_region	11997..12065
	/rpt_family="(TAGA)n"
repeat_region	12083..12200
	/rpt_family="Alu"
repeat_region	12214..12509
	/rpt_family="L2"



repeat\_region 12519..12565  
/rpt\_family="GA-rich"  
repeat\_region 12723..12743  
/rpt\_family="AT-rich"  
repeat\_region 12930..12965  
/rpt\_family="AT-rich"  
repeat\_region 13468..13770  
/rpt\_family="Alu"  
repeat\_region 13881..14194  
/rpt\_family="Alu"  
repeat\_region 14255..14316  
/rpt\_family="(CA)n"  
repeat\_region 14609..14696  
/rpt\_family="MIR"  
repeat\_region 15519..15572  
/rpt\_family="Alu"  
repeat\_region 15951..15997  
/rpt\_family="ERV1"  
repeat\_region 16430..16990  
/rpt\_family="MaLR"  
repeat\_region 18201..18343  
/rpt\_family="CR1"  
repeat\_region 18517..18822  
/rpt\_family="MER2\_type"  
repeat\_region 19982..20085  
/rpt\_family="MER1\_type"  
repeat\_region 20002..20087  
/rpt\_family="MER1\_type"  
repeat\_region 20106..20441  
/rpt\_family="MaLR"  
repeat\_region 20451..20530  
/rpt\_family="MIR"  
repeat\_region 20561..20610  
/rpt\_family="AT-rich"  
repeat\_region 21029..21147  
/rpt\_family="MER1\_type"  
repeat\_region 22035..22201  
/rpt\_family="MER1\_type"  
repeat\_region 22467..22528  
/rpt\_family="L2"  
repeat\_region 22922..23217  
/rpt\_family="Alu"  
repeat\_region 23765..23897  
/rpt\_family="L1"  
repeat\_region 23988..24016  
/rpt\_family="(CAAA)n"  
repeat\_region 24061..24481  
/rpt\_family="L1"  
repeat\_region 24482..24768  
/rpt\_family="L1"  
repeat\_region 25359..25381  
/rpt\_family="AT-rich"  
repeat\_region 26536..26845  
/rpt\_family="L2"  
repeat\_region 27442..27804  
/rpt\_family="MaLR"  
repeat\_region 28510..28537  
/rpt\_family="AT-rich"  
repeat\_region 29081..29469  
/rpt\_family="MER1\_type"

Query Match 100.0%; Score 15; DB 9; Length 34578;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGTT 15  
|||||  
Db 1831 CCTTCTCCCTGTT 1817

RESULT 14  
AL138734/c ALL138734 43347 bp DNA linear PRI 16-AUG-2000  
LOCUS

DEFINITION Human DNA sequence from clone RP1-310P17 on chromosome 6. Contains GSSs, complete sequence.  
ACCESSION AL138734  
VERSION AL138734.6 GI:8388469  
KEYWORDS HTG.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 43347)  
Tromans,A.  
AUTHORS Direct Submission  
TITLE Submitted (21-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
JOURNAL requests: clonerequest@sanger.ac.uk

COMMENT

On Jun 8, 2000 this sequence version replaced gi:8247412.  
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.  
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.  
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/projects/C.elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6  
RP1-310P17 is from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/VECTORS: PCYPAC2  
IMPORTANT: This sequence is not the entire insert of clone RP1-310P17 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.  
The true left end of clone RP1-310P17 is at 1 in this sequence. The true left end of clone RP3-413H6 is at 43244 in this sequence.

FEATURES

source location/Qualifiers  
1..43347  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="6"  
/clone="RP1-310P17"  
/clone\_lib="RPCI-1"  
132..426  
/note="AluSq repeat: matches 1..295 of consensus"  
complement(428..891)  
/note="match: GSS: Em:B53078"  
complement(580..878)  
/note="match: GSS: Em:AQ269829"  
1740..1867  
/note="MIR repeat: matches 20..146 of consensus"  
1924..2090  
/note="L1MB8 repeat: matches 6005..6171 of consensus"  
2151..2266  
/note="L1MB8 repeat: matches 5874..5991 of consensus"  
2281..2431  
/note="AluY repeat: matches 158..308 of consensus"  
2432..2878  
/note="L1MB8 repeat: matches 5429..5879 of consensus"  
2879..3641  
/note="LTR17 repeat: matches 1..780 of consensus"  
3516..4013  
/note="match: GSS: Em:AQ112069"

repeat\_region

misc\_feature

misc\_feature

repeat\_region

repeat\_region

repeat\_region

repeat\_region

repeat\_region

repeat\_region

misc\_feature



```
repeat_region 3642..3924
/note="L1MB8 repeat: matches 5147..5429 of consensus"
misc_feature 4063..4518
/note="match: GSS: Em:AQ508138"
/note="match: GSS: Em:AQ508138"
complement(4129..4662)
/note="match: GSS: Em:AQ316392"
4657..5169
/note="match: GSS: Em:AQ484379"
4665..5178
/note="match: GSS: Em:AQ432756"
5449..5596
/note="L2 repeat: matches 2580..2750 of consensus"
6304..6577
/note="AluSx repeat: matches 9..282 of consensus"
6589..6721
/note="AluSg/x repeat: matches 1..133 of consensus"
6732..7036
/note="AluSp repeat: matches 1..305 of consensus"
7164..7253
/note="MIR repeat: matches 47..147 of consensus"
7584..7643
/note="30 copies 2 mer gt 96% conserved"
7969..8079
/note="MIR repeat: matches 28..143 of consensus"
8265..8544
/note="AluJo repeat: matches 2..289 of consensus"
8711..8799
/note="MIR repeat: matches 59..145 of consensus"
9753..9893
/note="AluY repeat: matches 168..311 of consensus"
10697..11158
/note="L2 repeat: matches 2290..2750 of consensus"
11255..11286
/note="16 copies 2 mer ac 100% conserved"
11352..11558
/note="HERVL repeat: matches 1757..1969 of consensus"
12998..13299
/note="AluSx repeat: matches 1..311 of consensus"
14005..14200
/note="MIR repeat: matches 1..208 of consensus"
14674..14748
/note="L1ME3 repeat: matches 5872..5956 of consensus"
15052..15480
/note="L1M4 repeat: matches 3375..3822 of consensus"
15481..15498
/note="AluS repeat: matches 152..170 of consensus"
15499..15731
/note="AluSg/x repeat: matches 71..308 of consensus"
15732..15790
/note="AluS repeat: matches 1..152 of consensus"
15822..16105
/note="L1PA16 repeat: matches 5830..6110 of consensus"
16106..16416
/note="AluSp repeat: matches 1..313 of consensus"
16417..17711
/note="L1PA16 repeat: matches 4517..5830 of consensus"
17737..18032
/note="WER61A repeat: matches 7..314 of consensus"
18038..18426
/note="L1PA16 repeat: matches 4125..4510 of consensus"
18427..18706
/note="L1M4 repeat: matches 3826..4124 of consensus"
18703..19271
/note="L1MD2 repeat: matches 5774..6331 of consensus"
19272..19892
/note="L2 repeat: matches 1452..2147 of consensus"
19893..19948
/note="WADE1 repeat: matches 5..80 of consensus"
19949..20211
/note="L2 repeat: matches 1194..1452 of consensus"
20944..21113
/note="AluSg/x repeat: matches 129..299 of consensus"
21140..21264
```

```
repeat_region 21581..21650
/note="AluSc repeat: matches 1..125 of consensus"
21747..21896
/note="L1MD3 repeat: matches 7476..7579 of consensus"
complement(21823..22281)
/note="match: GSS: Em:AQ714858"
22304..22755
/note="match: GSS: Em:AQ357726"
22608..22697
/note="L2 repeat: matches 2620..2710 of consensus"
22829..22868
/note="20 copies 2 mer aa 80% conserved"
22998..23085
/note="L1TR22 repeat: matches 413..509 of consensus"
23148..23417
/note="L1TR22 repeat: matches 38..312 of consensus"
23454..23569
/note="L2 repeat: matches 2005..2146 of consensus"
23645..23819
/note="MIR repeat: matches 61..243 of consensus"
24043..25714
/note="L1MEC repeat: matches 281..1953 of consensus"
25721..26938
/note="L1MEC repeat: matches 2151..3045 of consensus"
complement(26913..27340)
/note="match: GSS: Em:AQ225006"
28135..28460
/note="MER7A repeat: matches 4..346 of consensus"
28538..29022
/note="L1MC3 repeat: matches 7250..7739 of consensus"
29898..30315
/note="MLT1B repeat: matches 6..390 of consensus"
30318..31382
/note="Charlie2 repeat: matches 2658..3755 of consensus"
31290..31766
/note="match: GSS: Em:AQ735362"
31390..31669
/note="L1TR16C repeat: matches 102..387 of consensus"
32151..32455
/note="AluJb repeat: matches 1..304 of consensus"
33318..33468
/note="Charlie2 repeat: matches 327..504 of consensus"
34076..34305
/note="MIR repeat: matches 6..260 of consensus"
34434..34535
/note="L2 repeat: matches 2574..2687 of consensus"
34633..35136
/note="MER9 repeat: matches 1..511 of consensus"
36692..37186
/note="Cheshire repeat: matches 27..548 of consensus"
37183..38826
/note="Cheshire repeat: matches 723..2420 of consensus"
```

Query Match 100.0%; Score 15; DB 9; Length 43347;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGTT 15  
Db 27556 CCTTCTCCCCCTGTT 27542  
|||||

RESULT 15  
AL583852  
LOCUS Human DNA sequence from clone RP11-17G2 on chromosome 10, complete  
DEFINITION sequence.  
ACCESSION AL583852 AC011691  
VERSION AL583852.6 GI:14702147  
KEYWORDS HTG.  
SOURCE human.  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 56701)  
Chapman, J.  
Direct Submission  
Submitted (03-DEC-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: hamquerry@sanger.ac.uk  
On or before Jul 12, 2001 this sequence version replaced gi:7381811, gi:13396759.  
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.  
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; SW; SWISSPROT; Tr; TREMBL; Wp; WORMPEP; Information on the WORMPEP database can be found at  
[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at  
<http://www.sanger.ac.uk/HGP/Chr10>  
RP11-17G2 is from the library RPCT-11.1 constructed by the group of Pieter de Jong. For further details see  
<http://www.chori.org/bacpac/home.htm>  
VECTOR: pBACe3.6  
IMPORTANT: This sequence is not the entire insert of clone RP11-17G2 it may be shorter because we sequence overlapping sections only once, except for a short overlap.  
The true right end of clone RP11-17G2 is at 56701 in this sequence. The true right end of clone RP11-397115 is at 2000 in this sequence.

## FEATURES

source  
1..56701  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="10"  
/clone="RP11-17G2"  
/clone\_lib="RPCT-11.1"  
1..284  
/note="MER1B repeat: matches 1..285 of consensus"  
285..400  
/note="MER20 repeat: matches 103..218 of consensus"  
1266..1301  
/note="L2 repeat: matches 2580..2615 of consensus"  
1305..1352  
/note="24 copies 2 mer ga 75% conserved"  
complement(2038..2454)  
/note="match: GSS: Em:AQ358591"  
2479..2823  
/note="match: GSS: Em:AQ812738"  
2586..2791  
/note="MIR repeat: matches 45..258 of consensus"  
2979..3119  
/note="MIR repeat: matches 61..212 of consensus"  
complement(3478..3937)  
/note="match: GSS: Em:AQ475942"  
4218..4317  
/note="L2 repeat: matches 2645..2749 of consensus"  
5477..5644  
/note="MLR1I repeat: matches 68..240 of consensus"  
complement(5738..6110)  
/note="match: STS: Em:G53244"

repeat\_region  
match: GSS: Em:AQ083388"  
6206..6292  
/note="MER91A repeat: matches 5..95 of consensus"  
6293..6521  
/note="MIR repeat: matches 9..234 of consensus"  
8688..8929  
/note="L2 repeat: matches 2284..2534 of consensus"  
8947..9112  
/note="MIR repeat: matches 70..248 of consensus"  
9173..9416  
/note="MT1A1 repeat: matches 337..568 of consensus"  
9753..10220  
/note="match: GSS: Em:AQ497216"  
10458..10642  
/note="L2 repeat: matches 2129..2318 of consensus"  
13448..13763  
/note="MT1A1 repeat: matches 1..341 of consensus"  
13847..13898  
/note="2 copies 26 mer 94% conserved"  
15428..15572  
/note="MER5A repeat: matches 18..178 of consensus"  
16288..16546  
/note="L2 repeat: matches 2242..2521 of consensus"  
16664..16777  
/note="L2 repeat: matches 2596..2708 of consensus"  
16779..16842  
/note="16 copies 4 mer gga 81% conserved"  
16817..16938  
/note="7 copies 26 mer 62% conserved"  
16861..16944  
/note="21 copies 4 mer gga 75% conserved"  
16951..16994  
/note="11 copies 4 mer gga 81% conserved"  
17973..18165  
/note="MIR repeat: matches 22..214 of consensus"  
18174..18509  
/note="MER46C repeat: matches 7..338 of consensus"  
18670..18785  
/note="MER5A repeat: matches 45..163 of consensus"  
18833..19044  
/note="MIR repeat: matches 28..260 of consensus"  
21936..22145  
/note="TIME repeat: matches 5599..5820 of consensus"  
22148..22199  
/note="13 copies 4 mer caca 82% conserved"  
22199..22596  
/note="MSTA repeat: matches 1..426 of consensus"  
22480..22743  
/note="match: STS: Em:HS094YH3"  
22597..22638  
/note="21 copies 2 mer ca 92% conserved"  
22599..22638  
/note="10 copies 4 mer caca 92% conserved"  
22770..22846  
/note="MIR repeat: matches 87..165 of consensus"  
22959..23149  
/note="MER3 repeat: matches 1..200 of consensus"  
23508..23698  
/note="L2 repeat: matches 2539..2748 of consensus"  
24378..24458  
/note="L1 repeat: matches 2136..2213 of consensus"  
24486..24581  
/note="48 copies 2 mer tt 63% conserved"  
25073..25451  
/note="MT1F repeat: matches 1..371 of consensus"  
complement(25325..25729)  
/note="match: GSS: Em:AQ507252"  
26471..26619  
/note="MT1F repeat: matches 105..257 of consensus"  
26933..27097  
/note="MER5A repeat: matches 1..188 of consensus"  
27101..27219  
/note="MIR repeat: matches 13..134 of consensus"

```
repeat_region 27767..27813
               /note="MIR repeat: matches 49..103 of consensus"
repeat_region 28697..28879
               /note="MIR repeat: matches 31..225 of consensus"
repeat_region 29356..29488
               /note="MERSA repeat: matches 50..184 of consensus"
repeat_region 29578..29664
               /note="MIR repeat: matches 82..175 of consensus"
repeat_region 31386..31508
               /note="MIR repeat: matches 42..164 of consensus"
repeat_region 31974..32354
               /note="MLTII repeat: matches 1..410 of consensus"
misc_feature 32596..33015
               /note="match: GSS: Em:AQ604754"
repeat_region 33407..33823
               /note="MLTII repeat: matches 128..547 of consensus"
repeat_region 33833..34015
               /note="MIR repeat: matches 50..251 of consensus"
misc_feature 34122..34214
               /note="match: GSS: Em:AQ551831"
repeat_region 35380..35474
               /note="MIR repeat: matches 46..140 of consensus"
repeat_region 37028..37195
               /note="MER63A repeat: matches 45..210 of consensus"
repeat_region 37274..37413
               /note="L2 repeat: matches 2137..2276 of consensus"
repeat_region 37801..38057
               /note="L2 repeat: matches 2469..2750 of consensus"
repeat_region 38541..39465
               /note="L2 repeat: matches 1655..2599 of consensus"
repeat_region 39625..39782
               /note="MIR repeat: matches 59..220 of consensus"
repeat_region 41102..41277
               /note="L2 repeat: matches 2517..2691 of consensus"
repeat_region 41278..41718
               /note="MLTIC repeat: matches 5..462 of consensus"
repeat_region 41719..41924
               /note="L2 repeat: matches 2308..2517 of consensus"
repeat_region 42387..42468
               /note="MIR repeat: matches 162..246 of consensus"
repeat_region 42496..42577
               /note="L2 repeat: matches 2605..2692 of consensus"
repeat_region 43328..43400
               /note="L2 repeat: matches 2646..2731 of consensus"
repeat_region 43505..43769
               /note="L2 repeat: matches 2161..2419 of consensus"
```

```
Query Match      100.0%; Score 15; DB 9; Length 56701;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 1 CCTTCTCCCCCTGTT 15
    |||||
DB 2530 CCTTCTCCCCCTGTT 2544
```

Search completed: December 11, 2002, 18:08:27  
Job time : 1740 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 15:29:02 ; Search time 213 Seconds  
(without alignments)  
158.591 Million cell updates/sec

Title: US-09-750-609-10

Perfect score: 15

Sequence: 1 cctctcccccgttt 15

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : N\_Geneseq\_101002:\*

- 1: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:\*
- 2: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*
- 3: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*
- 4: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:\*
- 5: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:\*
- 6: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:\*
- 7: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:\*
- 8: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:\*
- 9: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:\*
- 10: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:\*
- 11: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:\*
- 12: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:\*
- 13: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:\*
- 14: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:\*
- 15: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:\*
- 16: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:\*
- 17: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:\*
- 18: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:\*
- 19: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:\*
- 20: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:\*
- 21: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:\*
- 22: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*
- 23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*
- 24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	AAH28085	Probe for human no
c 2	15	100.0	352	AAC09241	Human secreted pro
3	15	100.0	445	ABV50337	Human prostate exp
4	15	100.0	549	23 AAS66052	DNA encoding novel
c 5	15	100.0	827	22 AAH04051	Human cDNA clone (
c 6	15	100.0	1689	22 AAH15437	Human cDNA sequenc
7	15	100.0	1854	22 AAH28083	DNA encoding human
8	15	100.0	1854	22 AAH28087	DNA encoding human
9	15	100.0	2159	23 ABK43728	DNA encoding novel

15	100.0	2451	23	AAS83288	DNA encoding novel
15	100.0	2520	24	ABL90474	Human polynucleoti
c 12	15	2522	23	ABK44004	DNA encoding novel
13	15	3580	21	AAH16697	Human secreted pro
c 14	15	3580	24	ABK35630	cDNA sequence #21
c 15	100.0	4215	23	ABV22746	Human prostate exp
c 16	15	4215	23	ABV28574	Human prostate exp
c 17	15	4366	22	AAH57556	Human brain cell s
18	15	15857	22	AA526730	Human genomic DNA
c 19	15	31122	14	AAO40706	Bacillus subtilis
c 20	14	389	24	ABN96737	Gene #3235 used to
c 21	14	389	24	ABL66267	Lung cancer relate
c 22	14	482	24	ABT04065	Human ovary specif
23	14	594	22	ABAG2115	Human foetal liver
24	14	594	22	AAK10435	Human brain expres
25	14	594	22	AAK36337	Human bone marrow
26	14	594	22	AAI42060	Probe #10746 used
c 27	14	599	23	AAS85439	DNA encoding novel
28	14	2349	21	AAA26376	Human secreted pro
c 29	14	2415	18	AAT62067	Fission yeast prot
30	14	2775	22	AAH13954	Human cDNA sequenc
c 31	14	6959	23	AAS85443	DNA encoding novel
32	14	8894	22	AAL36698	Human musculoskele
c 33	14	8894	22	ABA26718	Human genomic DNA
c 34	14	16877	22	ABA20494	Human nervous syst
c 35	14	16877	22	AAL36984	Human musculoskele
c 36	14	61710	22	AAK83782	Human immune/haema
c 37	13	193	16	AAT21956	Human gene signatu
38	13	209	22	ABA75403	Human foetal liver
39	13	209	22	ABA40037	Probe #18503 for g
40	13	209	22	AAK23963	Human brain expres
41	13	209	22	AAK50031	Human bone marrow
42	13	209	22	AAI27125	Probe #17058 for g
43	13	209	22	AAI55970	Probe #24656 used
44	13	209	22	ABS23521	Human genome-deriv
c 45	13	210	22	AAI29067	Colon tumour relat
c 46	13	285	24	ABL81791	Human ovarian canc
c 47	13	306	22	AAH71347	Human cervical can
c 48	13	315	22	AAH52042	Mycobacterium tube
49	13	322	22	ABA07823	Human ovarian and
50	13	322	22	AAL03625	Human reproductive
c 51	13	337	21	AAL11522	Human secreted pro
c 52	13	337	24	ABL87132	Human ovarian canc
c 53	13	373	22	AAK56539	Human immune/haema
c 54	13	381	23	AA564315	DNA encoding novel
c 55	13	383	24	ABN94579	Gene #1077 used to
c 56	13	383	24	ABL65582	Lung cancer relate
c 57	13	401	22	ABA08339	Human protein-tyr
c 58	13	435	22	AAK68265	Human immune/haema
c 59	13	435	22	AAK68266	Human immune/haema
c 60	13	435	22	AAK68267	Human immune/haema
61	13	444	20	AAV88767	EST clone HM280.
62	13	449	24	ABA37354	A2R20 adenylate ur
63	13	467	22	ABA07414	Human pancreatic c
64	13	467	22	AAK91145	Human digestive sy
c 65	13	469	22	ABA52284	Human foetal liver
c 66	13	469	22	ABA22085	Probe #551 for gen
c 67	13	469	22	ABA07060	Human pancreatic c
c 68	13	469	22	AAK00559	Human brain expres
c 69	13	469	22	AAK26008	Human bone marrow
c 70	13	469	22	AAK88801	Human digestive sy
c 71	13	469	22	AAI10637	Probe #570 for gen
c 72	13	469	22	AAI31891	Probe #577 used to
c 73	13	469	22	AAI00568	Probe #559 used to
c 74	13	469	24	ABS00589	Human genome-deriv
c 75	13	494	24	ABL83753	Human ovarian canc
c 76	13	500	22	ABA62303	Human foetal liver
c 77	13	500	22	ABA29646	Probe #8112 for ge
c 78	13	500	22	AAK10639	Human brain expres
c 79	13	500	22	AAK36525	Human bone marrow
c 80	13	500	22	AAI17384	Probe #7317 for ge
c 81	13	500	22	AAI42281	Probe #10967 used
c 82	13	500	24	ABS10523	Human genome-deriv

c 83	13	86.7	529	23	AAH88281	CNS disorder-relat	156	13	86.7	5514	23	ABL10818	Drosophila melanog
c 84	13	86.7	561	22	AAH13181	Human cDNA clone (	157	13	86.7	5728	20	ABK62572	Rat sequence diffe
c 85	13	86.7	565	22	ABA64032	Human foetal liver	c 158	13	86.7	5828	24	AAK84592	AML1-MTG16 fusion
c 86	13	86.7	596	17	AAT33226	Oryzacystatin-I de	c 159	13	86.7	5938	24	ABL66297	Lung cancer relate
c 87	13	86.7	598	22	ABA62898	Human foetal liver	c 160	13	86.7	5938	24	ABL68033	Ovary cancer relat
c 88	13	86.7	598	22	ABA30172	Probe #8638 for ge	161	13	86.7	6004	21	AAA07835	Human homologue of
c 89	13	86.7	598	22	AAK11302	Human brain expres	162	13	86.7	6032	19	AAV30268	Plasmid pMT1802 en
c 90	13	86.7	598	22	AAK37094	Human bone marrow	163	13	86.7	6032	19	AAV12368	Trichoderma harzia
c 91	13	86.7	598	22	AAI17935	Probe #7868 for ge	c 164	13	86.7	6056	20	AAK84593	AML1-MTG16 fusion
c 92	13	86.7	598	22	AAI42917	Probe #11603 used	c 165	13	86.7	6864	22	AAI26588	Human breast cance
c 93	13	86.7	598	24	ABSI11096	Human genome-deriv	c 166	13	86.7	7180	23	ABL04344	Drosophila melanog
c 94	13	86.7	616	23	ABV57123	Human prostate exp	c 167	13	86.7	8267	23	ABL09340	Drosophila melanog
c 95	13	86.7	673	22	AAI01792	Human reproductive	c 168	13	86.7	8448	22	AAK040680	DNA encoding human
c 96	13	86.7	673	23	ABU97085	Human testicular a	c 169	13	86.7	8448	22	AAI06568	Human reproductive
c 97	13	86.7	705	24	ABK78617	Bacillus clausii g	c 170	13	86.7	9566	22	AAK06568	DNA encoding human
c 98	13	86.7	705	24	ABK78618	Bacillus clausii g	c 171	13	86.7	9566	22	AAI06570	Human reproductive
c 99	13	86.7	788	22	AAI21413	Human breast cance	c 172	13	86.7	10828	22	ABA19208	Human immune syst
c 100	13	86.7	966	22	AAH31746	Human olfactory re	c 173	13	86.7	10828	22	AAK70743	Human immune/haema
c 101	13	86.7	991	24	ABT04187	Human G-protein co	c 174	13	86.7	13660	22	AAI199126	Human excretory re
c 102	13	86.7	1044	24	ABQ91421	M. capsulatus gene	c 175	13	86.7	13660	22	AAK67907	Human immune/haema
c 103	13	86.7	1046	22	AAK76385	T. harzianum alpha	c 176	13	86.7	13660	22	AAK81002	Human immune/haema
c 104	13	86.7	1059	22	AAK42429	Human cDNA encodin	c 177	13	86.7	13660	22	AAI63476	Human kidney relat
c 105	13	86.7	1059	24	ABK37715	DNA encoding G-cou	c 178	13	86.7	14221	22	AAK040681	DNA encoding human
c 106	13	86.7	1077	22	AAH75725	Human NOV 10 codin	c 179	13	86.7	14221	22	AAI06569	Human reproductive
c 107	13	86.7	1136	19	AAV37396	Streptococcus pneu	c 180	13	86.7	14537	24	ABL67781	Oesophagus cancer
c 108	13	86.7	1139	24	AAK15019	Rice 16S RNA-speci	c 181	13	86.7	21469	22	AAK89568	Human digestive sy
c 109	13	86.7	1167	22	AAK52030	Human polynucleoti	c 182	13	86.7	21475	22	AAK89569	Human digestive sy
c 110	13	86.7	1229	21	AAK47295	Arabidopsis thalia	c 183	13	86.7	22813	22	AAK65271	Human immune/haema
c 111	13	86.7	1356	22	AAH90777	CPE 81 coding sequ	c 184	13	86.7	22813	22	AAK82016	Human immune/haema
c 112	13	86.7	1379	22	AAH90886	2CFE 81 coding seq	c 185	13	86.7	22813	22	AAK86303	Human immune/haema
c 113	13	86.7	1448	22	AAI05887	Human reproductive	c 186	13	86.7	22813	22	AAK87333	Human immune/haema
c 114	13	86.7	1448	23	ABU98451	Human testicular a	c 187	13	86.7	23449	21	AAZ35393	Human digestive sy
c 115	13	86.7	1656	23	AAK55580	Streptococcus pneu	c 188	13	86.7	23449	21	AAK89569	Human immune/haema
c 116	13	86.7	1896	24	AAI40132	Isoprenoid related	c 189	13	86.7	24740	21	AAK87743	Human LMP-1 (HIMP-
c 117	13	86.7	1900	21	AAK77509	Human ORFX ORF3064	c 190	13	86.7	30352	22	AAK87743	Human LMP-1 (HIMP-
c 118	13	86.7	2007	24	ABK72714	Bacillus lichenifo	c 191	13	86.7	32217	22	AAK81742	Human cardiovascular
c 119	13	86.7	2037	23	AAK569761	DNA encoding novel	c 192	13	86.7	32217	22	AAK81742	Genomic sequence #
c 120	13	86.7	2037	23	AAK76456	DNA encoding novel	c 193	13	86.7	32217	22	AAK81742	Human immune/haema
c 121	13	86.7	2037	23	AAK83376	DNA encoding novel	c 194	13	86.7	32217	22	AAK83376	Human immune/haema
c 122	13	86.7	2040	24	AAI45342	Human T2 coding se	c 195	13	86.7	32217	22	AAK83376	Human GPCR protein
c 123	13	86.7	2256	22	AAK76384	Trichoderma harzia	c 196	13	86.7	32217	22	AAK83376	Genomic sequence e
c 124	13	86.7	2339	24	ABQ54676	Human ovarian anti	c 197	13	86.7	32217	22	AAK83376	Human osteoblast d
c 125	13	86.7	2364	22	AAH15873	Human cDNA sequenc	c 198	13	86.7	32217	22	AAK83376	Pyrococcus abyssi
c 126	13	86.7	2448	22	AAI58188	Human polynucleoti	c 199	13	86.7	32217	22	AAK83376	Mycobacterium tube
c 127	13	86.7	2499	23	AAK88464	DNA encoding novel	c 200	13	86.7	32217	22	AAK83376	Human PAH gene ass
c 128	13	86.7	2525	21	AAI16144	Human prostate can	c 201	13	86.7	32217	22	AAK83376	Human PAH gene ass
c 129	13	86.7	2687	15	AAO54896	Maize pollen-speci	c 202	13	86.7	32217	22	AAK83376	Human PAH gene ass
c 130	13	86.7	2873	15	AAO54889	Maize pollen-speci	c 203	13	86.7	32217	22	AAK83376	Human DNA containi
c 131	13	86.7	2874	22	AAK58134	Human polynucleoti	c 204	13	86.7	32217	22	AAK83376	Mouse spliced tran
c 132	13	86.7	2879	13	AAO23074	Bacterial alpha-1,	c 205	13	86.7	32217	22	AAK83376	Human breast cell
c 133	13	86.7	2902	24	AAK27895	Human ephrin-B2 cD	c 206	13	86.7	32217	22	AAK83376	Human foetal liver
c 134	13	86.7	2943	23	AAK84770	DNA encoding novel	c 207	13	86.7	32217	22	AAK83376	Probe #11091 for g
c 135	13	86.7	3045	22	AAI58133	Human polynucleoti	c 208	13	86.7	32217	22	AAK83376	Human brain expres
c 136	13	86.7	3069	22	AAI58135	Human polynucleoti	c 209	13	86.7	32217	22	AAK83376	Human bone marrow
c 137	13	86.7	3100	23	AAK77867	DNA encoding novel	c 210	13	86.7	32217	22	AAK83376	Probe #10425 for g
c 138	13	86.7	3383	24	ABQ72496	Human MDT encodin	c 211	13	86.7	32217	22	AAK83376	Probe #14385 used
c 139	13	86.7	3415	20	ABK28654	Human cDNA encodin	c 212	13	86.7	32217	22	AAK83376	Probe #6181 used t
c 140	13	86.7	3419	20	AAK28077	HS2ST coding sequ	c 213	13	86.7	32217	22	AAK83376	Human genome-deriv
c 141	13	86.7	3611	22	AAH18179	Human cDNA sequenc	c 214	13	86.7	32217	22	AAK83376	Human secreted pro
c 142	13	86.7	4254	23	ABK42317	Genomic sequence #	c 215	13	86.7	32217	22	AAK83376	Human immune/haema
c 143	13	86.7	4255	23	ABK42316	Genomic sequence #	c 216	13	86.7	32217	22	AAK83376	Human foetal liver
c 144	13	86.7	4287	15	AAQ58996	AML1-MTG8 fusion.	c 217	13	86.7	32217	22	AAK83376	Human brain expres
c 145	13	86.7	4287	19	AAV20475	Human AML1/MTG8 on	c 218	13	86.7	32217	22	AAK83376	Human bone marrow
c 146	13	86.7	4440	23	ABV25160	Human prostate exp	c 219	13	86.7	32217	22	AAK83376	Probe #23820 used
c 147	13	86.7	4503	18	AAK64783	Human oxygen regul	c 220	13	86.7	32217	22	AAK83376	Human breast cell
c 148	13	86.7	4503	24	ABK84398	Human cDNA diffe	c 221	13	86.7	32217	22	AAK83376	Human foetal liver
c 149	13	86.7	5108	23	AAK27692	DNA encoding novel	c 222	13	86.7	32217	22	AAK83376	Probe #13739 for g
c 150	13	86.7	5256	21	AAZ98619	RPPI-WSB genomic n	c 223	13	86.7	32217	22	AAK83376	Human brain expres
c 151	13	86.7	5265	23	AAK85296	DNA encoding novel	c 224	13	86.7	32217	22	AAK83376	Human bone marrow
c 152	13	86.7	5342	22	AAK81684	Human immune/haema	c 225	13	86.7	32217	22	AAK83376	Probe #13096 for g
c 153	13	86.7	5345	22	AAK81685	Human immune/haema	c 226	13	86.7	32217	22	AAK83376	Probe #17168 used
c 154	13	86.7	5345	22	AAK81686	Human immune/haema	c 227	13	86.7	32217	22	AAK83376	Probe #8809 used t
c 155	13	86.7	5416	23	ABL09341	Drosophila melanog	c 228	13	86.7	32217	22	AAK83376	Bacillus lichenifo

c 229	12	80.0	208	22	ABA76330	Human foetal liver	c 302	12	80.0	409	22	AAI81144	Human polynucleoti
c 230	12	80.0	208	22	ABA40860	Probe #19326 for g	c 303	12	80.0	410	22	ABA42506	Human breast cell
c 231	12	80.0	208	22	AKA24980	Human brain expres	c 304	12	80.0	410	22	ABA52935	Human foetal liver
c 232	12	80.0	208	22	AAK50978	Human bone marrow	c 305	12	80.0	410	22	ABA22714	Probe #1180 for ge
c 233	12	80.0	208	22	AAI28012	Probe #17945 for g	c 306	12	80.0	410	22	AAK01185	Human brain expres
c 234	12	80.0	208	22	AAI57003	Probe #25689 used	c 307	12	80.0	410	22	AAK26646	Human bone marrow
c 235	12	80.0	208	24	ABS24487	Human genome-deriv	c 308	12	80.0	410	22	AAI11273	Probe #1206 for ge
c 236	12	80.0	221	24	ABN16126	Human ORFX polynuc	c 309	12	80.0	410	22	AAI32539	Probe #1225 used t
c 237	12	80.0	238	22	ABA71748	Human foetal liver	c 310	12	80.0	410	22	AAI01188	Probe #1179 used t
c 238	12	80.0	238	22	ABA37838	Probe #16304 for g	c 311	12	80.0	410	22	ABS01238	Human genome-deriv
c 239	12	80.0	238	22	AAK20111	Human brain expres	c 312	12	80.0	410	22	ABA12382	Human nervous syst
c 240	12	80.0	238	22	AAK46164	Human bone marrow	c 313	12	80.0	415	22	AAK33940	Human cDNA encodin
c 241	12	80.0	238	22	AAI25549	Probe #15482 for g	c 314	12	80.0	419	22	AAI3780	Human polynucleoti
c 242	12	80.0	238	22	AAI52073	Probe #20759 used	c 315	12	80.0	437	23	ABV05483	Human prostate exp
c 243	12	80.0	238	24	ABS20473	Human genome-deriv	c 316	12	80.0	441	23	ABV36664	Human prostate exp
c 244	12	80.0	245	21	AAK29279	Human secreted pro	c 317	12	80.0	449	22	ABA59019	Human foetal liver
c 245	12	80.0	255	20	AAV89836	EST clone CW1150.	c 318	12	80.0	449	22	ABA27849	Probe #6315 for ge
c 246	12	80.0	258	21	AAK12892	Human secreted pro	c 319	12	80.0	449	22	AAK07189	Human brain expres
c 247	12	80.0	268	21	AAK19159	Human secreted pro	c 320	12	80.0	449	22	AAK32940	Human bone marrow
c 248	12	80.0	269	21	AAK45882	Human secreted exp	c 321	12	80.0	449	22	AAI16267	Probe #6200 for ge
c 249	12	80.0	270	24	ABK64644	Human benign prost	c 322	12	80.0	449	22	AAI38746	Probe #7432 used t
c 250	12	80.0	270	24	ABL65692	Lung cancer relate	c 323	12	80.0	449	24	ABS07746	Human genome-deriv
c 251	12	80.0	277	22	AAK36636	Human cardiovascular	c 324	12	80.0	450	22	AAK62933	Human immune/haema
c 252	12	80.0	277	22	AAK06330	Human reproductive	c 325	12	80.0	451	20	AAK40853	Human secreted pro
c 253	12	80.0	277	22	AAI06331	Human reproductive	c 326	12	80.0	460	22	AAK13384	Human nervous syst
c 254	12	80.0	277	22	AAI06331	Human ovarian canc	c 327	12	80.0	461	22	AAK54824	Rice glutamate 1-s
c 255	12	80.0	278	24	ABL83286	DNA encoding novel	c 328	12	80.0	467	22	ABA57318	Human foetal liver
c 256	12	80.0	291	23	AAK571802	Human foetal liver	c 329	12	80.0	467	22	ABA26868	Probe #5334 for ge
c 257	12	80.0	294	22	ABA72856	Probe #16919 for g	c 330	12	80.0	467	22	AAK05354	Human brain expres
c 258	12	80.0	294	22	ABA38453	Human brain expres	c 331	12	80.0	467	22	AAK30948	Human bone marrow
c 259	12	80.0	294	22	AAK21289	Human bone marrow	c 332	12	80.0	467	22	AAI36861	Probe #5547 used t
c 260	12	80.0	294	22	AAK47445	Probe #15871 for g	c 333	12	80.0	467	24	ABS05696	Human genome-deriv
c 261	12	80.0	294	22	AAI25938	Probe #21965 used	c 334	12	80.0	468	24	ABN65232	Human cancer relat
c 262	12	80.0	294	22	AAI53279	Human genome-deriv	c 335	12	80.0	473	22	ABA27977	Human foetal liver
c 263	12	80.0	294	22	ABS21568	Human colon cancer	c 336	12	80.0	473	22	ABA27977	Probe #6443 for ge
c 264	12	80.0	300	21	AAK01000	DNA encoding novel	c 337	12	80.0	473	22	AAK33211	Human brain expres
c 265	12	80.0	318	23	AAK65968	Human cDNA encodin	c 338	12	80.0	473	22	AAK33211	Human bone marrow
c 266	12	80.0	324	22	AAK26456	CDNA encoding colo	c 339	12	80.0	473	22	AAI16368	Probe #6301 for ge
c 267	12	80.0	325	24	ABK45574	Human nervous syst	c 340	12	80.0	473	22	AAI39008	Probe #7694 used t
c 268	12	80.0	326	22	ABA12341	Human polynucleoti	c 341	12	80.0	473	22	ABS08041	Human genome-deriv
c 269	12	80.0	330	22	AAI87249	Human foetal liver	c 342	12	80.0	477	24	ABK62794	Rat sequence diffe
c 270	12	80.0	342	22	ABA59241	Probe #6452 for ge	c 343	12	80.0	486	24	ABK55193	Human colon cancer
c 271	12	80.0	342	22	ABA27986	Novel human diagno	c 344	12	80.0	490	23	ABV56974	Human prostate exp
c 272	12	80.0	342	22	AAK38882	Human brain expres	c 345	12	80.0	494	22	AAK33594	Human bone marrow
c 273	12	80.0	342	22	AAK07449	Human bone marrow	c 346	12	80.0	494	22	AAI39329	Probe #8015 used t
c 274	12	80.0	342	22	AAK33231	Probe #6308 for ge	c 347	12	80.0	494	24	ABS08485	Human genome-deriv
c 275	12	80.0	342	22	AAI16375	Probe #7712 used t	c 348	12	80.0	495	23	AAK585941	DNA encoding novel
c 276	12	80.0	342	22	AAI39026	Human genome-deriv	c 349	12	80.0	496	22	ABA57350	Human foetal liver
c 277	12	80.0	342	24	ABS08062	Human ORFX polynuc	c 350	12	80.0	496	22	AAK05386	Human brain expres
c 278	12	80.0	348	24	ABN21180	Human secreted exp	c 351	12	80.0	496	22	AAK30982	Human bone marrow
c 279	12	80.0	349	21	AAK44806	Human polynucleoti	c 352	12	80.0	496	22	AAI36894	Probe #5580 used t
c 280	12	80.0	354	22	AAI81113	SCA2 gene fragment	c 353	12	80.0	496	24	ABS05731	Human genome-deriv
c 281	12	80.0	355	19	AAV17224	Human nervous syst	c 354	12	80.0	506	22	AAK62150	Human foetal liver
c 282	12	80.0	355	22	ABA17378	Human nervous syst	c 355	12	80.0	506	22	AAK10469	Human brain expres
c 283	12	80.0	355	22	ABA17379	Human nervous syst	c 356	12	80.0	506	22	AAK36370	Human bone marrow
c 284	12	80.0	363	22	AAK65614	Novel human polynu	c 357	12	80.0	506	22	AAI42101	Probe #10787 used
c 285	12	80.0	366	22	AAK59344	Human immune/haema	c 358	12	80.0	512	22	ABA47826	Human breast cell
c 286	12	80.0	376	21	AAK19930	Human secreted pro	c 359	12	80.0	512	22	ABA65714	Human foetal liver
c 287	12	80.0	378	22	AAK77411	Human immune/haema	c 360	12	80.0	512	22	ABA32801	Probe #11267 for g
c 288	12	80.0	378	22	AAK60314	Human immune/haema	c 361	12	80.0	512	22	AAK14119	Human brain expres
c 289	12	80.0	379	22	AAK60314	Novel human polynu	c 362	12	80.0	512	22	AAK39860	Human bone marrow
c 290	12	80.0	381	22	AAK64655	Novel human polynu	c 363	12	80.0	512	22	AAI20671	Probe #10604 for g
c 291	12	80.0	386	21	AAK57268	Eucalyptus grandis	c 364	12	80.0	512	22	AAI45882	Probe #14568 used
c 292	12	80.0	388	22	AAI81345	Human polynucleoti	c 365	12	80.0	512	22	AAI06370	Probe #6361 used t
c 293	12	80.0	389	24	ABN76304	Human transcriptio	c 366	12	80.0	512	24	ABS13958	Human genome-deriv
c 294	12	80.0	397	21	AAK09645	Human secreted pro	c 367	12	80.0	516	19	AAV06551	SCA2 gene fragment
c 295	12	80.0	398	22	AAK75100	Human immune/haema	c 368	12	80.0	519	24	ABQ18838	Oligonucleotide fo
c 296	12	80.0	399	22	AAK66792	Novel human polynu	c 369	12	80.0	519	24	ABQ18839	Oligonucleotide fo
c 297	12	80.0	401	22	AAK96121	Human neuroregulin g	c 370	12	80.0	522	22	AAH33128	Human colon cancer
c 298	12	80.0	401	22	AAK97614	Human neuroregulin g	c 371	12	80.0	522	24	ABL89713	Human polynucleoti
c 299	12	80.0	403	24	ABN16862	Human ORFX polynuc	c 372	12	80.0	537	21	ABL15158	Trichoderma reesei
c 300	12	80.0	406	21	AAK43968	Human secreted exp	c 373	12	80.0	546	24	ABK55070	Human colon cancer
c 301	12	80.0	406	22	AAH89970	Human bone marrow	c 374	12	80.0	557	22	ABA60528	Human foetal liver

c 375	12	80.0	557	22	ABA28694	Probe #7160 for ge	448	12	80.0	839	22	AAI63352	Human kidney relat
c 376	12	80.0	557	22	AAK08809	Human brain expres	449	12	80.0	849	20	AX97676	Extended human sec
c 377	12	80.0	557	22	AAK34696	Human bone marrow	450	12	80.0	852	22	ABA89428	Escherichia coli p
c 378	12	80.0	557	22	AAI16811	Probe #6744 for ge	c 451	12	80.0	870	23	AS76112	DNA encoding novel
c 379	12	80.0	557	22	AAI40417	Probe #9103 used t	452	12	80.0	889	23	ABL56865	Plant resistance g
c 380	12	80.0	557	24	ABS09288	Human genome-deriv	453	12	80.0	895	21	AAF08172	Fusarium venenatum
c 381	12	80.0	558	24	ABQ17980	Oligonucleotide fo	c 454	12	80.0	895	23	AA578132	DNA encoding novel
c 382	12	80.0	558	24	ABQ17981	Oligonucleotide fo	455	12	80.0	899	24	ABL42277	Pancreatic tumour
c 383	12	80.0	559	22	AAH98842	Human EST-derived	456	12	80.0	910	22	ABA06989	Human pancreatic c
c 384	12	80.0	560	22	AAH13526	Human cDNA clone (	457	12	80.0	910	22	ABA088474	Human digestive sy
c 385	12	80.0	565	24	ABK79051	Bacillus clausii g	c 458	12	80.0	936	24	ABK73545	Bacillus lichenifo
c 386	12	80.0	576	23	AA568618	DNA encoding novel	c 459	12	80.0	965	22	AAH98528	Canine EST-derived
c 387	12	80.0	582	22	ABA4212	Human foetal liver	c 460	12	80.0	970	24	ABK74580	Bacillus lichenifo
c 388	12	80.0	582	22	ABA31358	Probe #9824 for ge	461	12	80.0	987	22	AAH22670	Mouse Bcl-G polype
c 389	12	80.0	582	22	AAK12692	Human brain expres	c 462	12	80.0	1001	21	AA527810	Arachidonic acid m
c 390	12	80.0	582	22	AAK38410	Human bone marrow	c 463	12	80.0	1012	22	ABA47193	Human breast cell
c 391	12	80.0	582	22	AAI19204	Probe #9137 for ge	c 464	12	80.0	1012	22	ABA65077	Human foetal liver
c 392	12	80.0	582	22	AAI44365	Probe #13051 used	c 465	12	80.0	1012	22	ABA32183	Probe #10649 for g
c 393	12	80.0	582	24	ABS12465	Human genome-deriv	c 466	12	80.0	1012	22	AAK13500	Human brain expres
c 394	12	80.0	582	24	ABN79151	Human transcriptio	c 467	12	80.0	1012	22	AAK39239	Human bone marrow
c 395	12	80.0	585	24	ABQ16892	Oligonucleotide fo	c 468	12	80.0	1012	22	AAI20049	Probe #9982 for ge
c 396	12	80.0	585	24	ABQ16893	Oligonucleotide fo	c 469	12	80.0	1012	22	AAI45247	Probe #13933 used
c 397	12	80.0	586	24	ABQ50528	Oligonucleotide fo	c 470	12	80.0	1012	22	AAI05756	Probe #5747 used t
c 398	12	80.0	586	24	ABQ50529	Oligonucleotide fo	c 471	12	80.0	1012	22	ABS13323	Human genome-deriv
c 399	12	80.0	594	21	AAA82223	N. meningitidis pa	c 472	12	80.0	1040	21	AA655525	Porcine BAC-PiGF2-
c 400	12	80.0	594	23	AA580695	DNA encoding novel	c 473	12	80.0	1046	23	AA582954	DNA encoding novel
c 401	12	80.0	595	22	ABA60317	Human foetal liver	c 474	12	80.0	1057	21	AAF13375	Aspergillus oryzae
c 402	12	80.0	595	22	ABA28576	Probe #7042 for ge	c 475	12	80.0	1074	19	AAV23874	Plant OMT enzyme D
c 403	12	80.0	595	22	AAK08597	Human brain expres	c 476	12	80.0	1074	20	AAZ06877	Pine O-methyl tran
c 404	12	80.0	595	22	AAK34479	Human bone marrow	c 477	12	80.0	1074	21	AA67961	Pinus radiata OMT
c 405	12	80.0	595	22	AAI16743	Probe #6676 for ge	c 478	12	80.0	1075	19	AAV23875	Plant OMT enzyme D
c 406	12	80.0	595	22	AAI40200	Probe #8886 used t	c 479	12	80.0	1075	20	AAZ06878	Pinus O-methyl tran
c 407	12	80.0	595	24	ABS09136	Human genome-deriv	c 480	12	80.0	1075	21	AA607962	Pinus radiata OMT
c 408	12	80.0	618	23	ABV52614	Human prostate exp	c 481	12	80.0	1089	22	AAZ07902	Human secreted pro
c 409	12	80.0	621	21	AA280330	Human colon cancer	c 482	12	80.0	1106	24	ABL49511	Sequence #113 used
c 410	12	80.0	623	19	AAV17229	SCA2 gene fragment	c 483	12	80.0	1106	24	ABK30706	Plant dwarfing/stu
c 411	12	80.0	631	23	ABV17229	Human prostate exp	c 484	12	80.0	1136	21	AA47827	Arabidopsis thalia
c 412	12	80.0	638	22	AAH04944	Human cDNA clone (	c 485	12	80.0	1149	24	AA55807	S. lavendulae Mth
c 413	12	80.0	638	24	ABQ22262	Oligonucleotide fo	c 486	12	80.0	1169	24	ABQ68781	Listeria monocytog
c 414	12	80.0	638	24	ABQ22262	Oligonucleotide fo	c 487	12	80.0	1189	21	AAAL3953	Resveratrol syntha
c 415	12	80.0	642	23	AA55185	DNA encoding novel	c 488	12	80.0	1192	24	ABQ68954	Listeria monocytog
c 416	12	80.0	642	23	AA583320	DNA encoding novel	c 489	12	80.0	1197	23	AA565911	DNA encoding novel
c 417	12	80.0	680	22	AA817163	Human ion channel-	c 490	12	80.0	1203	18	AA764815	Tumour suppressor
c 418	12	80.0	682	24	ABQ44992	Oligonucleotide fo	c 491	12	80.0	1208	22	AA32760	Human secreted pro
c 419	12	80.0	682	24	ABQ44993	Oligonucleotide fo	c 492	12	80.0	1235	24	AA515005	Rice 4-CL-specific
c 420	12	80.0	685	22	AA586047	CABF-1 partial seq	c 493	12	80.0	1242	22	AAI19045	Human excretory re
c 421	12	80.0	686	22	AA531375	Human cDNA encodin	c 494	12	80.0	1242	22	AAI63395	Human kidney relat
c 422	12	80.0	686	24	ABQ66699	Human polynucleoti	c 495	12	80.0	1244	24	ABK94958	Human novel polynu
c 423	12	80.0	695	21	AA801719	N. meningitidis pa	c 496	12	80.0	1250	9	AAH80316	Transcription cont
c 424	12	80.0	704	24	ABQ36594	Oligonucleotide fo	c 497	12	80.0	1260	16	AA700618	Megakaryocyte kina
c 425	12	80.0	704	24	ABQ36595	Oligonucleotide fo	c 498	12	80.0	1273	22	AAK60835	Human immune/haema
c 426	12	80.0	719	24	ABK53743	Human eosinophil-m	c 499	12	80.0	1274	19	AAV34215	Human secreted pro
c 427	12	80.0	729	23	AA555912	DNA encoding novel	c 500	12	80.0	1282	20	AAV84597	Human secreted pro
c 428	12	80.0	732	15	AAQ70304	Mouse NF-Atp cDNA	c 501	12	80.0	1282	22	ABA83380	Human secreted pro
c 429	12	80.0	732	15	AAQ70314	Human NF-Atp cDNA	c 502	12	80.0	1296	19	AAV34269	Human secreted pro
c 430	12	80.0	741	22	AAQ60771	Human immune/haema	c 503	12	80.0	1327	24	ABQ68452	Listeria monocytog
c 431	12	80.0	742	22	AAH01395	Human reproductive	c 504	12	80.0	1343	21	AAF16344	Human prostate can
c 432	12	80.0	742	22	AAH01395	Human colon cancer	c 505	12	80.0	1347	22	AAH86035	CABF-1 coding sequ
c 433	12	80.0	742	23	ABL96848	Human testicular a	c 506	12	80.0	1352	22	AAH46065	Sigma-34 factor 9
c 434	12	80.0	747	23	AA582292	DNA encoding novel	c 507	12	80.0	1389	23	AA559778	Propionibacterium
c 435	12	80.0	748	20	AAZ00430	Human secreted pro	c 508	12	80.0	1424	22	AAK78381	Human immune/haema
c 436	12	80.0	753	22	AA580395	Nucleotide sequenc	c 509	12	80.0	1449	22	AA544882	Human contig polyn
c 437	12	80.0	761	20	AA216588	Human gene express	c 510	12	80.0	1458	23	ABL27923	Drosophila melanog
c 438	12	80.0	768	22	AAK80034	Human immune/haema	c 511	12	80.0	1459	23	AA573909	DNA encoding novel
c 439	12	80.0	768	22	AAK86147	Human immune/haema	c 512	12	80.0	1474	15	AAQ70311	Mouse NF-Atp. Mus
c 440	12	80.0	776	22	AAI17954	Human breast cance	c 513	12	80.0	1486	21	AAF18228	Lung cancer associ
c 441	12	80.0	783	22	AAU23724	Human breast cance	c 514	12	80.0	1492	24	ABK30508	Human glioma-associ
c 442	12	80.0	784	21	AAAO2448	Human colon cancer	c 515	12	80.0	1493	19	AAV27207	cDNA clone ethb001
c 443	12	80.0	788	22	AAH07874	Human cDNA clone (	c 516	12	80.0	1494	23	ABL28079	Drosophila melanog
c 444	12	80.0	791	24	AA520988	DNA sequence #19 r	c 517	12	80.0	1522	23	AA590487	DNA encoding novel
c 445	12	80.0	815	20	AA216195	Human gene express	c 518	12	80.0	1539	23	ABV23163	Human prostate exp
c 446	12	80.0	834	22	AA580394	Nucleotide sequenc	c 519	12	80.0	1539	23	ABV29003	Human prostate exp
c 447	12	80.0	839	22	AA199002	Human excretory re	c 520	12	80.0	1551	21	AAZ35757	Strongylocentrotus



521	12	80.0	1561	21	AAF21032	Human low adenosin	c 594	12	80.0	2545	22	AAS63205	Human purified sec
522	12	80.0	1561	21	AAA34910	Human adenosine re	595	12	80.0	2549	22	AAH15872	Human cDNA sequenc
c 523	12	80.0	1584	24	ABK72940	Bacillus lichenifo	c 596	12	80.0	2563	19	AAV28617	Nucleotide sequenc
c 524	12	80.0	1608	22	AAS23120	DNA encoding novel	597	12	80.0	2576	22	RAI59194	Human polynucleoti
c 525	12	80.0	1613	23	AAS94510	DNA encoding novel	598	12	80.0	2590	22	AAH99062	Murine muscle ring
526	12	80.0	1622	24	ABK09766	Human ovarian tumo	c 599	12	80.0	2642	22	AAH99048	Human EST-derived
c 527	12	80.0	1634	22	AAF59613	Human cell cycle a	c 600	12	80.0	2656	22	AAH16132	Human cDNA sequenc
c 528	12	80.0	1643	22	AAF54825	Rice glutamate 1-s	601	12	80.0	2675	15	AAQ70312	Human NF-ATP. Hom
529	12	80.0	1650	21	AAZ90020	Human phenylalanin	602	12	80.0	2679	24	ABN95721	Gene #2219 used to
c 530	12	80.0	1650	23	AAZ67603	DNA encoding novel	c 603	12	80.0	2689	22	AAK78265	Human immune/haema
c 531	12	80.0	1650	23	AAZ67603	DNA encoding novel	c 604	12	80.0	2714	22	AAK78265	Rat p-HYDE coding
532	12	80.0	1652	22	AAZ67603	Human FLEXHT-3 nuc	c 605	12	80.0	2723	21	AAZ67603	Human ORF for pote
c 533	12	80.0	1667	22	AAZ67603	Human cDNA encodin	c 606	12	80.0	2753	21	AAZ67603	Human ORF ORF2359
c 534	12	80.0	1667	24	ABK66538	Human polynucleoti	c 607	12	80.0	2806	24	ABA94778	Human BSTP-CAD pol
c 535	12	80.0	1672	24	ABK13773	DNA encoding huma	c 608	12	80.0	2807	22	AAK78265	Human LTC4 recepto
c 536	12	80.0	1690	22	AAH01056	Streptococcus pneu	c 609	12	80.0	2863	22	AAK78265	Human secreted pro
c 537	12	80.0	1715	24	ABK63724	Rat sequence diffe	c 610	12	80.0	2872	22	AAI60426	Human polynucleoti
538	12	80.0	1724	20	AAZ20442	Human secreted pro	c 611	12	80.0	2895	22	AAK78265	Human immune/haema
c 539	12	80.0	1735	21	AAZ77448	Human ORF ORF3003	612	12	80.0	2920	23	AAS87293	DNA encoding novel
540	12	80.0	1746	22	AAI58640	Human polynucleoti	613	12	80.0	2957	22	AAH14691	Human cDNA sequenc
541	12	80.0	1756	21	AAZ98993	Human pancreatic c	c 614	12	80.0	2969	24	ABN85026	Murine Tumour Supp
542	12	80.0	1761	20	AAZ20412	Human secreted pro	c 615	12	80.0	2980	6	AAZ50139	Sequence of Hepati
c 543	12	80.0	1776	23	AAZ74532	DNA encoding novel	c 616	12	80.0	2980	6	AAZ50139	Partial sequence o
c 544	12	80.0	1777	23	AAZ74532	Canine IgA gene.	617	12	80.0	2983	19	AAZ69281	Mouse chromodomain
c 545	12	80.0	1789	17	AAZ29825	Human polynucleoti	618	12	80.0	2998	21	AAZ21180	Human low adenosin
546	12	80.0	1820	22	AAI60980	Human cDNA sequenc	619	12	80.0	3063	23	AAZ35058	Human adenosine re
c 547	12	80.0	1834	22	AAH18015	DNA encoding novel	c 620	12	80.0	3063	23	AAZ35058	DNA encoding novel
c 548	12	80.0	1848	23	AAZ90056	Heat resistant car	c 621	12	80.0	3097	19	AAV19609	Homo sapiens EPCR
c 549	12	80.0	1860	13	AAZ26728	C glutamicum codin	622	12	80.0	3113	22	AAH02892	Human reproductive
c 550	12	80.0	1866	22	AAH67164	Nuclear matrix-ass	c 623	12	80.0	3125	22	AAH17859	Human cDNA sequenc
551	12	80.0	1909	20	AAH84356	Human EST-derived	624	12	80.0	3160	24	ABK84122	Human cDNA differe
c 552	12	80.0	1909	22	AAH98561	AML 1 gene. Homo	c 625	12	80.0	3262	21	AAAI6623	Human secreted pro
553	12	80.0	1912	14	AAQ34443	Human polynucleoti	c 626	12	80.0	3343	22	AAI60763	Human polynucleoti
554	12	80.0	1922	22	AAI93648	Human cDNA sequenc	627	12	80.0	3360	19	AAV19608	Mus musculus EPCR
555	12	80.0	1934	22	AAH16761	Human cDNA sequenc	c 628	12	80.0	3372	9	AAZ80755	Encodes all HAV st
c 556	12	80.0	1941	22	AAH13893	Human cancer cell	629	12	80.0	3380	24	ABK15372	DNA encoding novel
557	12	80.0	1949	24	AAI45652	Human cancer cell	c 630	12	80.0	3394	18	AAZ84484	A. oryzae pacC (Sp
c 558	12	80.0	1949	24	AAI45653	Human Her-2/neu ov	c 631	12	80.0	3394	24	AAZ84484	Drosophila melanog
559	12	80.0	1981	22	AAZ04172	A. oryzae pacC (No	c 632	12	80.0	3394	24	AAZ84484	Human alpha-1 coll
560	12	80.0	1989	24	ABL41076	Human polynucleoti	c 633	12	80.0	3399	24	ABL41071	Human alpha-1 coll
c 561	12	80.0	2002	22	AAI58794	Human polynucleoti	c 634	12	80.0	3402	23	AAZ88989	Gene #2178 used to
c 562	12	80.0	2013	24	ABK49349	RNA polymerase II	c 635	12	80.0	3402	23	AAZ88989	A. oryzae pacC (No
c 563	12	80.0	2016	22	AAK89499	Human digestive sy	c 636	12	80.0	3414	24	ABL41081	DNA encoding novel
c 564	12	80.0	2020	14	AAQ40092	PHD1 gene. Saccha	c 637	12	80.0	3458	23	ABL27922	Drosophila melanog
565	12	80.0	2040	24	ABQ54224	Human ovarian anti	c 638	12	80.0	3478	17	AAZ36866	Human transcriptio
c 566	12	80.0	2057	22	AAZ72803	Secreted protein g	c 639	12	80.0	3483	22	AAH62757	Shrimp white spot
c 567	12	80.0	2065	23	AAZ73478	DNA encoding novel	c 640	12	80.0	3512	20	AAZ59396	Mouse topoisomeras
c 568	12	80.0	2067	21	AAZ59065	Human secreted pro	641	12	80.0	3512	24	ABI99291	Mouse ischaemic co
569	12	80.0	2084	21	AAZ76364	Human ORF ORF1919	c 642	12	80.0	3516	19	AAV71082	Green fluorescent
c 570	12	80.0	2087	21	AAZ77154	Human ORF ORF2709	643	12	80.0	3526	21	AAZ77511	Human ORF ORF3066
c 571	12	80.0	2103	22	AAZ79464	Human immune/haema	c 644	12	80.0	3546	19	AAV71083	NFAT1-green fluore
572	12	80.0	2108	22	AAI60580	Human polynucleoti	c 645	12	80.0	3616	20	AAV73924	Human SAHH DNA #1
573	12	80.0	2127	17	AAI12461	Human K+ channel 1	646	12	80.0	3617	22	AAI99001	Human excretory re
c 574	12	80.0	2127	19	AAV04873	DNA sequence of t	c 647	12	80.0	3617	22	AAI99001	Human kidney relat
c 575	12	80.0	2137	22	AAH15653	Human cDNA sequenc	c 648	12	80.0	3634	23	ABV23195	Human prostate exp
c 576	12	80.0	2152	22	ABAI5445	Human nervous syst	c 649	12	80.0	3634	23	ABV29032	Human prostate exp
c 577	12	80.0	2211	24	ABK12859	DNA encoding huma	c 650	12	80.0	3656	17	AAZ36751	VLDL receptor gene
c 578	12	80.0	2238	23	AAZ71124	DNA encoding novel	c 651	12	80.0	3741	22	AAI99573	Human expressed po
c 579	12	80.0	2259	23	AAZ79424	DNA encoding novel	c 652	12	80.0	3747	23	ABK43741	DNA encoding novel
c 580	12	80.0	2310	22	AAZ46734	Tumour suppressor	c 653	12	80.0	3799	23	ABL20995	Drosophila melanog
c 581	12	80.0	2323	22	AAH75165	Nucleotide sequenc	c 654	12	80.0	3885	22	AAZ89169	ADRSVPHYDE region
c 582	12	80.0	2356	11	AAZ80140	Human X chromosome	655	12	80.0	3912	22	AAZ89169	Human late stage o
583	12	80.0	2383	21	AAZ96495	DNA encoding a hu	c 656	12	80.0	3929	22	ABL26450	Human breast cance
c 584	12	80.0	2387	22	AAH16135	Human cDNA sequenc	c 657	12	80.0	4112	23	ABL08835	Drosophila melanog
c 585	12	80.0	2407	23	AAZ68797	DNA encoding novel	c 658	12	80.0	4152	21	AAZ15924	Human prostate can
c 586	12	80.0	2415	22	AAH73802	Phosphatidyl trans	c 659	12	80.0	4184	23	ABL20999	Drosophila melanog
587	12	80.0	2448	18	AAZ91639	Human phenylalanin	660	12	80.0	4200	18	AAZ70999	Spinocerebellar at
c 588	12	80.0	2448	20	AAZ30664	Human phenylalanin	c 661	12	80.0	4201	24	ABK83757	Human cDNA differe
c 589	12	80.0	2467	22	AAZ94847	Human full-length	c 662	12	80.0	4277	23	ABL20997	Drosophila melanog
c 590	12	80.0	2512	23	AAZ83556	DNA encoding novel	c 663	12	80.0	4278	23	AAZ87531	DNA encoding novel
591	12	80.0	2518	18	AAZ90702	RD114 env gene. S	c 664	12	80.0	4367	23	AAZ30270	Gene causative of
c 592	12	80.0	2523	12	AAQ12712	Phenylalanine hydr	665	12	80.0	4434	23	ABL16404	Drosophila melanog
c 593	12	80.0	2539	24	ABI99857	Mouse ischaemic co	666	12	80.0	4481	19	AAZ06552	Human SCA2 cDNA in
											20	AAZ23428	Human SCA2 DNA. H

c 567	12	80.0	4551	24	ABN05301	Human collagen XVI	c 740	12	80.0	7802	24	ABL32765	Human immune syste
c 568	12	80.0	4620	24	ABK30161	Human GLI1 genomic	c 741	12	80.0	7802	24	ABK28184	DNA transcripction
c 569	12	80.0	4875	24	ABQ54955	Human ovarian anti	c 742	12	80.0	7911	22	AAS36238	Human cardiovascular
c 570	12	80.0	4881	24	AAD23738	Maize streak gemin	c 743	12	80.0	7911	22	AL03223	Human reproductive
c 571	12	80.0	4961	24	AAD23740	Maize streak gemin	c 744	12	80.0	7938	23	ABL04780	Drosophila melanog
c 572	12	80.0	5044	23	ABL03142	Drosophila melanog	c 745	12	80.0	8000	23	ABL07372	Drosophila melanog
c 573	12	80.0	5174	20	AAV65142	Thrichia sp. B82	c 746	12	80.0	8043	24	AAD23742	Maize streak gemin
c 574	12	80.0	5212	9	AAH80317	Transcription cont	c 747	12	80.0	8246	22	AAD23742	Maize streak gemin
c 575	12	80.0	5216	20	AAH07548	PKS90 TIR coupling	c 748	12	80.0	8526	22	ABA18356	Human nervous syst
c 576	12	80.0	5227	22	ABA20781	Human nervous syst	c 749	12	80.0	8939	22	ABA15471	Human nervous syst
c 577	12	80.0	5230	20	AAH07549	pPREX1 mutant beta	c 750	12	80.0	8939	22	ABA16243	Human nervous syst
c 578	12	80.0	5230	21	AAA15041	Nucleotide sequenc	c 751	12	80.0	8939	22	ABA18915	Human nervous syst
c 579	12	80.0	5231	20	AAH07550	pPREX1A mutant bet	c 752	12	80.0	8965	22	AAK79591	Human immune/haema
c 580	12	80.0	5235	22	ABA20782	Human nervous syst	c 753	12	80.0	9121	21	AAK79591	Human immune/haema
c 581	12	80.0	5271	20	AAH20505	Polynucleotide seq	c 754	12	80.0	9202	8	AAH70608	Human ORFX ORF1956
c 582	12	80.0	5281	22	AAH04261	Human reproductive	c 755	12	80.0	9289	22	AAK90960	VISNA sheep lentiv
c 583	12	80.0	5288	22	AAK52070	Human polynucleoti	c 756	12	80.0	9289	22	AAK90960	Human digestive sy
c 584	12	80.0	5292	21	AAH21374	Human low adenosin	c 757	12	80.0	9289	22	AAH31995	Human liver associ
c 585	12	80.0	5292	21	AAH35252	Human adenosine re	c 758	12	80.0	9401	22	ABA08648	Human liver antige
c 586	12	80.0	5391	24	ABK39938	Human chemically p	c 759	12	80.0	9402	22	AAK46672	Human FLAMINGO 1 h
c 587	12	80.0	5391	24	ABL32242	Human immune syste	c 760	12	80.0	9439	19	AAV69284	Tumour suppressor
c 588	12	80.0	5408	20	AAH77720	Human collagen 18	c 761	12	80.0	9592	17	AAK36752	Human variably cha
c 589	12	80.0	5448	22	AAH78267	Human immune/haema	c 762	12	80.0	9592	17	AAK36752	Adenovirus vector
c 590	12	80.0	5484	24	ABN59750	Human immune coding	c 763	12	80.0	9751	22	AAH18386	Recombinant viral
c 591	12	80.0	5497	22	AAH29646	Novel human coding	c 764	12	80.0	9751	22	AAH18386	Recombinant viral
c 592	12	80.0	5559	20	AAH02982	Human IL-1ra BAC c	c 765	12	80.0	10695	22	AAK65420	FIV-Oma3 recombina
c 593	12	80.0	5586	24	ABL32649	Human immune syste	c 766	12	80.0	10766	22	AAK39895	Human immune/haema
c 594	12	80.0	5704	22	AAH03350	Human reproductive	c 767	12	80.0	10766	22	AAK39895	Genomic sequence #
c 595	12	80.0	5736	22	AAH04572	Human reproductive	c 768	12	80.0	10872	24	ABL70336	Human digestive sy
c 596	12	80.0	5736	22	AAH05108	Human reproductive	c 769	12	80.0	10872	24	AAK31389	Chemically treated
c 597	12	80.0	5736	23	ABL97495	Human reproductive	c 770	12	80.0	11172	22	AAH41188	Human gene regulat
c 598	12	80.0	5736	23	ABL98000	Human testicular a	c 771	12	80.0	11301	22	AAK71591	Signal transductio
c 599	12	80.0	5770	21	AAH15043	Human testicular a	c 772	12	80.0	11330	23	AAH59544	Murine oligonucleo
c 600	12	80.0	5819	22	AAK73716	Nucleotide sequenc	c 773	12	80.0	11982	23	AAH59544	Human immune/haema
c 601	12	80.0	5819	22	AAK73717	Human immune/haema	c 774	12	80.0	12020	23	ABL20994	Propionibacterium
c 602	12	80.0	5819	22	AAK77589	Human immune/haema	c 775	12	80.0	12020	23	ABL20994	Drosophila melanog
c 603	12	80.0	5819	22	AAK77592	Human immune/haema	c 776	12	80.0	12047	23	ABL20998	Drosophila melanog
c 604	12	80.0	5865	18	AAH90692	Plasmid FBDELPRDSA	c 777	12	80.0	12308	23	AAH23451	Human lung tumour
c 605	12	80.0	5870	21	AAH15044	Nucleotide sequenc	c 778	12	80.0	12309	22	AAK89483	Human digestive sy
c 606	12	80.0	5906	21	AAH15042	Nucleotide sequenc	c 779	12	80.0	12328	22	AAK90834	Human immune/haema
c 607	12	80.0	5954	21	AAH76439	Human ORFX ORF1994	c 780	12	80.0	12775	23	AAK79156	Human immune/haema
c 608	12	80.0	6109	23	AAH78667	Murine Col5a3 cDNA	c 781	12	80.0	12881	22	AAK85861	Drosophila melanog
c 609	12	80.0	6161	23	AAH12556	Drosophila melanog	c 782	12	80.0	13123	22	AAH04954	Human immune/haema
c 610	12	80.0	6167	22	AAS45337	Chemically pretrea	c 783	12	80.0	13123	23	ABL97848	Human reproductive
c 611	12	80.0	6167	24	ABL70194	Chemically treated	c 784	12	80.0	13189	22	AAH06063	Human testicular a
c 612	12	80.0	6167	24	ABL32643	Human immune syste	c 785	12	80.0	13189	23	ABL98628	Human reproductive
c 613	12	80.0	6167	24	AAH61152	Human gene regulat	c 786	12	80.0	13202	23	ABL13830	Human testicular a
c 614	12	80.0	6167	24	ABK28172	DNA transcripction	c 787	12	80.0	13371	22	AAH199114	Drosophila melanog
c 615	12	80.0	6211	24	ABL32806	Human immune syste	c 788	12	80.0	13371	22	AAH199114	Human excretory re
c 616	12	80.0	6212	21	AAH21375	Human low adenosin	c 789	12	80.0	13596	23	ABL02138	Human kidney relat
c 617	12	80.0	6212	21	AAH35253	Human adenosine re	c 790	12	80.0	14147	22	AAS46743	Drosophila melanog
c 618	12	80.0	6228	23	ABL11144	Drosophila melanog	c 791	12	80.0	14147	24	ABK33955	Tumour suppressor
c 619	12	80.0	6309	24	AAD23741	Maize streak gemin	c 792	12	80.0	14148	24	ABK33955	Human DNA for stag
c 620	12	80.0	6314	22	AAK90962	Human digestive sy	c 793	12	80.0	14160	22	AAK65583	Human immune/haema
c 621	12	80.0	6314	22	AAH31997	Human liver associ	c 794	12	80.0	14301	23	AAH82709	Human immune/haema
c 622	12	80.0	6314	24	ABN90352	Human liver associ	c 795	12	80.0	14452	23	AAH22986	DNA encoding novel
c 623	12	80.0	6324	24	ABK31543	Signal transductio	c 796	12	80.0	14452	23	ABV22986	Human prostate exp
c 624	12	80.0	6368	22	AAK79592	Human immune/haema	c 797	12	80.0	14456	23	ABV24304	Human prostate exp
c 625	12	80.0	6638	22	AAK83770	Human immune/haema	c 798	12	80.0	14458	23	ABL10220	Human prostate exp
c 626	12	80.0	6804	23	ABL13824	Drosophila melanog	c 799	12	80.0	14800	22	AAH06039	Drosophila melanog
c 627	12	80.0	6898	24	ABN80223	Human chemically m	c 800	12	80.0	15512	19	AAH59470	Angiotensin conver
c 628	12	80.0	6911	22	AAK69352	Human immune/haema	c 801	12	80.0	15512	19	AAH59470	Human ryanodin rec
c 629	12	80.0	6911	22	AAK82578	Human immune/haema	c 802	12	80.0	15662	23	AAH76501	DNA encoding novel
c 630	12	80.0	7236	22	AAK64793	Human immune/haema	c 803	12	80.0	15662	23	ABL13832	Drosophila melanog
c 631	12	80.0	7404	24	AAD23743	Maize streak gemin	c 804	12	80.0	15820	23	AAH87533	DNA encoding novel
c 632	12	80.0	7408	24	AAH47851	Murine basic helix	c 805	12	80.0	16271	22	ABA19209	Human nervous syst
c 633	12	80.0	7408	24	ABN83211	Mouse transcriptio	c 806	12	80.0	16271	22	ABA19210	Human nervous syst
c 634	12	80.0	7482	22	AAK66961	Human immune/haema	c 807	12	80.0	16676	22	AAK68313	Human immune/haema
c 635	12	80.0	7581	23	ABL10234	Drosophila melanog	c 808	12	80.0	17069	21	AAH21185	Human low adenosin
c 636	12	80.0	7661	22	AAH16545	Human novel protei	c 809	12	80.0	17069	21	AAH21185	Human adenosine re
c 637	12	80.0	7661	22	AAH162954	Human genomic DNA	c 810	12	80.0	17123	22	AAK86738	Human immune/haema
c 638	12	80.0	7661	22	AAH162954	Human polynucleoti	c 811	12	80.0	17150	22	AAH82982	Human DNA methyltr
c 639	12	80.0	7802	22	AAH45351	Chemically pretrea	c 812	12	80.0	17583	22	AAK89484	Human digestive sy
c 640	12	80.0	7802	22	AAH45351	Chemically pretrea	c 813	12	80.0	17865	22	AAK90961	Human digestive sy

813	12	80.0	17865	22	AAS31996	Human liver associ	c 886	12	80.0	160271	22	AAS04858	Human chromosome 1
814	12	80.0	17865	24	ABN90351	Human liver antige	c 887	12	80.0	160271	22	AAS04864	Human chromosome 1
815	12	80.0	18073	20	AVB83948	Bacterial artifici	c 888	12	80.0	160271	22	AAS06667	Human chromosome 1
c 816	12	80.0	18664	22	AAK65421	Human immune/haema	c 889	12	80.0	160271	22	AAH40997	160kb fragment of
c 817	12	80.0	18664	22	AAK84438	Human immune/haema	c 890	12	80.0	160271	22	AAH23764	Human chromosome 1
818	12	80.0	19062	21	AAF21280	Human low adenosin	c 891	12	80.0	160271	22	AAF85116	Nucleotide sequenc
819	12	80.0	19186	20	AAK20620	Polynucleotide seq	c 892	12	80.0	198161	24	ABK83564	Human cDNA differe
820	12	80.0	19334	22	AAS36443	Human cardiovascular	c 893	12	80.0	213251	24	ABQ67193	Listeria innocua c
c 821	12	80.0	19345	22	AAS36444	Human cardiovascular	c 894	12	80.0	235033	19	AAV57926	Hereditary haemoch
c 822	12	80.0	19559	24	ABL32766	Human immune syste	c 895	12	80.0	302250	24	ABL67703	Oesophagus cancer
c 823	12	80.0	19738	23	ABL20992	Drosophila melanog	c 896	12	80.0	305107	22	AAH62689	Shrimp white spot
c 824	12	80.0	19942	22	AAK87416	Human immune/haema	c 897	12	80.0	349980	21	AAF21610	Neisseria meningit
c 825	12	80.0	20155	23	ABL13688	Drosophila melanog	c 898	12	80.0	349980	22	AAH41224	Pyrococcus abyssi
826	12	80.0	20510	23	ABL19710	Drosophila melanog	c 899	12	80.0	349980	22	AAH68530	C glutamicum codin
827	12	80.0	20775	24	AAK47852	Murine basic helix	900	12	80.0	349980	22	AAH68531	C glutamicum codin
828	12	80.0	20775	24	ABN83212	Mouse transcriptio	901	12	80.0	349980	22	AAH68532	C glutamicum codin
c 829	12	80.0	20829	23	ABL14502	Drosophila melanog	902	12	80.0	349980	22	AAH68533	C glutamicum codin
c 830	12	80.0	20933	24	ABQ67124	Human angiogenesis	c 903	12	80.0	611590	21	AAF22303	Arabidopsis thalia
831	12	80.0	21010	22	AAK05888	Human reproductive	c 904	12	80.0	1437668	21	AAH81490	N. meningitidis B
832	12	80.0	21010	22	AAK89247	Human digestive sy	905	12	80.0	3011208	24	ABQ69245	Listeria innocua D
833	12	80.0	21010	23	ABL98452	Human testicular a	c 906	11	73.3	13	23	ABH56156	Oligonucleotide SE
834	12	80.0	21024	22	AAK05989	Human reproductive	c 907	11	73.3	13	23	ABH56157	Oligonucleotide SE
835	12	80.0	21024	22	AAK89248	Human digestive sy	c 908	11	73.3	19	21	AAH21545	Fas ligand promote
836	12	80.0	21024	23	ABL98453	Human testicular a	c 909	11	73.3	20	20	AAZ06144	PCR primer used to
837	12	80.0	21729	23	ABL06154	Drosophila melanog	910	11	73.3	20	24	ABL59023	Nucleotide sequenc
c 838	12	80.0	23142	21	AAK35158	Human adenosine re	c 911	11	73.3	20	24	ABK47106	Mouse Ots2-G2 reve
c 839	12	80.0	23532	21	AAK81455	N. meningitidis pa	c 912	11	73.3	23	22	AAH39057	SNP specific upper
840	12	80.0	25325	22	ABK19375	Human nervous syst	c 913	11	73.3	27	12	AAQ14480	Consensus tandem r
c 841	12	80.0	25975	22	AAK04955	Human reproductive	914	11	73.3	27	12	AAQ14496	Tandem repeat vari
c 842	12	80.0	25975	23	ABL97849	Human testicular a	915	11	73.3	27	18	AAH68284	Human flt1 VEGF re
c 843	12	80.0	26668	24	ABL67771	Oesophagus cancer	916	11	73.3	29	20	AAA22249	Integrin subunit b
844	12	80.0	27423	23	ABL04268	Drosophila melanog	917	11	73.3	29	20	AAK33249	Primer for amplif
c 845	12	80.0	28444	24	ABK86948	Human glutathione	918	11	73.3	29	20	AAK18665	Human p53 gene PCR
846	12	80.0	29376	23	ABL08834	Drosophila melanog	919	11	73.3	29	21	AAK06694	Hammerhead ribozym
847	12	80.0	30013	22	ABL36932	Human musculoskele	c 920	11	73.3	29	21	AAA04353	Polymorphic fragme
c 848	12	80.0	30013	22	AAK41960	Genomic sequence #	c 921	11	73.3	30	22	AAK87641	Human acetylcholin
849	12	80.0	30352	22	AAS36268	Human cardiovascular	c 922	11	73.3	30	22	AAC90394	Acetylcholinestera
850	12	80.0	30417	21	AAF21282	Human low adenosin	c 923	11	73.3	32	19	AAV33214	Fibroblast growth
851	12	80.0	30417	21	AAK35160	Human adenosine re	c 924	11	73.3	32	22	AAC90675	Human FGF-13 PCR p
852	12	80.0	30568	22	AAK37486	Human musculoskele	c 925	11	73.3	33	22	AAK16982	Human peroxidase 1
853	12	80.0	32189	22	AAS30115	Human lung antigen	c 926	11	73.3	35	22	AAC90683	Human FGF-13 PCR p
854	12	80.0	32196	22	ABK18857	Human nervous syst	c 927	11	73.3	40	21	AAZ96111	Polynucleotide seq
855	12	80.0	32221	22	AAS30113	Human lung antigen	c 928	11	73.3	41	22	AAI69984	Human peroxidase 1
856	12	80.0	32222	22	AAK34734	Human DNA for a no	c 929	11	73.3	41	22	AAI69985	Human peroxidase 1
857	12	80.0	32367	19	AAV35620	Human SHOX (short	c 930	11	73.3	49	20	AAK88488	Human MIP-1 beta p
c 858	12	80.0	33472	23	ABL19792	Drosophila melanog	c 931	11	73.3	50	22	AAH44831	Probe used to dete
c 859	12	80.0	36194	23	ABL20582	Drosophila melanog	c 932	11	73.3	50	23	ABL01061	Human SNP involvin
c 860	12	80.0	39328	24	ABL91800	Human lipase endot	c 933	11	73.3	51	22	AAK27148	Human SNP oligonuc
861	12	80.0	42519	22	AAK81318	Human immune/haema	c 934	11	73.3	51	22	AAK29389	Human SNP oligonuc
c 862	12	80.0	43795	21	AAZ92583	Human DA2 genomic	c 935	11	73.3	52	16	AAK5554	Human rela hairpin
863	12	80.0	50000	20	AAK23517	Human kidney amino	c 936	11	73.3	60	24	ABN39619	Human spliced tran
864	12	80.0	50000	24	AAK26400	Human glutamate re	c 937	11	73.3	60	24	ABN44563	Human spliced tran
865	12	80.0	50000	24	AAK26437	Human GRM3 gene fr	c 938	11	73.3	65	24	ABN56975	Mouse spliced tran
866	12	80.0	50849	24	AAK87883	Human glutathione	c 939	11	73.3	66	16	AAK02938	Human glucose-6-ph
c 867	12	80.0	53500	21	AAK55842	Complete nucleotid	940	11	73.3	68	15	AAQ65989	COL2A1 5'-primer (
c 868	12	80.0	53552	22	AAS13655	Genomic DNA sequen	c 941	11	73.3	74	22	AAC90685	Human FGF-13 PCR p
869	12	80.0	54548	21	AAZ45596	DNA sequence of th	c 942	11	73.3	74	22	AAC90692	Human FGF-13 PCR p
c 870	12	80.0	65608	24	ABL62910	Breast cancer rela	c 943	11	73.3	74	22	AAC90695	Human FGF-13 PCR p
c 871	12	80.0	65608	24	ABL64414	Stomach cancer rel	944	11	73.3	81	16	AAK06211	HIV-1 reverse tran
c 872	12	80.0	65608	24	ABL67668	Oesophagus cancer	945	11	73.3	81	21	AAK19610	Human secreted pro
c 873	12	80.0	74037	24	ABK94412	DNA encoding endot	946	11	73.3	87	21	AAK19478	Human secreted pro
874	12	80.0	83946	21	ABQ88101	Human osteoblast d	947	11	73.3	93	21	AAK29544	Human secreted pro
875	12	80.0	101786	21	AAK22293	BAC containing rep	c 948	11	73.3	96	18	AAK49246	HVR1 region of E2
c 876	12	80.0	107820	22	AAK16230	Human ATP-binding	949	11	73.3	96	20	AAV81027	De-immunised 340 v
c 877	12	80.0	112190	22	AAH44801	Human GPCR protein	950	11	73.3	104	20	AAH86705	Human single nucle
c 878	12	80.0	113515	22	ABL34175	Human immune syste	c 951	11	73.3	105	21	AAK81453	Chitin-binding apt
879	12	80.0	117574	24	AAK45288	Human immune syste	c 952	11	73.3	108	19	AAK10384	Human foetal po
c 880	12	80.0	117574	24	AAK45288	Human KCNB1 gene.	c 953	11	73.3	112	22	ABK76653	Human foetal liver
c 881	12	80.0	125910	21	AAK64370	Human KCNQ5 (KCN6q	c 954	11	73.3	112	22	ABK41158	Probe #19624 for g
882	12	80.0	134525	11	AAK04525	Total base sequenc	c 955	11	73.3	112	22	AAK25285	Human brain expres
c 883	12	80.0	134525	11	AAK04525	Total base sequenc	c 956	11	73.3	112	22	AAK51292	Human bone marrow
c 884	12	80.0	160271	22	AAK85750	Bipolar affective	c 957	11	73.3	112	22	AAI28302	Probe #18235 for g
c 885	12	80.0	160271	22	AAK85756	Human chromosome 1	c 958	11	73.3	112	22	AAI57348	Probe #26034 used

c 959 11 73.3 112 24 ABS24832  
 960 11 73.3 114 22 ABA75521  
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 963 11 73.3 114 22 AAK24095  
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 965 11 73.3 114 22 AAI27237  
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 968 11 73.3 118 21 AAC29550  
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 970 11 73.3 121 22 ABA77503  
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 973 11 73.3 135 22 ABA12275  
 974 11 73.3 135 22 AAL09214  
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 976 11 73.3 136 22 AAC90679  
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 983 11 73.3 153 22 AAK15609  
 984 11 73.3 153 22 AAI22087  
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 987 11 73.3 153 24 ABS15349  
 988 11 73.3 157 22 ABA75854  
 989 11 73.3 157 22 ABA40420  
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ALIGNMENTS

RESULT 1  
 AAH28085  
 ID AAH28085 standard; DNA; 15 BP.  
 XX  
 AC AAH28085;  
 XX  
 DT 05-SEP-2001 (first entry)  
 XX  
 DE Probe for human norepinephrine transporter gene A457P variant allele.  
 XX  
 KW Norepinephrine transporter; orthostatic intolerance; gene therapy;  
 KW mental illness; hypertension; heart disease; stimulant abuse; cocaine;  
 KW amphetamine abuse; probe; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200148246-A1.  
 PD 05-JUL-2001.  
 XX  
 PF 28-DEC-2000; 2000WO-US35491.  
 XX  
 PR 29-DEC-1999; 9905-0173682.  
 PR 11-JAN-2000; 2000US-0175456.  
 XX  
 RA (UYVA-) UNIV VANDERBILT.  
 XX

Robertson D, Blakely RD;  
 WPI; 2001-425681/45.  
 Screening for susceptibility to sub-optimal norepinephrine transporter,  
 particularly orthostatic intolerance in a subject by detecting a  
 polymorphism of norepinephrine transporter gene -  
 Claim 15; Page 69; 133pp; English.  
 The present sequence represents a probe for the A457P variant allele of  
 a human norepinephrine transporter gene. The specification a method  
 for screening for susceptibility to sub-optimal norepinephrine transporter  
 in a subject. The method comprises obtaining a biological sample from  
 the subject and detecting a polymorphism of a norepinephrine transporter  
 gene in the sample from the subject, the presence of the polymorphism  
 indicating the susceptibility of the subject to sub-optimal  
 norepinephrine transporter. The method is useful for screening for  
 susceptibility of a subject to orthostatic intolerance. Norepinephrine  
 transporter genes are useful for gene therapy for modulating  
 norepinephrine transporter in a target cell and treating susceptibility  
 to impaired norepinephrine transporter function, orthostatic intolerance  
 or other relevant diseases in humans and animals such as mental illness,  
 hypertension, heart disease, psycho stimulant abuse e.g. cocaine or  
 amphetamine abuse.  
 Sequence 15 BP; 0 A; 8 C; 1 G; 6 T; 0 other;  
 Query Match 100.0%; Score 15; DB 22; Length 15;  
 Best Local Similarity 100.0%; Pred No. 38;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CCTTCTCCCTGTT 15  
 Db 1 CCTTCTCCCTGTT 15  
 RESULT 2  
 AAC09241/c  
 ID AAC09241 standard; cDNA; 352 BP.  
 XX  
 AC AAC09241;  
 XX  
 DT 06-OCT-2000 (first entry)  
 XX  
 DE Human secreted protein 5' EST, SEQ ID NO: 13316.  
 XX  
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
 KW gene therapy; chromosome mapping; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1033401-A2.  
 PD 06-SEP-2000.  
 XX  
 PF 21-FEB-2000; 2000EP-0200610.  
 XX  
 PR 26-FEB-1999; 9905-0122487.  
 XX  
 PA (GEST ) GENSET.  
 XX  
 PI Dumas Milne Edwards J, Duclert A, Giordano J;  
 DR WPI; 2000-500381/45.  
 XX  
 PF New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
 obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for  
 diagnostic, forensic, gene therapy and chromosome mapping procedures -  
 Claim 1; SEQ ID 13316; 71pp + CD-ROM; English.  
 XX

CC The present sequence is one of a large number of 5' ESTs derived from  
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively  
 CC identified within the present sequence. The 5' ESTs were prepared from  
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST  
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)  
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA  
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences  
 CC derived from the 5' ends of mRNAs and even in those cases where longer  
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included.  
 CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be  
 CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used  
 CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.  
 CC They are used to obtain upstream regulatory sequences and to design  
 CC expression and secretion vectors.

XX  
 SQ Sequence 352 BP; 111 A; 73 C; 97 G; 69 T; 2 other;

Query Match 100.0%; Score 15; DB 21; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 33;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGTT 15  
 |||||

Db 149 CCTTCTCCCCCTGTT 135

RESULT 3

ABV50337

ID ABV50337 standard; cDNA; 445 BP.

XX  
 AC ABV50337;

XX  
 DT 17-SEP-2002 (first entry)

XX  
 DE Human prostate expression marker cDNA 50328.

XX  
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

XX  
 KW pharmacogenomic marker; gene; ss.

XX  
 OS Homo sapiens.

XX  
 PN WO200160860-A2.

XX  
 PD 23-AUG-2001.

XX  
 PF 20-FEB-2001; 2001WO-US05171.

XX  
 PR 17-FEB-2000; 2000US-183319P.

XX  
 PR 16-MAR-2000; 2000US-189862P.

XX  
 PR 25-MAY-2000; 2000US-207454P.

XX  
 PR 09-JUN-2000; 2000US-211314P.

XX  
 PR 18-JUL-2000; 2000US-219007P.

XX  
 PR 13-DEC-2000; 2000US-255281P.

XX  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX  
 PI Schlegel R, Endege WO, Monahan JE;

XX  
 WPI; 2001-662795/76.

XX  
 PT Novel isolated nucleic acid molecule associated with cancerous state of

XX  
 PT prostate cells and correlating with presence of prostate cancer, useful

XX  
 PT for detecting presence of prostate cancer, stage of prostate cancer

XX  
 PS Claim 1; Page 9798; 11750pp; English.

XX  
 CC The invention relates to an isolated nucleic acid molecule (I) comprising

CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the

CC specification or its complement. (I) is useful for:

CC (a) assessing whether a patient is afflicted with prostate cancer;

CC (b) monitoring the progression of prostate cancer in a patient;

CC (c) assessing the efficacy of a test compound to inhibit prostate

CC cancer in a patient;

CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer

CC in a patient;

CC (e) selecting a composition for inhibiting prostate cancer in a patient;

CC (f) assessing the prostate cell carcinogenic potential of a compound;

CC (g) determining whether prostate cancer has metastasized in a patient;

CC (h) assessing the aggressiveness or indolence of prostate cancer in a

CC patient;

CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX  
 SQ Sequence 445 BP; 109 A; 118 C; 109 G; 107 T; 2 other;

Query Match 100.0%; Score 15; DB 23; Length 445;  
 Best Local Similarity 100.0%; Pred. No. 32;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGTT 15  
 |||||

Db 370 CCTTCTCCCCCTGTT 384

RESULT 4

AAS66052

ID AAS66052 standard; cDNA; 549 BP.

XX  
 AC AAS66052;

XX  
 DT 13-FEB-2002 (first entry)

XX  
 DE DNA encoding novel human diagnostic protein #1856.

XX  
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX  
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX  
 OS Homo sapiens.

XX  
 PN WO200175067-A2.

XX  
 PD 11-OCT-2001.

XX  
 PF 30-MAR-2001; 2001WO-US08631.

XX  
 PR 31-MAR-2000; 2000US-0540217.

XX  
 PR 23-AUG-2000; 2000US-0649167.

XX  
 PA (HYSE-) HYSEQ INC.

XX  
 PI Drmanac RT, Liu C, Tang YT;

XX  
 WPI; 2001-639362/73.

XX  
 P-PSDB; ABG01865.

XX  
 PT New isolated polynucleotide and encoded polypeptides, useful in

XX  
 PT diagnostics, forensics, gene mapping, identification of mutations

XX  
 PT responsible for genetic disorders or other traits and to assess

XX  
 PT biodiversity

XX  
 PS Claim 1; SEQ ID No 1856; 103pp; English.

XX  
 CC The invention relates to isolated polynucleotide (I) and

XX  
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,

XX  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

XX  
 CC and gene mapping, and in recombinant production of (II). The

XX  
 CC polynucleotides are also used in diagnostics as expressed sequence tags

XX  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques

XX  
 CC to restore normal activity of (II) or to treat disease states involving

XX  
 CC (II). (II) is useful for generating antibodies against it, detecting or

XX  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as

XX  
 CC a food supplement. (II) and its binding partners are useful in medical

XX  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating

XX  
 CC disorders involving aberrant protein expression or biological activity.

XX  
 CC The polypeptide and polynucleotide sequences have applications in

XX  
 CC diagnostics, forensics, gene mapping, identification of mutations

XX  
 CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AAS64197-AAS94564 represent novel human  
CC diagnostic coding sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
CC  
XX  
SQ Sequence 549 BP; 114 A; 178 C; 140 G; 117 T; 0 other;

Query Match 100.0%; Score 15; DB 23; Length 549;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15  
|||||  
Db 423 CCTTCTCCCCCTGTT 437

RESULT 5  
AAH04051/c  
ID AAH04051 standard; cDNA; 827 BP.  
XX  
AC AAH04051;  
XX  
XX 26-JUN-2001 (first entry)  
XX  
XX Human cDNA clone (5'-primer) SEQ ID NO:886.  
XX  
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.  
XX Homo sapiens.  
XX EP1074617-A2.  
XX  
XX 07-FEB-2001.  
XX  
XX 28-JUL-2000; 2000EP-0116126.  
XX  
XX 29-JUL-1999; 99JP-0248036.  
XX  
XX 27-AUG-1999; 99JP-0300253.  
XX  
XX 11-JAN-2000; 2000JP-0118776.  
XX  
XX 02-MAY-2000; 2000JP-0183767.  
XX  
XX 09-JUN-2000; 2000JP-0241899.  
XX  
XX (HELI-) HELIX RES INST.  
XX  
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
XX WPI; 2001-318749/34.  
XX  
XX Primer sets for synthesizing polynucleotides, particularly the 5602  
XX full-length cDNAs defined in the specification, and for the detection  
XX and/or diagnosis of the abnormality of the proteins encoded by the  
XX full-length cDNAs -  
XX  
XX Claim 1; SEQ ID 886; 2537pp + CD ROM; English.  
XX  
XX The present invention describes primer sets for synthesizing 5602  
XX full-length cDNAs defined in the specification. Where a primer set  
XX comprises: (a) an oligo-dr primer and an oligonucleotide complementary  
XX to the complementary strand of a polynucleotide which comprises one of  
XX the 5602 nucleotide sequences defined in the specification, where the  
XX oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
XX of an oligonucleotide comprising a sequence complementary to the  
XX complementary strand of a polynucleotide which comprises a 5'-end  
XX sequence and an oligonucleotide comprising a sequence complementary to a  
XX polynucleotide which comprises a 3'-end sequence, where the  
XX oligonucleotide comprises at least 15 nucleotides and the combination  
XX of the 5'-end sequence/3'-end sequence is selected from those defined in  
XX the specification. The primer sets can be used in antisense therapy and  
XX in gene therapy. The primers are useful for synthesizing polynucleotides,  
XX particularly full-length cDNAs. The primers are also useful for the

CC detection and/or diagnosis of the abnormality of the proteins encoded by  
CC the full-length cDNAs. The primers allow obtaining of the full-length  
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to  
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632  
CC represent oligonucleotides, all of which are used in the exemplification  
CC of the present invention.  
XX  
SQ Sequence 827 BP; 264 A; 138 C; 199 G; 223 T; 3 other;

Query Match 100.0%; Score 15; DB 22; Length 827;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15  
|||||  
Db 123 CCTTCTCCCCCTGTT 109

RESULT 6  
AAH15437/c  
ID AAH15437 standard; cDNA; 1689 BP.  
XX  
AC AAH15437;  
XX  
XX 26-JUN-2001 (first entry)  
XX  
XX Human cDNA sequence SEQ ID NO:13660.  
XX  
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.  
XX Homo sapiens.  
XX EP1074617-A2.  
XX  
XX 07-FEB-2001.  
XX  
XX 28-JUL-2000; 2000EP-0116126.  
XX  
XX 29-JUL-1999; 99JP-0248036.  
XX  
XX 27-AUG-1999; 99JP-0300253.  
XX  
XX 11-JAN-2000; 2000JP-0118776.  
XX  
XX 02-MAY-2000; 2000JP-0183767.  
XX  
XX 09-JUN-2000; 2000JP-0241899.  
XX  
XX (HELI-) HELIX RES INST.  
XX  
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
XX WPI; 2001-318749/34.  
XX  
XX Primer sets for synthesizing polynucleotides, particularly the 5602  
XX full-length cDNAs defined in the specification, and for the detection  
XX and/or diagnosis of the abnormality of the proteins encoded by the  
XX full-length cDNAs -  
XX  
XX Claim 8; SEQ ID 13660; 2537pp + CD ROM; English.  
XX  
XX The present invention describes primer sets for synthesizing 5602  
XX full-length cDNAs defined in the specification. Where a primer set  
XX comprises: (a) an oligo-dr primer and an oligonucleotide complementary  
XX to the complementary strand of a polynucleotide which comprises one of  
XX the 5602 nucleotide sequences defined in the specification, where the  
XX oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
XX of an oligonucleotide comprising a sequence complementary to the  
XX complementary strand of a polynucleotide which comprises a 5'-end  
XX sequence and an oligonucleotide comprising a sequence complementary to a  
XX polynucleotide which comprises a 3'-end sequence, where the  
XX oligonucleotide comprises at least 15 nucleotides and the combination  
XX of the 5'-end sequence/3'-end sequence is selected from those defined in  
XX the specification. The primer sets can be used in antisense therapy and  
XX in gene therapy. The primers are useful for synthesizing polynucleotides,  
XX particularly full-length cDNAs. The primers are also useful for the

CC particularly full-length cDNAs. The primers are also useful for the  
CC detection and/or diagnosis of the abnormality of the proteins encoded by  
CC the full-length cDNAs. The primers allow obtaining of the full-length  
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to  
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632  
CC represent oligonucleotides, all of which are used in the exemplification  
CC of the present invention.

XX Sequence 1689 BP; 555 A; 309 C; 366 G; 459 T; 0 other;

Query Match 100.0%; Score 15; DB 22; Length 1689;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCGCTGTT 15  
|||||

Db 123 CCTTCTCCCGCTGTT 109

## RESULT 7

AAH28083  
ID AAH28083 standard; cDNA; 1854 BP.

XX AC

XX AC

XX 05-SEP-2001 (first entry)

DE DNA encoding human norepinephrine transporter variant A457P.

XX Norepinephrine transporter; orthostatic intolerance; gene therapy;  
KW mental illness; hypertension; heart disease; stimulant abuse; cocaine;  
KW amphetamine abuse; ss.

XX Homo sapiens.

Key Location/Qualifiers  
FH 1..1854  
CDS /\*tag= a

FT /\*product= "norepinephrine transporter"

XX WO200148246-A1.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US35491.

XX 29-DEC-1999; 99US-0173682.

XX 11-JAN-2000; 2000US-0175456.

XX (UYVA-) UNIV VANDERBILT.

XX Robertson D, Blakely RD;

XX WPI; 2001-425681/45.

XX P-PSDB; AAB84533.

XX Screening for susceptibility to sub-optimal norepinephrine transporter,  
PT particularly orthostatic intolerance in a subject by detecting a  
PT polymorphism of norepinephrine transporter gene

XX Claim 43; Page 104-108; 133pp; English.

XX The present sequence encodes a variant norepinephrine transporter. The  
CC specification a method for screening for susceptibility to sub-optimal  
CC norepinephrine (NE) transport in a subject. The method comprises  
CC obtaining a biological sample from the subject and detecting a  
CC polymorphism of a norepinephrine transporter gene in the sample from  
CC the subject, the presence of the polymorphism indicating the  
CC susceptibility of the subject to sub-optimal norepinephrine transporter.  
CC The method is useful for screening for susceptibility of a subject to  
CC orthostatic intolerance. Norepinephrine transporter genes are useful  
CC for gene therapy for modulating norepinephrine transport in a target

CC cell and treating susceptibility to impaired norepinephrine transporter  
CC function, orthostatic intolerance or other relevant diseases in humans  
CC and animals such as mental illness, hypertension, heart disease, psycho  
CC stimulant abuse e.g. cocaine or amphetamine abuse.

XX Sequence 1854 BP; 356 A; 555 C; 493 G; 450 T; 0 other;

Query Match 100.0%; Score 15; DB 22; Length 1854;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCGCTGTT 15

|||||

Db 1362 CCTTCTCCCGCTGTT 1376

## RESULT 8

AAH28087  
ID AAH28087 standard; cDNA; 1854 BP.

XX AC

XX AAH28087;

XX 05-SEP-2001 (first entry)

DE DNA encoding human norepinephrine transporter variant.

XX Norepinephrine transporter; orthostatic intolerance; gene therapy;  
KW mental illness; hypertension; heart disease; stimulant abuse; cocaine;  
KW amphetamine abuse; ss.

XX Homo sapiens.

Key Location/Qualifiers  
FH 1..1854  
CDS /\*tag= a

FT /\*product= "norepinephrine transporter"

XX WO200148246-A1.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US35491.

XX 29-DEC-1999; 99US-0173682.

XX 11-JAN-2000; 2000US-0175456.

XX (UYVA-) UNIV VANDERBILT.

XX Robertson D, Blakely RD;

XX WPI; 2001-425681/45.

XX P-PSDB; AAB84533.

XX Screening for susceptibility to sub-optimal norepinephrine transporter,  
PT particularly orthostatic intolerance in a subject by detecting a  
PT polymorphism of norepinephrine transporter gene

XX Claim 43; Page 119-121; 133pp; English.

XX The present sequence encodes a variant norepinephrine transporter. The  
CC specification a method for screening for susceptibility to sub-optimal  
CC norepinephrine (NE) transport in a subject. The method comprises  
CC obtaining a biological sample from the subject and detecting a  
CC polymorphism of a norepinephrine transporter gene in the sample from  
CC the subject, the presence of the polymorphism indicating the  
CC susceptibility of the subject to sub-optimal norepinephrine transporter.  
CC The method is useful for screening for susceptibility of a subject to  
CC orthostatic intolerance. Norepinephrine transporter genes are useful  
CC for gene therapy for modulating norepinephrine transport in a target  
CC cell and treating susceptibility to impaired norepinephrine transporter  
CC function, orthostatic intolerance or other relevant diseases in humans  
CC and animals such as mental illness, hypertension, heart disease, psycho  
CC stimulant abuse e.g. cocaine or amphetamine abuse.

```
XX SQ Sequence 1854 BP; 357 A; 554 C; 493 G; 450 T; 0 other;
Query Match 100.0%; Score 15; DB 22; Length 1854;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGTT 15
      |||||
Db 1362 CCTTCTCCCTGTT 1376

RESULT 9
ABK43728
ID ABK43728 standard; cDNA; 2159 BP.
XX AC ABK43728;
XX DT 05-JUN-2002 (first entry)
XX DE DNA encoding novel central nervous system protein #308.
XX KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; ischemia; angiogenesis;
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
KW adenocarcinoma; reproductive system disorder; testicular feminisation;
KW endocrine disorder; diabetes; cancer; leukemia; neovascularisation;
KW respiratory disorder; renal disorder; kidney failure; blood disorder;
KW myocardial infarction; wound healing; cell proliferation; skin aging;
KW food additive; food preservative; gene therapy; gene; ss.
XX OS Homo sapiens.
XX PN WO200155318-A2.
XX PD 02-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US01332.
XX PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 17-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
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PR 17-NOV-2000; 2000US-0249208.  
PR 17-NOV-2000; 2000US-0249209.  
PR 17-NOV-2000; 2000US-0249210.  
PR 17-NOV-2000; 2000US-0249211.  
PR 17-NOV-2000; 2000US-0249212.  
PR 17-NOV-2000; 2000US-0249213.  
PR 17-NOV-2000; 2000US-0249214.  
PR 17-NOV-2000; 2000US-0249215.  
PR 17-NOV-2000; 2000US-0249216.  
PR 17-NOV-2000; 2000US-0249217.  
PR 17-NOV-2000; 2000US-0249218.  
PR 17-NOV-2000; 2000US-0249244.  
PR 17-NOV-2000; 2000US-0249245.  
PR 17-NOV-2000; 2000US-0249264.  
PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249297.  
PR 17-NOV-2000; 2000US-0249299.  
PR 17-NOV-2000; 2000US-0249300.  
PR 01-DEC-2000; 2000US-0250160.  
PR 01-DEC-2000; 2000US-0250391.  
PR 05-DEC-2000; 2000US-0251030.  
PR 05-DEC-2000; 2000US-0251988.  
PR 05-DEC-2000; 2000US-0256719.  
PR 06-DEC-2000; 2000US-0251479.  
PR 08-DEC-2000; 2000US-0251856.  
PR 08-DEC-2000; 2000US-0251868.  
PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251989.  
PR 08-DEC-2000; 2000US-0251990.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Barash SC, Ruben SM;

XX WPI; 2001-581633/65.

DR P-PSDB; AAU87398.

PT New isolated nucleic acid encoding a protein for diagnosing,  
PT preventing, treating or ameliorating medical conditions and used as  
PT food additives or preservatives -

XX Claim 1; SEQ ID No 318; 837pp; English.

PS The invention describes an isolated nucleic acid molecule (I) encoding a  
XX novel central nervous system protein. (I) and polypeptides (III) encoded  
CC by (I), are used to treat a medical condition and in diagnosis of a  
CC pathological condition. Disorders which are diagnosed or treated include  
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative  
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders  
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,  
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease and  
CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses  
CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders  
CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,  
CC adenocarcinomas and irritable bowel syndrome, reproductive system  
CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes  
CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.  
CC leukaemia, disorders involving neovascularisation e.g. malignancies,  
CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.  
CC acute kidney failure and blood related disorders e.g. myocardial  
CC infarction. The polypeptides can also be used to aid wound healing and  
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to  
CC maintain organs before transplantation, for supporting cell culture of  
CC primary tissues, to regenerate tissues and in chemotaxis. The  
CC polypeptides can also be used as a food additive or preservative to  
CC increase or decrease storage capabilities, fat content, lipid, protein,

Query Match 100.0%; Score 15; DB 23; Length 2159;

Best Local Similarity 100.0%; Pred. No. 30;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15  
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Db 1070 CCTTCTCCCCCTGTT 1084

RESULT 10  
AAS83288/c

ID AAS83288 standard; cDNA; 2451 BP.

XX AAS83288;

AC AAS83288;

XX 13-FEB-2002 (first entry)

XX DNA encoding novel human diagnostic protein #19092.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

XX 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

DR P-PSDB; ABG19101.

PT New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess

PT biodiversity -

XX Claim 1; SEQ ID No 19092; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AAS64197-AAS94564 represent novel human  
CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 2451 BP; 670 A; 631 C; 671 G; 479 T; 0 other;

Query Match 100.0%; Score 15; DB 23; Length 2451;

Best Local Similarity 100.0%; Pred. No. 30;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15

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PR	08-SEP-2000;	2000US-02311413;
PR	08-SEP-2000;	2000US-02311414;
PR	08-SEP-2000;	2000US-02320800;
PR	08-SEP-2000;	2000US-02320801;
PR	12-SEP-2000;	2000US-02321968;
PR	14-SEP-2000;	2000US-02323997;
PR	14-SEP-2000;	2000US-02323998;
PR	14-SEP-2000;	2000US-02323999;
PR	14-SEP-2000;	2000US-02324000;
PR	14-SEP-2000;	2000US-02324001;
PR	14-SEP-2000;	2000US-02324063;
PR	14-SEP-2000;	2000US-02323064;
PR	14-SEP-2000;	2000US-02323065;
PR	21-SEP-2000;	2000US-02342223;
PR	21-SEP-2000;	2000US-02342274;
PR	25-SEP-2000;	2000US-02349999;
PR	25-SEP-2000;	2000US-02349998;
PR	26-SEP-2000;	2000US-02354884;
PR	27-SEP-2000;	2000US-02358334;
PR	27-SEP-2000;	2000US-02358336;
PR	29-SEP-2000;	2000US-02363277;
PR	29-SEP-2000;	2000US-02363677;
PR	29-SEP-2000;	2000US-02363688;
PR	29-SEP-2000;	2000US-02363689;
PR	02-OCT-2000;	2000US-02363770;
PR	02-OCT-2000;	2000US-02368002;
PR	02-OCT-2000;	2000US-02370377;
PR	02-OCT-2000;	2000US-02370378;
PR	02-OCT-2000;	2000US-02370389;
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PR	13-OCT-2000;	2000US-02393937;
PR	20-OCT-2000;	2000US-02409660;
PR	20-OCT-2000;	2000US-02411221;
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PR	20-OCT-2000;	2000US-02417866;
PR	20-OCT-2000;	2000US-02417877;
PR	20-OCT-2000;	2000US-02418008;
PR	20-OCT-2000;	2000US-02418009;
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PR	08-NOV-2000;	2000US-02446617;
PR	08-NOV-2000;	2000US-02464745;
PR	08-NOV-2000;	2000US-02464757;
PR	08-NOV-2000;	2000US-02464676;
PR	08-NOV-2000;	2000US-02464677;
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PR	08-NOV-2000;	2000US-02465523;
PR	08-NOV-2000;	2000US-02465524;
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PR	08-NOV-2000;	2000US-02465626;
PR	08-NOV-2000;	2000US-02465627;
PR	08-NOV-2000;	2000US-02465528;
PR	08-NOV-2000;	2000US-02465532;
PR	08-NOV-2000;	2000US-02466009;
PR	08-NOV-2000;	2000US-02466010;
PR	08-NOV-2000;	2000US-02466111;
PR	17-NOV-2000;	2000US-02466613;
PR	17-NOV-2000;	2000US-02492007;
PR	17-NOV-2000;	2000US-02492008;
PR	17-NOV-2000;	2000US-02492009;
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PR	17-NOV-2000;	2000US-02492112;
PR	17-NOV-2000;	2000US-02492113;
PR	17-NOV-2000;	2000US-02492114;
PR	17-NOV-2000;	2000US-02492115;
PR	17-NOV-2000;	2000US-02492116;
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PR	17-NOV-2000;	2000US-02492125;
PR	17-NOV-2000;	2000US-02492126;
PR	17-NOV-2000;	2000US-02492127;
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PR	17-NOV-2000;	2000US-02492245.
PR	17-NOV-2000;	2000US-02492264.
PR	17-NOV-2000;	2000US-02492265.
PR	17-NOV-2000;	2000US-02492297.
PR	17-NOV-2000;	2000US-02492299.
PR	17-NOV-2000;	2000US-02493300.
PR	01-DEC-2000;	2000US-02501160.
PR	01-DEC-2000;	2000US-02503391.
PR	05-DEC-2000;	2000US-02510330.
PR	05-DEC-2000;	2000US-02511988.
PR	06-DEC-2000;	2000US-02567119.
PR	08-DEC-2000;	2000US-0251479.
PR	08-DEC-2000;	2000US-0251856.
PR	08-DEC-2000;	2000US-0251868.
PR	08-DEC-2000;	2000US-0251869.
PR	08-DEC-2000;	2000US-0251989.
PR	11-DEC-2000;	2000US-0251990.
PR	11-DEC-2000;	2000US-0254097.
PR	05-JAN-2001;	2001US-0259678.
PA	(HUMA-) HUMAN GENOME SCI INC	
XX		
XX		
PI	Rosen CA, Barash SC, Ruben	
XX		
XX	WPI; 2001-581633/65.	
DR	P-PSDB: AAU87674.	
DR		

Query Match	Score 15:	DB 23:	Length 2522:
Best Local Similarity	100.0%		
Matches	100.0%	Pred. No. 30:	
15: Conservative	0:	Mismatches	0:
Indels	0:	Gaps	0:

Qy 1 CCTTCTCCCCCTGTT 15  
Db 1460 CCTTCTCCCCCTGTT 1446

RESULT 13	
AAA16697	
ID	AAA16697 standard; cDNA; 3580 BP.
XX	
AC	AAA16697;
XX	
DT	16-JUN-2000 (first entry)

XX DE Human secreted protein clone as180\_1 nucleotide sequence SEQ ID NO:159.  
XX KW Human; secreted protein; immunestimulant; immunosuppressant; virucide;  
KW antibacterial; antifungal; cytostatic; antiinflammatory; dermatological;  
KW antidiabetic; antiasthmatic; antiarthritic; antirheumatic; protozoacide;  
KW antithyroid; immune deficiency; severe combined immunodeficiency; SCID;  
KW infection; HIV; hepatitis; malaria; autoimmune disorder; systemic lupus;  
KW connective tissue disease; multiple sclerosis; erythematosis;  
KW rheumatoid arthritis; autoimmune pulmonary inflammation; asthma;  
KW Guillain-Barre syndrome; autoimmune thyroiditis; myasthenia gravis;  
KW insulin dependent diabetes mellitus; graft-versus-host-disease;  
KW autoimmune inflammatory eye disease; allergy; ss.  
XX OS Homo sapiens.  
XX KW WO200009552-A1.  
XX PN 24-FEB-2000.  
XX PD 13-AUG-1999; 99WO-US18298.  
XX PF 14-AUG-1998; 98US-0096622.  
XX PR 17-AUG-1998; 98US-0096815.  
XX PR 04-SEP-1998; 98US-0099229.  
XX PR 23-OCT-1998; 98US-0105368.  
XX PR 08-JAN-1999; 99US-0115234.  
XX PR 12-FEB-1999; 99US-0119931.  
XX PR 18-FEB-1999; 99US-0120575.  
XX PR 30-APR-1999; 99US-0132020.  
XX PR 11-AUG-1999; 99US-0096622.  
XX PA (GEMY ) GENETICS INST INC.  
XX PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;  
PI Merberg D, Treacy M, Agostino MJ, Steininger RJ, Spaulding V;  
PI Wong GG, Clark HF, Fechtcl K;  
XX WPI; 2000-205979/18.  
XX P-PSDB; AAY94977.  
XX New polynucleotides encoding secreted proteins, which may have e.g.  
XX nutritional, chemokine, immune stimulating or suppressing,  
XX hematopoiesis regulating, tissue growth, activin/inhibin  
XX antiinflammatory or tumor inhibition activity  
XX Claim 168; Page 613-614; 64lpp; English.  
XX AAAL6618 to AAAL6697 encode the human secreted proteins given in  
XX AAY94898 to AAY94980, isolated from human adult brain, adult thyroid,  
XX adult retina, foetal carcinoma, adult blood, adult neural, foetal kidney,  
XX adult placenta, adult testis, whole embryo, adult cartilage, kidney,  
XX foetal brain, adult thymus, foetal placenta, adult uterus, adult tumour,  
XX and adult bladder, cDNA libraries. The polynucleotides and proteins are  
XX predicted to have biological activities which would make them suitable  
XX for treating, preventing or ameliorating medical conditions in humans  
XX and animals. The polynucleotides can be used as markers for tissues in  
XX which the protein is preferentially expressed, as molecular weight  
XX markers on Southern gels, and as chromosome markers or tags to identify  
XX chromosomes or to map gene positions. The proteins can be used in the  
XX treatment of immune deficiencies and disorders, such as severe combined  
XX immunodeficiency (SCID), as well as viral, bacterial, fungal and other  
XX infections. These infections include human immunodeficiency virus (HIV),  
XX hepatitis, herpesviruses, mycobacteria, Leishmania spp., malaria and  
XX candidiasis. The proteins can be used to treat autoimmune disorders such  
XX as connective tissue disease, multiple sclerosis, systemic lupus  
XX erythematosis, rheumatoid arthritis, autoimmune pulmonary inflammation,  
XX Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent  
XX diabetes mellitus, myasthenia gravis, graft-versus-host-disease and  
XX autoimmune inflammatory eye disease. The proteins can also be used to  
XX treat allergic conditions, such as asthma. AAAL6698 to AAAL6774 represent  
XX probes for the human secreted proteins from the present invention.

SQ Sequence 3580 BP; 734 A; 942 C; 1024 G; 880 T; 0 other;  
Query Match 100.0%; Score 15; DB 21; Length 3580;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCTTCTCCCCCTGTT 15  
Db 2528 CCTTCTCCCCCTGTT 2542  
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ABK35630/c  
ID ABK35630 standard; cDNA; 3580 BP.  
XX AC ABK35630;  
XX XX  
XX DT 08-MAY-2002 (first entry)  
XX DE cDNA sequence #21 encoding novel human secreted protein.  
XX KW Human secreted protein; hyperproliferative disorder; autoimmune disorder;  
KW immune deficiency disorder; blood disorder; inflammatory disorder;  
KW infectious disorder; allergic condition; neurodegenerative disorder;  
KW liver fibrosis; coagulation disorder; gene therapy; antimicrobial;  
KW tumour; cancer; hepatotropic; immunosuppressive; antirheumatic; gene; ss.  
XX OS Homo sapiens.  
XX PN WO200177289-A2.  
XX PD 18-OCT-2001.  
XX PF 29-MAR-2001; 2001WO-US10232.  
XX PR 06-APR-2000; 2000US-195605P.  
XX PA (GEMY ) GENETICS INST INC.  
XX PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;  
PI Merberg D, Treacy M, Agostino MJ, Bowman MR, Spaulding V, Wong GG;  
PI Clark HF, Fechtcl K, Howes SH, Resnick RJ, Gulukota K, Graham JR;  
XX WPI; 2002-179322/23.  
XX Six hundred and twenty three polynucleotides derived from a variety of  
XX human tissue sources which encode secreted proteins, useful for  
XX treating immune deficiencies and disorders such as autoimmune disorders  
XX Claim 1; Page 85-86; 393pp; English.  
XX The present invention relates to the isolation of novel cDNA sequences  
XX which encode human secreted proteins. The cDNA sequences have been  
XX derived from a variety of human tissues. The invention also provides  
XX a method for producing proteins from these polynucleotide sequences.  
XX The proteins are useful for identifying compounds that modulate their  
XX activity and production. The sequences of the invention are  
XX useful for treating diseases such as hyperproliferative disorders  
XX (e.g. cancer), immune deficiency disorders (e.g. severe combined  
XX immunodeficiency (SCID)), autoimmune disorders (e.g. multiple  
XX sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory  
XX disorders (e.g. arthritis), infectious disorders (e.g. hepatitis),  
XX allergic conditions (e.g. asthma), neurodegenerative disorders (e.g.  
XX Alzheimer's disease), liver fibrosis, coagulation disorders (e.g.  
XX haemophilia), and tumours. The polynucleotide sequences of the  
XX invention are also useful in gene therapy. ABK35610-ABK36232 represent  
XX the cDNA sequences of the invention that encode for novel human  
XX secreted proteins.  
SQ Sequence 3580 BP; 880 A; 1024 C; 942 G; 734 T; 0 other;  
Query Match 100.0%; Score 15; DB 24; Length 3580;

Best Local Similarity 100.0%; Pred. No. 29;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CCTTCTCCCGCTGT 15  
DB 1053 CCTTCTCCCGCTGT 1039

RESULT 15  
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ID ABV22746 standard; cDNA; 4215 BP.  
XX AC ABV22746;  
XX 13-SEP-2002 (first entry)  
XX Human prostate expression marker cDNA 22737.  
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
KW pharmacogenomic marker; gene; ss.  
XX OS Homo sapiens.  
XX PN WO200160860-A2.  
XX PD 23-AUG-2001.  
XX PF 20-FEB-2001; 2001WO-US05171.  
XX PR 17-FEB-2000; 2000US-183319P.  
PR 16-MAR-2000; 2000US-189862P.  
PR 25-MAY-2000; 2000US-207454P.  
PR 09-JUN-2000; 2000US-211314P.  
PR 18-JUL-2000; 2000US-219007P.  
PR 13-DEC-2000; 2000US-255281P.  
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
XX PI Schlegel R, Endege WO, Monahan JE;  
XX WPI; 2001-662795/76.

Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer  
PS Claim 1; Page 4005-4006; 11750pp; English.

The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:  
CC (a) assessing whether a patient is afflicted with prostate cancer;  
CC (b) monitoring the progression of prostate cancer in a patient;  
CC (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;  
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound;  
CC (g) determining whether prostate cancer has metastasized in a patient;  
CC (h) assessing the aggressiveness or indolence of prostate cancer in a patient;  
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.

SQ Sequence 4215 BP; 1325 A; 808 C; 818 G; 1251 T; 13 other;

Query Match 100.0%; Score 15; DB 23; Length 4215;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCGCTGT 15  
DB 166 CCTTCTCCCGCTGT 152

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 16:59:33 : Search time 47 seconds  
(without alignments)  
97.876 Million cell updates/sec

Title: US-09-750-609-10  
Perfect score: 15  
Sequence: 1 cctctccccctgtt 15

Scoring table: OLIGO\_NUC  
Gapop 50.0 , Gapext 50.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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1	13	86.7	776	US-09-484-970B-82	Sequence 82, Appl
2	13	86.7	1419	US-08-619-542B-29	Sequence 29, Appl
3	13	86.7	1905	US-09-295-744A-1	Sequence 1, Appl
4	13	86.7	2431	US-09-221-017B-351	Sequence 351, App
5	13	86.7	2687	US-08-149-695-8	Sequence 8, Appl
6	13	86.7	2687	US-08-377-228-8	Sequence 8, Appl
7	13	86.7	2873	US-08-149-695-1	Sequence 1, Appl
8	13	86.7	2873	US-08-377-228-1	Sequence 1, Appl
9	13	86.7	4287	US-08-244-189-1	Sequence 1, Appl
10	13	86.7	4287	US-08-306-691B-53	Sequence 53, Appl
11	13	86.7	4503	US-08-770-301A-2	Sequence 2, Appl
12	13	86.7	4503	US-09-175-581-2	Sequence 2, Appl
13	13	86.7	6032	US-09-295-744A-12	Sequence 12, Appl
14	13	86.7	55827	US-09-813-133A-3	Sequence 3, Appl
15	13	86.7	4411529	US-09-103-840A-1	Sequence 1, Appl
16	12	80.0	355	US-09-043-303-1	Sequence 1, Appl
17	12	80.0	621	US-09-328-111-414	Sequence 414, App
18	12	80.0	623	US-09-043-303-5	Sequence 5, Appl
19	12	80.0	732	US-08-145-006C-21	Sequence 8, Appl
20	12	80.0	732	US-08-145-006C-8	Sequence 21, Appl
21	12	80.0	732	PCT-US94-00545-8	Sequence 8, Appl
22	12	80.0	732	PCT-US94-00545-22	Sequence 22, Appl
23	12	80.0	1001	US-09-641-638-444	Sequence 444, App
24	12	80.0	1065	US-08-145-006C-11	Sequence 11, Appl
25	12	80.0	1074	US-08-975-316-54	Sequence 54, Appl
26	12	80.0	1074	US-09-615-192A-54	Sequence 54, Appl
27	12	80.0	1075	US-08-975-316-55	Sequence 55, Appl

Sequence 55, Appl  
Sequence 10, Appl  
Sequence 19, Appl  
Sequence 6, Appl  
Sequence 6, Appl  
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c 104	11	73.3	392	4	US-09-345-882-5	Sequence 5, Appli	177	11	73.3	1322	1	US-08-468-709B-5	Sequence 5, Appli
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c 107	11	73.3	439	4	US-09-397-787-308	Sequence 308, App	180	11	73.3	1323	4	US-09-651-200-9	Sequence 9, Appli
108	11	73.3	450	6	5437995-1	Patent No. 5437995	181	11	73.3	1374	4	US-08-482-746-9	Sequence 9, Appli
109	11	73.3	454	3	US-09-030-613-14	Sequence 14, Appl	182	11	73.3	1451	4	US-09-310-463-37	Sequence 37, Appl
110	11	73.3	454	3	US-09-451-905-14	Sequence 14, Appl	183	11	73.3	1498	3	US-09-173-581-14	Sequence 14, Appl
c 111	11	73.3	454	6	5175147-1	Patent No. 5175147	184	11	73.3	1498	4	US-09-420-915-14	Sequence 14, Appl
c 112	11	73.3	462	4	US-09-712-016-68	Sequence 68, Appl	185	11	73.3	1508	4	US-09-404-390-14	Sequence 14, Appl
c 113	11	73.3	463	4	US-09-132-316-52	Sequence 52, Appl	186	11	73.3	1514	1	US-08-381-433A-1	Sequence 1, Appli
c 114	11	73.3	474	4	US-09-149-476-13	Sequence 13, Appl	187	11	73.3	1539	3	US-09-058-725B-6	Sequence 6, Appli
c 115	11	73.3	499	6	5242821-2	Patent No. 5242821	188	11	73.3	1539	3	US-09-232-857-6	Sequence 6, Appli
116	11	73.3	500	4	US-09-328-111-5	Sequence 5, Appli	c 189	11	73.3	1549	4	US-09-206-344A-13	Sequence 13, Appl
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119	11	73.3	501	2	US-08-487-231-2	Sequence 2, Appli	c 192	11	73.3	1572	3	US-09-234-613-93	Sequence 93, Appl
120	11	73.3	501	4	US-09-201-912-2	Sequence 2, Appli	c 193	11	73.3	1602	4	US-09-651-200-11	Sequence 11, Appl
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128	11	73.3	576	1	US-08-086-428B-2	Sequence 2, Appli	201	11	73.3	1789	4	US-09-428-219-3	Sequence 3, Appli
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154	11	73.3	1021	4	US-09-177-650-127	Sequence 127, App	c 227	11	73.3	2091	4	US-09-126-121-22	Sequence 22, Appl
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c 248	11	73.3	2333	4	US-09-404-390-15	Sequence 15, Appl	321	11	73.3	4823	4	US-08-461-819-5	Sequence 5, Appl
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c 251	11	73.3	2478	4	US-08-485-355B-47	Sequence 47, Appl	324	11	73.3	4823	5	PCT-US95-16626-5	Sequence 5, Appl
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c 255	11	73.3	2502	3	US-08-899-437-5	Sequence 5, Appl	328	11	73.3	5100	1	US-08-164-292B-17	Sequence 17, Appl
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c 271	11	73.3	2885	4	US-09-651-200-3	Sequence 3, Appl	344	11	73.3	5100	3	US-08-815-927-25	Sequence 25, Appl
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c 273	11	73.3	3000	1	US-09-361-707-74	Sequence 74, Appl	346	11	73.3	5100	4	US-09-103-330-17	Sequence 17, Appl
c 274	11	73.3	3000	1	US-08-393-985-3	Sequence 3, Appl	347	11	73.3	5100	4	US-09-103-330-19	Sequence 19, Appl
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c 284	11	73.3	3528	1	US-08-362-652-36	Sequence 36, Appl	357	11	73.3	5152	4	US-09-690-364-10	Sequence 10, Appl
c 285	11	73.3	3528	1	US-08-605-672-36	Sequence 36, Appl	358	11	73.3	5159	2	US-08-146-930-3	Sequence 3, Appl
c 286	11	73.3	3528	2	US-08-482-293A-36	Sequence 36, Appl	359	11	73.3	5159	3	US-08-458-240-3	Sequence 3, Appl
c 287	11	73.3	3528	2	US-08-943-363-36	Sequence 36, Appl	360	11	73.3	5159	5	PCT-US93-03993-3	Sequence 3, Appl
c 288	11	73.3	3528	4	US-09-193-043-36	Sequence 36, Appl	c 361	11	73.3	5408	1	US-08-471-058-20	Sequence 20, Appl
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c 290	11	73.3	3539	4	US-08-853-948B-1	Sequence 1, Appl	c 363	11	73.3	5410	4	US-09-221-017B-70	Sequence 70, Appl
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c 301	11	73.3	3789	1	US-08-454-455-5	Sequence 5, Appl	c 374	11	73.3	5975	1	US-08-404-354B-1	Sequence 1, Appl
c 302	11	73.3	4046	1	US-07-793-961A-1	Sequence 1, Appl	c 375	11	73.3	5975	1	US-08-314-083B-1	Sequence 1, Appl
c 303	11	73.3	4046	1	US-08-240-357-1	Sequence 1, Appl	c 376	11	73.3	5975	1	US-08-435-675B-1	Sequence 1, Appl
c 304	11	73.3	4091	4	US-08-630-915A-33	Sequence 33, Appl	c 377	11	73.3	5975	1	US-08-336-257A-3	Sequence 3, Appl
c 305	11	73.3	4112	1	US-08-340-203A-2	Sequence 2, Appl	c 378	11	73.3	5975	3	US-08-884-599-1	Sequence 1, Appl
c 306	11	73.3	4112	2	US-08-452-567-2	Sequence 2, Appl	c 379	11	73.3	6002	4	US-09-345-882-4	Sequence 4, Appl
c 307	11	73.3	4112	2	US-08-452-421-2	Sequence 2, Appl	c 380	11	73.3	6574	4	US-09-221-017B-1097	Sequence 1097, Ap
c 308	11	73.3	4112	3	US-09-085-407-2	Sequence 2, Appl	c 381	11	73.3	6709	4	US-09-285-601-3	Sequence 3, Appl
c 309	11	73.3	4294	1	US-08-152-483B-2	Sequence 2, Appl	c 382	11	73.3	6756	2	US-08-151-574-31	Sequence 31, Appl
c 310	11	73.3	4317	4	US-08-961-527-124	Sequence 124, App	c 383	11	73.3	6756	2	US-08-419-448-31	Sequence 31, Appl
c 311	11	73.3	4414	5	PCT-US95-04567-1	Sequence 1, Appl	c 384	11	73.3	6756	4	US-09-233-510-31	Sequence 31, Appl
c 312	11	73.3	4417	4	US-07-741-453A-57	Sequence 57, Appl	c 385	11	73.3	6803	3	US-08-665-259-19	Sequence 19, Appl
c 313	11	73.3	4616	1	US-08-340-203A-1	Sequence 1, Appl	c 386	11	73.3	6803	3	US-08-762-500-19	Sequence 19, Appl
c 314	11	73.3	4616	2	US-08-452-567-1	Sequence 1, Appl	c 387	11	73.3	7011	1	US-08-306-691B-42	Sequence 42, Appl
c 315	11	73.3	4616	2	US-08-452-427-1	Sequence 1, Appl	c 388	11	73.3	7301	4	US-09-816-088-3	Sequence 3, Appl
c 316	11	73.3	4616	3	US-09-085-407-1	Sequence 1, Appl	c 389	11	73.3	7319	4	US-09-221-017B-510	Sequence 510, App
c 317	11	73.3	4800	3	US-08-941-445A-4	Sequence 4, Appl	c 390	11	73.3	7571	4	US-08-961-527-16	Sequence 2, Appl
c 318	11	73.3	4823	2	US-08-457-254-5	Sequence 5, Appl	c 391	11	73.3	8411	4	US-08-961-527-16	Sequence 16, Appl
c 319	11	73.3	4823	2	US-08-484-257-20	Sequence 20, Appl	c 392	11	73.3	8501	3	US-08-793-900-1	Sequence 1, Appl

393	11	73.3	9541	4	US-08-961-527-132	Sequence 132, App	c 466	10	66.7	48	3	US-08-297-431B-26	Sequence 26, Appl
394	11	73.3	11384	4	US-08-961-527-45	Sequence 45, Appl	467	10	66.7	48	4	US-07-875-790B-4	Sequence 4, Appl
c 395	11	73.3	12284	2	US-08-876-991-1	Sequence 1, Appl	468	10	66.7	48	4	US-07-875-790B-5	Sequence 5, Appl
c 396	11	73.3	12284	2	US-09-059-853-1	Sequence 1, Appl	469	10	66.7	48	4	US-07-875-790B-6	Sequence 6, Appl
c 397	11	73.3	12732	4	US-09-060-756-1	Sequence 1, Appl	470	10	66.7	48	4	US-07-875-790B-7	Sequence 7, Appl
c 398	11	73.3	13965	4	US-09-453-702B-48	Sequence 48, Appl	471	10	66.7	48	4	US-07-875-790B-8	Sequence 8, Appl
c 399	11	73.3	14747	4	US-09-608-285A-42	Sequence 42, Appl	472	10	66.7	48	4	US-07-875-790B-9	Sequence 9, Appl
400	11	73.3	15602	4	US-09-844-634-17	Sequence 17, Appl	473	10	66.7	48	4	US-07-875-790B-9	Sequence 9, Appl
401	11	73.3	15977	4	US-09-608-285A-59	Sequence 59, Appl	c 474	10	66.7	50	3	US-08-985-162-1676	Sequence 1676, Ap
c 402	11	73.3	17606	4	US-08-943-731-4	Sequence 4, Appl	475	10	66.7	54	1	US-08-311-486C-1118	Sequence 1118, Ap
c 403	11	73.3	18627	4	US-08-961-527-113	Sequence 113, App	476	10	66.7	54	4	US-09-282-147-49	Sequence 49, Appl
404	11	73.3	19446	4	US-08-961-527-51	Sequence 51, Appl	c 476	10	66.7	54	4	US-08-584-040-8282	Sequence 8282, Ap
c 405	11	73.3	19446	4	US-08-961-527-51	Sequence 51, Appl	c 477	10	66.7	54	4	US-08-679-645-1150	Sequence 1150, Ap
c 406	11	73.3	20199	4	US-08-961-527-6	Sequence 6, Appl	478	10	66.7	60	4	US-08-538-526-3	Sequence 3, Appl
c 407	11	73.3	20303	1	US-08-370-975B-6	Sequence 6, Appl	c 479	10	66.7	64	3	US-08-205-428-24	Sequence 24, Appl
408	11	73.3	20710	1	US-08-420-235B-1	Sequence 1, Appl	c 480	10	66.7	66	2	US-08-868-162A-1	Sequence 1, Appl
409	11	73.3	20710	3	US-08-793-62A-1	Sequence 1, Appl	481	10	66.7	66	3	US-09-205-428-23	Sequence 23, Appl
410	11	73.3	20710	5	PCT-US95-10194-1	Sequence 1, Appl	482	10	66.7	81	4	US-08-477-928A-43	Sequence 43, Appl
411	11	73.3	21126	1	US-08-008-216-19	Sequence 19, Appl	483	10	66.7	84	2	US-08-426-599B-10	Sequence 10, Appl
412	11	73.3	21126	1	US-08-459-569-19	Sequence 19, Appl	484	10	66.7	90	4	US-08-943-731-10	Sequence 10, Appl
413	11	73.3	21126	1	US-08-458-831-19	Sequence 19, Appl	485	10	66.7	91	4	US-08-050-482A-19	Sequence 19, Appl
414	11	73.3	21126	1	US-08-472-217-1	Sequence 1, Appl	c 486	10	66.7	91	4	US-08-050-482A-20	Sequence 20, Appl
415	11	73.3	26700	1	US-08-488-199-5	Sequence 5, Appl	487	10	66.7	96	1	US-08-361-708-25	Sequence 25, Appl
416	11	73.3	26700	2	US-08-760-534A-1	Sequence 1, Appl	488	10	66.7	96	1	US-08-536-277-25	Sequence 25, Appl
c 417	11	73.3	26764	1	US-08-370-975B-1	Sequence 1, Appl	c 489	10	66.7	96	3	US-08-484-322-12	Sequence 12, Appl
418	11	73.3	34446	4	US-09-103-330-35	Sequence 35, Appl	490	10	66.7	96	4	US-09-342-681C-107	Sequence 107, App
419	11	73.3	35060	3	US-08-814-095-7	Sequence 7, Appl	491	10	66.7	97	3	US-09-106-638-6	Sequence 6, Appl
c 420	11	73.3	35060	3	US-08-814-095-7	Sequence 7, Appl	492	10	66.7	100	4	US-09-575-574-6	Sequence 6, Appl
421	11	73.3	35100	2	US-08-770-379-18	Sequence 18, Appl	493	10	66.7	102	4	US-08-943-731-9	Sequence 9, Appl
422	11	73.3	35100	4	US-08-757-669A-18	Sequence 18, Appl	494	10	66.7	109	1	US-07-640-476-3	Sequence 3, Appl
423	11	73.3	35100	4	US-09-230-770A-18	Sequence 18, Appl	c 495	10	66.7	110	1	US-08-487-890A-91	Sequence 91, Appl
424	11	73.3	49272	1	US-08-614-770A-1	Sequence 1, Appl	496	10	66.7	110	2	US-08-478-435-91	Sequence 91, Appl
c 425	11	73.3	61663	4	US-09-453-702B-62	Sequence 62, Appl	c 497	10	66.7	110	2	US-08-337-483-91	Sequence 91, Appl
c 426	11	73.3	61663	4	US-09-784-316-3	Sequence 3, Appl	c 498	10	66.7	110	2	US-08-478-373-91	Sequence 91, Appl
427	11	73.3	72928	3	US-09-009-913-1	Sequence 1, Appl	c 499	10	66.7	110	3	US-08-478-373-91	Sequence 91, Appl
c 428	11	73.3	72928	3	US-09-009-913-1	Sequence 1, Appl	c 500	10	66.7	110	3	US-08-478-373-91	Sequence 91, Appl
c 429	11	73.3	81001	4	US-09-750-580-1	Sequence 1, Appl	c 501	10	66.7	110	4	US-09-037-990B-46	Sequence 46, Appl
c 430	11	73.3	90050	4	US-09-245-041-5	Sequence 5, Appl	c 502	10	66.7	110	4	US-09-037-990B-48	Sequence 48, Appl
c 431	11	73.3	162450	4	US-09-345-882-1	Sequence 1, Appl	c 503	10	66.7	110	4	US-08-897-438-91	Sequence 91, Appl
c 432	11	73.3	176373	3	US-09-128-155-17	Sequence 17, Appl	c 504	10	66.7	110	4	US-08-637-654-91	Sequence 91, Appl
c 433	11	73.3	4403765	4	US-09-103-840A-2	Sequence 2, Appl	c 505	10	66.7	110	4	US-08-649-518-91	Sequence 91, Appl
c 434	10	66.7	19	4	US-09-061-764A-3	Sequence 3, Appl	c 506	10	66.7	116	1	US-08-487-890A-89	Sequence 89, Appl
435	10	66.7	20	2	US-08-173-489C-18	Sequence 18, Appl	c 507	10	66.7	116	2	US-08-478-435-89	Sequence 89, Appl
436	10	66.7	20	4	US-08-961-810-64	Sequence 64, Appl	c 508	10	66.7	116	2	US-08-337-483-89	Sequence 89, Appl
437	10	66.7	20	4	US-08-352-902D-64	Sequence 64, Appl	c 509	10	66.7	116	2	US-08-478-373-89	Sequence 89, Appl
c 438	10	66.7	20	4	US-09-150-999-11	Sequence 11, Appl	c 510	10	66.7	116	3	US-08-474-671-89	Sequence 89, Appl
c 439	10	66.7	21	2	US-08-117-952-47	Sequence 47, Appl	c 511	10	66.7	116	3	US-08-474-671-89	Sequence 89, Appl
c 440	10	66.7	24	2	US-08-811-897A-53	Sequence 53, Appl	c 512	10	66.7	116	4	US-08-897-438-89	Sequence 89, Appl
c 441	10	66.7	24	2	US-08-855-213-53	Sequence 53, Appl	c 513	10	66.7	116	4	US-08-637-654-89	Sequence 89, Appl
c 442	10	66.7	24	4	US-09-201-47A-53	Sequence 53, Appl	c 514	10	66.7	116	4	US-08-649-518-89	Sequence 89, Appl
c 443	10	66.7	25	1	US-08-153-848-55	Sequence 55, Appl	c 515	10	66.7	119	1	US-08-487-890A-93	Sequence 93, Appl
c 444	10	66.7	25	3	US-09-299-843A-55	Sequence 55, Appl	c 516	10	66.7	119	2	US-08-478-435-93	Sequence 93, Appl
c 445	10	66.7	25	3	US-09-088-337B-55	Sequence 55, Appl	c 517	10	66.7	119	2	US-08-337-483-93	Sequence 93, Appl
c 446	10	66.7	25	5	PCT-US93-11153-55	Sequence 55, Appl	c 518	10	66.7	119	2	US-08-478-373-93	Sequence 93, Appl
447	10	66.7	26	1	US-08-379-078-55A	Sequence 55A, App	c 519	10	66.7	119	3	US-08-474-671-93	Sequence 93, Appl
448	10	66.7	26	4	US-07-974-409C-177	Sequence 177, App	c 520	10	66.7	119	3	US-08-483-577A-93	Sequence 93, Appl
449	10	66.7	26	5	PCT-US93-00977-177	Sequence 177, App	c 521	10	66.7	119	4	US-08-897-438-93	Sequence 93, Appl
450	10	66.7	31	3	US-08-431-0081B-9	Sequence 9, Appl	c 522	10	66.7	119	4	US-08-637-654-93	Sequence 93, Appl
451	10	66.7	31	3	US-08-608-016-9	Sequence 9, Appl	c 523	10	66.7	119	4	US-08-637-654-93	Sequence 93, Appl
452	10	66.7	31	4	US-07-875-790B-16	Sequence 16, Appl	524	10	66.7	122	3	US-08-411-768B-19	Sequence 19, Appl
453	10	66.7	31	4	US-09-497-933A-9	Sequence 9, Appl	525	10	66.7	124	1	US-08-229-444B-3	Sequence 3, Appl
c 454	10	66.7	35	1	US-08-458-423A-8	Sequence 8, Appl	526	10	66.7	125	3	US-08-411-768B-17	Sequence 17, Appl
c 455	10	66.7	35	1	US-08-458-424B-8	Sequence 8, Appl	527	10	66.7	126	3	US-08-411-768B-18	Sequence 18, Appl
c 456	10	66.7	35	4	US-08-973-124-8	Sequence 8, Appl	528	10	66.7	130	4	US-09-037-990B-20	Sequence 20, Appl
c 457	10	66.7	35	5	PCT-US96-08014-8	Sequence 8, Appl	529	10	66.7	131	4	US-09-037-990B-18	Sequence 18, Appl
458	10	66.7	38	1	US-08-049-264C-64	Sequence 64, Appl	530	10	66.7	131	4	US-08-943-731-25	Sequence 25, Appl
459	10	66.7	38	1	US-08-476-562-64	Sequence 64, Appl	531	10	66.7	132	1	US-08-479-577-1	Sequence 1, Appl
460	10	66.7	38	5	PCT-US94-04310-64	Sequence 64, Appl	532	10	66.7	132	2	US-08-756-977-1	Sequence 1, Appl
461	10	66.7	38	5	US-08-479-723A-64	Sequence 64, Appl	533	10	66.7	132	5	PCT-US93-05331-5	Sequence 5, Appl
462	10	66.7	39	4	US-08-961-810-103	Sequence 103, App	c 534	10	66.7	143	3	US-08-650-275-9	Sequence 9, Appl
463	10	66.7	39	4	US-08-352-902D-103	Sequence 103, App	c 535	10	66.7	143	3	US-09-181-318-9	Sequence 9, Appl
464	10	66.7	42	5	PCT-US92-10421-6	Sequence 6, Appl	536	10	66.7	180	4	US-09-575-574-1	Sequence 1, Appl
c 465	10	66.7	44	5	PCT-US92-10421-9	Sequence 9, Appl	537	10	66.7	185	4	US-08-905-223-163	Sequence 163, App
							538	10	66.7	200	1	US-07-623-953-6	Sequence 6, Appl

c 539	10	66.7	204	4	US-08-991-789A-23	Sequence 23, Appl	c 612	10	66.7	384	4	US-08-619-491-1	Sequence 1, Appl
c 540	10	66.7	204	4	US-09-062-451-23	Sequence 23, Appl	c 613	10	66.7	384	4	US-08-232-246A-14	Sequence 14, Appl
c 541	10	66.7	204	4	US-09-598-326-23	Sequence 23, Appl	c 614	10	66.7	384	4	US-08-475-815B-6	Sequence 6, Appl
c 542	10	66.7	215	4	US-09-177-650-103	Sequence 103, Appl	c 615	10	66.7	384	5	PCT-US95-07302-1	Sequence 1, Appl
c 543	10	66.7	218	4	US-08-943-731-41	Sequence 41, Appl	c 616	10	66.7	387	2	US-08-449-287-1	Sequence 1, Appl
c 544	10	66.7	240	4	US-09-116-032-28	Sequence 28, Appl	c 617	10	66.7	390	1	US-08-482-882-79	Sequence 79, Appl
c 545	10	66.7	241	4	US-09-470-191-71	Sequence 71, Appl	c 618	10	66.7	390	2	US-08-483-389-79	Sequence 79, Appl
c 546	10	66.7	246	1	US-08-165-304A-1	Sequence 1, Appl	c 619	10	66.7	390	2	US-08-487-113D-79	Sequence 79, Appl
c 547	10	66.7	249	1	US-08-439-132-1	Sequence 1, Appl	c 620	10	66.7	390	2	US-08-473-503-79	Sequence 79, Appl
c 548	10	66.7	249	6	5223407-1	Patent No. 5223407	c 621	10	66.7	390	2	US-08-483-932-79	Sequence 79, Appl
c 549	10	66.7	250	4	US-09-605-785-409	Sequence 409, App	c 622	10	66.7	390	2	US-08-720-420A-79	Sequence 79, Appl
c 550	10	66.7	250	4	US-09-439-313-409	Sequence 409, App	c 623	10	66.7	390	3	US-08-714-011-79	Sequence 79, Appl
c 551	10	66.7	250	4	US-09-352-616A-409	Sequence 409, App	c 624	10	66.7	390	3	US-08-475-680-79	Sequence 79, Appl
c 552	10	66.7	252	1	US-08-253-155A-6	Sequence 6, Appl	c 625	10	66.7	393	2	US-08-116-778B-39	Sequence 39, Appl
c 553	10	66.7	254	3	US-08-866-340-31	Sequence 31, Appl	c 626	10	66.7	393	2	US-08-438-562-39	Sequence 39, Appl
c 554	10	66.7	254	4	US-09-103-875-37	Sequence 37, Appl	c 627	10	66.7	393	2	US-08-483-528B-2	Sequence 2, Appl
c 555	10	66.7	284	4	US-08-905-223-219	Sequence 219, App	c 628	10	66.7	393	3	US-08-673-739B-2	Sequence 2, Appl
c 556	10	66.7	286	2	US-08-332-766A-6	Sequence 6, Appl	c 629	10	66.7	393	4	US-09-393-385B-2	Sequence 2, Appl
c 557	10	66.7	287	2	US-08-332-766A-27	Sequence 27, Appl	c 630	10	66.7	396	4	US-09-199-637A-396	Sequence 396, App
c 558	10	66.7	287	3	US-08-881-037-55	Sequence 55, Appl	c 631	10	66.7	400	1	US-08-301-718-1	Sequence 1, Appl
c 559	10	66.7	290	4	US-08-896-164-18	Sequence 18, Appl	c 632	10	66.7	401	4	US-09-221-298-38	Sequence 38, Appl
c 560	10	66.7	292	2	US-08-308-494A-12	Sequence 12, Appl	c 633	10	66.7	405	4	US-08-905-223-93	Sequence 38, Appl
c 561	10	66.7	292	4	US-09-280-028-3	Sequence 3, Appl	c 634	10	66.7	413	4	US-09-657-453A-23	Sequence 23, Appl
c 562	10	66.7	297	4	US-09-042-353-93	Sequence 93, Appl	c 635	10	66.7	415	4	US-09-615-192A-177	Sequence 177, App
c 563	10	66.7	297	4	US-08-758-417A-357	Sequence 357, App	c 636	10	66.7	416	1	US-07-653-091A-12	Sequence 12, Appl
c 564	10	66.7	300	2	US-08-308-494A-20	Sequence 20, Appl	c 637	10	66.7	416	1	US-08-485-068-12	Sequence 12, Appl
c 565	10	66.7	300	3	US-08-881-037-27	Sequence 27, Appl	c 638	10	66.7	416	1	US-08-481-598-12	Sequence 12, Appl
c 566	10	66.7	300	3	US-08-881-037-30	Sequence 30, Appl	c 639	10	66.7	416	2	US-08-483-353-12	Sequence 12, Appl
c 567	10	66.7	301	4	US-09-222-575-8	Sequence 8, Appl	c 640	10	66.7	416	2	US-08-473-702-12	Sequence 12, Appl
c 568	10	66.7	309	1	US-08-467-393-3	Sequence 3, Appl	c 641	10	66.7	420	1	US-08-470-179-108	Sequence 108, App
c 569	10	66.7	311	2	US-08-611-757-23	Sequence 23, Appl	c 642	10	66.7	420	2	US-08-726-306A-46	Sequence 46, Appl
c 570	10	66.7	311	5	PCT-US95-05980-23	Sequence 3, Appl	c 643	10	66.7	423	4	US-09-199-637A-394	Sequence 394, App
c 571	10	66.7	315	1	US-08-459-310-3	Sequence 3, Appl	c 644	10	66.7	434	2	US-08-997-080-50	Sequence 50, Appl
c 572	10	66.7	318	3	US-08-783-853A-104	Sequence 104, App	c 645	10	66.7	434	2	US-08-997-362-50	Sequence 50, Appl
c 573	10	66.7	318	4	US-09-344-050-104	Sequence 104, App	c 646	10	66.7	434	3	US-08-873-970-50	Sequence 50, Appl
c 574	10	66.7	321	3	US-08-783-853A-6	Sequence 6, Appl	c 647	10	66.7	434	4	US-09-095-855-50	Sequence 50, Appl
c 575	10	66.7	321	4	US-09-344-050-6	Sequence 6, Appl	c 648	10	66.7	434	4	US-08-705-347A-50	Sequence 50, Appl
c 576	10	66.7	322	3	US-08-434-000A-11	Sequence 11, Appl	c 649	10	66.7	434	4	US-09-324-542-50	Sequence 50, Appl
c 577	10	66.7	322	4	US-09-312-157-11	Sequence 11, Appl	c 650	10	66.7	434	4	US-09-205-426-50	Sequence 50, Appl
c 578	10	66.7	324	3	US-08-483-749A-7	Sequence 7, Appl	c 651	10	66.7	434	4	US-09-200-643-50	Sequence 50, Appl
c 579	10	66.7	324	3	US-08-881-037-56	Sequence 56, Appl	c 652	10	66.7	435	4	US-09-641-638-534	Sequence 534, App
c 580	10	66.7	330	1	US-08-207-996-28	Sequence 28, Appl	c 653	10	66.7	435	4	US-09-641-638-535	Sequence 535, App
c 581	10	66.7	330	2	US-08-760-840A-29	Sequence 29, Appl	c 654	10	66.7	435	4	US-09-641-638-536	Sequence 536, App
c 582	10	66.7	330	2	US-08-760-840A-31	Sequence 31, Appl	c 655	10	66.7	435	4	US-09-641-638-537	Sequence 537, App
c 583	10	66.7	330	3	US-09-266-119-29	Sequence 29, Appl	c 656	10	66.7	435	4	US-09-641-638-538	Sequence 538, App
c 584	10	66.7	330	3	US-09-266-119-31	Sequence 31, Appl	c 657	10	66.7	435	4	US-09-641-638-539	Sequence 539, App
c 585	10	66.7	330	4	US-09-602-709-29	Sequence 29, Appl	c 658	10	66.7	441	1	US-07-781-254A-8	Sequence 8, Appl
c 586	10	66.7	330	4	US-09-602-709-31	Sequence 31, Appl	c 659	10	66.7	441	1	US-08-149-091-4	Sequence 4, Appl
c 587	10	66.7	331	3	US-08-836-561-32	Sequence 32, Appl	c 660	10	66.7	441	2	US-08-637-761-4	Sequence 4, Appl
c 588	10	66.7	334	3	US-08-581-918A-24	Sequence 24, Appl	c 661	10	66.7	441	5	PCT-US94-12672-4	Sequence 4, Appl
c 589	10	66.7	334	4	US-08-346-147B-24	Sequence 24, Appl	c 662	10	66.7	442	4	US-09-397-787-325	Sequence 325, App
c 590	10	66.7	334	4	US-08-497-214D-24	Sequence 24, Appl	c 663	10	66.7	443	4	US-09-397-787-202	Sequence 202, App
c 591	10	66.7	334	4	US-09-311-625B-41	Sequence 41, Appl	c 664	10	66.7	443	4	US-09-397-787-281	Sequence 281, App
c 592	10	66.7	335	3	US-08-783-853A-102	Sequence 102, App	c 665	10	66.7	449	4	US-09-397-787-175	Sequence 175, App
c 593	10	66.7	335	4	US-09-344-050-102	Sequence 102, App	c 666	10	66.7	456	4	US-09-040-984-79	Sequence 79, Appl
c 594	10	66.7	344	2	US-08-875-972-17	Sequence 17, Appl	c 667	10	66.7	456	4	US-09-123-912-79	Sequence 79, Appl
c 595	10	66.7	347	4	US-09-397-787-309	Sequence 309, App	c 668	10	66.7	456	4	US-09-643-597-79	Sequence 79, Appl
c 596	10	66.7	357	4	US-09-171-945-8	Sequence 8, Appl	c 669	10	66.7	456	4	US-09-920-672-11	Sequence 11, Appl
c 597	10	66.7	359	3	US-09-184-658-6	Sequence 6, Appl	c 670	10	66.7	458	1	US-08-751-782-1	Sequence 1, Appl
c 598	10	66.7	366	4	US-09-380-190A-3	Sequence 3, Appl	c 671	10	66.7	458	2	US-08-925-171-1	Sequence 1, Appl
c 599	10	66.7	377	4	US-09-453-702B-139	Sequence 139, App	c 672	10	66.7	458	4	US-08-961-810-16	Sequence 16, Appl
c 600	10	66.7	380	4	US-09-037-990B-4	Sequence 4, Appl	c 673	10	66.7	458	4	US-08-352-902D-16	Sequence 16, Appl
c 601	10	66.7	381	4	US-09-037-990B-3	Sequence 3, Appl	c 674	10	66.7	461	1	US-08-454-720A-37	Sequence 37, Appl
c 602	10	66.7	384	1	US-07-634-278-30	Sequence 30, Appl	c 675	10	66.7	462	1	US-07-946-421-25	Sequence 25, Appl
c 603	10	66.7	384	1	US-08-477-728-30	Sequence 30, Appl	c 676	10	66.7	462	4	US-09-227-357-124	Sequence 124, App
c 604	10	66.7	384	1	US-08-474-040-30	Sequence 30, Appl	c 677	10	66.7	470	4	US-09-615-192A-149	Sequence 149, App
c 605	10	66.7	384	1	US-08-487-200-30	Sequence 30, Appl	c 678	10	66.7	474	1	US-07-730-853-2	Sequence 2, Appl
c 606	10	66.7	384	1	US-08-149-099C-6	Sequence 6, Appl	c 679	10	66.7	474	1	US-08-280-041-2	Sequence 2, Appl
c 607	10	66.7	384	1	US-08-476-275-3	Sequence 3, Appl	c 680	10	66.7	478	4	US-09-227-357-50	Sequence 50, Appl
c 608	10	66.7	384	2	US-08-656-586-1	Sequence 1, Appl	c 681	10	66.7	484	4	US-09-056-556-224	Sequence 224, App
c 609	10	66.7	384	2	US-08-478-967A-6	Sequence 6, Appl	c 682	10	66.7	484	4	US-09-072-596-219	Sequence 219, App
c 610	10	66.7	384	3	US-08-444-644-14	Sequence 14, Appl	c 683	10	66.7	487	4	US-09-380-190A-2	Sequence 2, Appl
c 611	10	66.7	384	4	US-08-484-537-30	Sequence 30, Appl	c 684	10	66.7	492	3	US-08-729-416C-12	Sequence 12, Appl

c 685	10	66.7	494	4	US-09-404-879A-196	Sequence 196, App	c 758	10	66.7	726	2	US-08-553-497A-27	Sequence 27, Appl
686	10	66.7	497	4	US-09-328-111-114	Sequence 114, App	c 759	10	66.7	726	4	US-09-134-001C-2656	Sequence 2656, Ap
687	10	66.7	500	4	US-09-575-574-2	Sequence 2, App	c 760	10	66.7	732	4	US-08-553-497A-19	Sequence 19, Appl
c 688	10	66.7	500	4	US-09-370-838-269	Sequence 269, App	c 761	10	66.7	732	2	US-08-553-497A-21	Sequence 21, Appl
c 689	10	66.7	504	4	US-09-328-111-340	Sequence 340, App	c 762	10	66.7	732	2	US-08-860-862A-26	Sequence 26, Appl
690	10	66.7	504	4	US-09-328-111-104	Sequence 104, App	c 763	10	66.7	732	4	US-09-423-439-57	Sequence 57, Appl
691	10	66.7	517	4	US-09-052-469-4	Sequence 4, Appl	c 764	10	66.7	732	4	US-08-965-087-1	Sequence 1, Appl
692	10	66.7	531	4	US-08-991-789A-220	Sequence 220, App	c 765	10	66.7	732	4	US-09-011-769A-22	Sequence 22, Appl
693	10	66.7	531	4	US-09-062-451-220	Sequence 220, App	c 766	10	66.7	735	1	US-08-466-033-118	Sequence 118, App
694	10	66.7	531	4	US-09-598-326-220	Sequence 220, App	c 767	10	66.7	735	1	US-08-444-733-118	Sequence 118, App
c 695	10	66.7	535	4	US-09-603-785-596	Sequence 596, App	c 768	10	66.7	735	2	US-08-464-134-118	Sequence 118, App
c 696	10	66.7	552	1	US-08-149-091-3	Sequence 3, Appl	c 769	10	66.7	735	2	US-08-461-361-118	Sequence 118, App
c 697	10	66.7	552	1	US-08-637-761-3	Sequence 3, Appl	c 770	10	66.7	735	2	US-08-485-910-118	Sequence 118, App
c 698	10	66.7	552	5	PCT-US94-12672-3	Sequence 3, Appl	c 771	10	66.7	735	4	US-09-502-653-11	Sequence 11, Appl
c 699	10	66.7	555	4	US-08-479-089A-4	Sequence 4, Appl	c 772	10	66.7	738	2	US-08-553-497A-23	Sequence 23, Appl
700	10	66.7	561	4	US-09-392-184-28	Sequence 28, Appl	c 773	10	66.7	755	4	US-09-484-970B-158	Sequence 158, App
c 701	10	66.7	562	5	PCT-US92-03993-6	Sequence 6, Appl	c 774	10	66.7	758	3	US-08-279-772A-5	Sequence 5, Appl
c 702	10	66.7	564	3	US-08-545-809A-8	Sequence 8, Appl	c 775	10	66.7	759	3	US-08-902-486-8	Sequence 8, Appl
703	10	66.7	568	4	US-09-247-155-136	Sequence 136, App	c 776	10	66.7	765	4	US-08-861-774E-57	Sequence 57, Appl
704	10	66.7	569	4	US-09-276-531-69	Sequence 69, App	c 777	10	66.7	769	4	US-09-404-879A-320	Sequence 320, App
c 705	10	66.7	578	4	US-09-328-111-744	Sequence 744, App	c 778	10	66.7	778	3	US-09-188-930-27	Sequence 27, Appl
c 706	10	66.7	581	4	US-09-643-597-133	Sequence 133, App	c 779	10	66.7	778	3	US-09-188-930-202	Sequence 202, App
c 707	10	66.7	588	4	US-09-473-310A-105	Sequence 105, App	c 780	10	66.7	785	4	US-09-812-484-9	Sequence 9, Appl
708	10	66.7	590	2	US-08-600-999-1	Sequence 1, Appl	c 781	10	66.7	786	4	US-08-635-928-31	Sequence 31, Appl
c 709	10	66.7	591	2	US-08-481-814A-4	Sequence 4, Appl	c 782	10	66.7	786	4	US-09-142-623-10	Sequence 10, Appl
c 710	10	66.7	591	4	US-09-385-982-77	Sequence 77, App	c 783	10	66.7	790	1	US-08-393-985-22	Sequence 22, Appl
711	10	66.7	591	4	US-09-602-877A-89	Sequence 89, App	c 784	10	66.7	795	2	US-08-967-101-119	Sequence 119, App
712	10	66.7	593	2	US-08-443-639-12	Sequence 12, Appl	c 785	10	66.7	796	2	US-08-592-541-119	Sequence 119, App
713	10	66.7	593	3	US-08-577-483-12	Sequence 12, Appl	c 786	10	66.7	796	3	US-09-124-698-119	Sequence 119, App
c 714	10	66.7	596	4	US-09-385-982-304	Sequence 304, App	c 787	10	66.7	796	4	US-09-127-480-119	Sequence 119, App
715	10	66.7	598	4	US-09-385-982-267	Sequence 267, App	c 788	10	66.7	796	4	US-08-496-841C-119	Sequence 119, App
716	10	66.7	602	4	US-09-385-982-369	Sequence 369, App	c 789	10	66.7	796	4	US-09-124-523-119	Sequence 119, App
717	10	66.7	603	2	US-08-924-838-6	Sequence 6, Appl	c 790	10	66.7	801	4	US-09-276-531-111	Sequence 111, App
718	10	66.7	611	4	US-08-642-274D-16	Sequence 16, Appl	c 791	10	66.7	803	4	US-09-221-017B-684	Sequence 684, App
719	10	66.7	611	4	US-08-952-014C-16	Sequence 16, Appl	c 792	10	66.7	810	2	US-08-632-507-1	Sequence 1, Appl
c 720	10	66.7	612	4	US-09-385-982-506	Sequence 506, App	c 793	10	66.7	811	3	US-08-961-083-63	Sequence 63, Appl
c 721	10	66.7	612	4	US-09-222-575-56	Sequence 56, App	c 794	10	66.7	815	4	US-08-998-416-441	Sequence 441, App
722	10	66.7	614	4	US-09-920-672-3	Sequence 3, Appl	c 795	10	66.7	820	4	US-08-998-416-343	Sequence 343, App
723	10	66.7	616	4	US-09-289-349-5	Sequence 5, Appl	c 796	10	66.7	825	2	US-08-486-148B-1	Sequence 1, Appl
c 724	10	66.7	616	4	US-09-292-097-7	Sequence 7, Appl	c 797	10	66.7	829	4	US-08-998-416-495	Sequence 495, App
c 725	10	66.7	617	4	US-09-328-111-158	Sequence 158, App	c 798	10	66.7	843	4	US-09-423-439-43	Sequence 43, Appl
726	10	66.7	624	2	US-08-426-599B-3	Sequence 3, Appl	c 799	10	66.7	845	4	US-09-105-390-14	Sequence 14, Appl
c 727	10	66.7	625	4	US-09-328-111-734	Sequence 734, App	c 800	10	66.7	850	4	US-08-998-416-314	Sequence 314, App
728	10	66.7	631	4	US-09-385-982-322	Sequence 322, App	c 801	10	66.7	851	3	US-09-126-646-3	Sequence 3, Appl
c 729	10	66.7	640	4	US-09-385-982-2	Sequence 2, Appl	c 802	10	66.7	851	4	US-09-421-491-3	Sequence 3, Appl
c 730	10	66.7	646	2	US-08-737-129A-3	Sequence 3, Appl	c 803	10	66.7	853	2	US-08-179-557-19	Sequence 19, Appl
c 731	10	66.7	646	4	US-09-438-906-5	Sequence 5, Appl	c 804	10	66.7	864	1	US-08-396-650-2	Sequence 2, Appl
c 732	10	66.7	650	4	US-08-961-527-286	Sequence 286, App	c 805	10	66.7	864	1	US-08-768-626-2	Sequence 2, Appl
733	10	66.7	663	1	US-08-555-394-18	Sequence 18, App	c 806	10	66.7	864	4	US-09-199-637A-392	Sequence 392, App
734	10	66.7	663	3	US-08-745-892-18	Sequence 18, App	c 807	10	66.7	866	4	US-09-257-583-6	Sequence 6, Appl
c 735	10	66.7	672	2	US-08-190-199A-62	Sequence 62, Appl	c 808	10	66.7	872	3	US-08-581-148C-5	Sequence 5, Appl
c 736	10	66.7	678	1	US-08-149-091-5	Sequence 5, Appl	c 809	10	66.7	872	3	US-08-581-148C-6	Sequence 6, Appl
c 737	10	66.7	678	2	PCT-US94-12672-5	Sequence 5, Appl	c 810	10	66.7	874	3	US-08-462-436-1	Sequence 1, Appl
c 738	10	66.7	678	5	US-09-056-285A-5	Sequence 5, Appl	c 811	10	66.7	874	3	US-08-465-275-1	Sequence 1, Appl
c 739	10	66.7	680	4	US-09-328-111-115	Sequence 115, App	c 812	10	66.7	879	4	US-08-640-877-1	Sequence 1, Appl
c 740	10	66.7	687	4	US-09-328-111-115	Sequence 115, App	c 813	10	66.7	879	4	US-09-605-785-531	Sequence 531, App
c 741	10	66.7	695	4	US-09-328-111-67	Sequence 67, App	c 814	10	66.7	879	4	US-09-439-313-531	Sequence 531, App
742	10	66.7	697	2	US-08-401-638-1	Sequence 1, Appl	c 815	10	66.7	883	3	US-09-184-658-7	Sequence 7, Appl
c 743	10	66.7	697	2	US-08-411-920-1	Sequence 1, Appl	c 816	10	66.7	900	4	US-09-105-058C-3	Sequence 3, Appl
c 744	10	66.7	704	3	US-09-048-889-7	Sequence 7, Appl	c 817	10	66.7	909	4	US-09-228-986-67	Sequence 67, Appl
c 745	10	66.7	705	4	US-09-998-416-1080	Sequence 1080, Ap	c 818	10	66.7	910	4	US-09-221-017B-969	Sequence 969, App
c 746	10	66.7	705	4	US-09-171-945-16	Sequence 16, App	c 819	10	66.7	921	1	US-08-396-650-3	Sequence 3, Appl
c 747	10	66.7	705	4	US-09-423-439-17	Sequence 17, Appl	c 820	10	66.7	921	1	US-08-396-650-4	Sequence 4, Appl
c 748	10	66.7	711	1	US-08-061-092A-1	Sequence 1, Appl	c 821	10	66.7	921	1	US-08-270-985-11	Sequence 11, Appl
c 749	10	66.7	711	2	US-08-190-199A-64	Sequence 64, Appl	c 822	10	66.7	921	1	US-08-768-626-3	Sequence 3, Appl
c 750	10	66.7	711	2	US-08-468-252-4	Sequence 4, Appl	c 823	10	66.7	921	1	US-08-768-626-4	Sequence 4, Appl
c 751	10	66.7	711	3	US-08-668-706B-4	Sequence 4, Appl	c 824	10	66.7	924	2	US-08-478-208-19	Sequence 19, Appl
c 752	10	66.7	711	5	PCT-US95-10740-4	Sequence 4, Appl	c 825	10	66.7	924	2	US-08-860-174A-9	Sequence 9, Appl
c 753	10	66.7	717	4	US-09-142-974B-1	Sequence 1, Appl	c 826	10	66.7	930	4	US-09-171-025-26	Sequence 26, Appl
c 754	10	66.7	719	3	US-08-279-772A-7	Sequence 7, Appl	c 827	10	66.7	934	4	US-09-171-025-3	Sequence 3, Appl
c 755	10	66.7	720	3	US-08-902-486-10	Sequence 10, Appl	c 828	10	66.7	933	4	US-09-347-803-21	Sequence 21, Appl
c 756	10	66.7	720	4	US-08-913-014A-4	Sequence 4, Appl	c 829	10	66.7	943	2	US-08-303-569B-4	Sequence 4, Appl
c 757	10	66.7	726	2	US-08-553-497A-25	Sequence 25, Appl	c 830	10	66.7	943	2	US-08-116-247-4	Sequence 4, Appl

c 831	10	66.7	951	1	US-08-221-750A-12	Sequence 12, Appl	c 904	10	66.7	1256	4	US-09-553-498-7	Sequence 7, Appl
c 832	10	66.7	952	4	US-08-943-731-87	Sequence 87, Appl	c 905	10	66.7	1256	4	US-09-618-869-7	Sequence 7, Appl
c 833	10	66.7	959	3	US-08-297-431B-11	Sequence 11, Appl	c 906	10	66.7	1257	4	US-08-791-115B-8	Sequence 8, Appl
c 834	10	66.7	969	4	US-08-346-147B-23	Sequence 23, Appl	c 907	10	66.7	1277	2	US-08-555-568B-18	Sequence 18, Appl
c 835	10	66.7	975	2	US-08-637-761-7	Sequence 7, Appl	c 908	10	66.7	1277	4	US-09-519-223-18	Sequence 18, Appl
c 836	10	66.7	975	5	PCT-US94-12672-7	Sequence 7, Appl	c 909	10	66.7	1281	3	US-09-063-893A-1	Sequence 1, Appl
c 837	10	66.7	980	4	US-09-171-209-8	Sequence 8, Appl	c 910	10	66.7	1281	4	US-09-082-092-7	Sequence 7, Appl
c 838	10	66.7	987	4	US-08-910-722-1	Sequence 1, Appl	c 911	10	66.7	1281	4	US-09-082-092-8	Sequence 8, Appl
c 839	10	66.7	987	4	US-09-457-568-27	Sequence 27, Appl	c 912	10	66.7	1288	2	US-09-172-977-2	Sequence 2, Appl
c 840	10	66.7	987	4	US-09-457-646-27	Sequence 27, Appl	c 913	10	66.7	1290	4	US-09-149-476-176	Sequence 176, App
c 841	10	66.7	987	4	US-09-370-838-289	Sequence 289, App	c 914	10	66.7	1302	3	US-08-932-823A-1	Sequence 1, Appl
c 842	10	66.7	994	2	US-08-627-610-1	Sequence 1, Appl	c 915	10	66.7	1314	4	US-09-242-737-1	Sequence 1, Appl
c 843	10	66.7	994	2	US-08-306-511A-1	Sequence 1, Appl	c 916	10	66.7	1320	4	US-09-210-748A-1	Sequence 1, Appl
c 844	10	66.7	994	2	US-08-893-274-1	Sequence 1, Appl	c 917	10	66.7	1322	4	US-09-128-450-27	Sequence 27, Appl
c 845	10	66.7	994	3	US-08-581-918A-1	Sequence 1, Appl	c 918	10	66.7	1322	4	US-09-823-494-27	Sequence 27, Appl
c 846	10	66.7	994	4	US-08-346-147B-1	Sequence 1, Appl	c 919	10	66.7	1329	4	US-09-296-284-23	Sequence 23, Appl
c 847	10	66.7	994	4	US-08-822-936-1	Sequence 1, Appl	c 920	10	66.7	1340	3	US-09-184-658-8	Sequence 8, Appl
c 848	10	66.7	994	4	US-08-497-214D-1	Sequence 1, Appl	c 921	10	66.7	1341	4	US-09-018-633-30	Sequence 30, Appl
c 849	10	66.7	999	5	PCT-US95-04636-1	Sequence 1, Appl	c 922	10	66.7	1345	1	US-08-592-214A-7	Sequence 7, Appl
c 850	10	66.7	999	2	US-08-860-174B-6	Sequence 6, Appl	c 923	10	66.7	1345	3	US-08-659-188-7	Sequence 7, Appl
c 851	10	66.7	999	4	US-09-171-025-25	Sequence 25, Appl	c 924	10	66.7	1345	3	US-08-655-227-7	Sequence 7, Appl
c 852	10	66.7	1000	4	US-09-128-450-25	Sequence 25, Appl	c 925	10	66.7	1345	3	US-08-655-241-7	Sequence 7, Appl
c 853	10	66.7	1000	4	US-09-823-494-25	Sequence 25, Appl	c 926	10	66.7	1345	3	US-09-149-976-7	Sequence 7, Appl
c 854	10	66.7	1001	4	US-09-641-638-320	Sequence 320, App	c 927	10	66.7	1345	4	US-09-398-328-7	Sequence 7, Appl
c 855	10	66.7	1011	4	US-09-134-001C-1342	Sequence 1342, Ap	c 928	10	66.7	1351	1	US-07-816-283-5	Sequence 5, Appl
c 856	10	66.7	1024	3	US-08-934-494-3	Sequence 3, Appl	c 929	10	66.7	1351	1	US-08-417-103-5	Sequence 5, Appl
c 857	10	66.7	1024	3	US-09-143-068-3	Sequence 3, Appl	c 930	10	66.7	1353	4	US-08-913-014A-6	Sequence 6, Appl
c 858	10	66.7	1024	4	US-09-143-707-3	Sequence 3, Appl	c 931	10	66.7	1357	4	US-09-448-176-9	Sequence 9, Appl
c 859	10	66.7	1024	4	US-09-202-089-3	Sequence 3, Appl	c 932	10	66.7	1357	4	US-09-448-176-10	Sequence 10, Appl
c 860	10	66.7	1024	4	US-09-511-133-3	Sequence 3, Appl	c 933	10	66.7	1357	4	US-09-448-176-11	Sequence 11, Appl
c 861	10	66.7	1024	4	US-09-690-169-3	Sequence 3, Appl	c 934	10	66.7	1359	1	US-08-275-488A-1	Sequence 1, Appl
c 862	10	66.7	1024	4	US-09-511-631-3	Sequence 3, Appl	c 935	10	66.7	1359	1	US-08-275-490-1	Sequence 1, Appl
c 863	10	66.7	1035	1	US-07-601-094-30	Sequence 30, Appl	c 936	10	66.7	1359	1	US-08-446-380-1	Sequence 1, Appl
c 864	10	66.7	1035	1	US-08-012-735-30	Sequence 30, Appl	c 937	10	66.7	1359	1	US-08-446-374-1	Sequence 1, Appl
c 865	10	66.7	1053	5	PCT-US91-06418-2	Sequence 2, Appl	c 938	10	66.7	1359	1	US-08-446-382-1	Sequence 1, Appl
c 866	10	66.7	1075	4	US-09-276-531-95	Sequence 95, Appl	c 939	10	66.7	1359	1	US-08-445-801-1	Sequence 1, Appl
c 867	10	66.7	1092	4	US-09-134-001C-1382	Sequence 1382, Ap	c 940	10	66.7	1359	1	US-08-275-487-1	Sequence 1, Appl
c 868	10	66.7	1094	2	US-08-902-294-1	Sequence 1, Appl	c 941	10	66.7	1359	3	US-08-275-487-1	Sequence 1, Appl
c 869	10	66.7	1094	3	US-09-178-637-1	Sequence 1, Appl	c 942	10	66.7	1359	5	PCT-US95-08919-1	Sequence 17, Appl
c 870	10	66.7	1098	4	US-09-221-017B-928	Sequence 928, App	c 943	10	66.7	1362	1	US-08-275-488A-11	Sequence 11, Appl
c 871	10	66.7	1100	2	US-08-481-814B-5	Sequence 5, Appl	c 944	10	66.7	1362	1	US-08-275-490-11	Sequence 11, Appl
c 872	10	66.7	1102	4	US-09-641-638-586	Sequence 586, App	c 945	10	66.7	1362	1	US-08-446-380-11	Sequence 11, Appl
c 873	10	66.7	1108	5	PCT-US93-03035-1	Sequence 1, Appl	c 946	10	66.7	1362	1	US-08-446-374-11	Sequence 11, Appl
c 874	10	66.7	1111	4	US-09-221-017B-56	Sequence 56, Appl	c 947	10	66.7	1362	1	US-08-446-382-11	Sequence 11, Appl
c 875	10	66.7	1114	3	US-09-048-889-10	Sequence 10, Appl	c 948	10	66.7	1362	1	US-08-445-801-11	Sequence 11, Appl
c 876	10	66.7	1116	4	US-09-221-017B-125	Sequence 125, App	c 949	10	66.7	1362	1	US-08-275-487-11	Sequence 11, Appl
c 877	10	66.7	1128	1	US-07-872-678A-11	Sequence 11, Appl	c 950	10	66.7	1362	5	PCT-US95-08919-11	Sequence 11, Appl
c 878	10	66.7	1138	3	US-08-913-842-8	Sequence 8, Appl	c 951	10	66.7	1362	6	5290690-8	Patent No. 5290690
c 879	10	66.7	1147	1	US-08-417-103-15	Sequence 15, Appl	c 952	10	66.7	1365	1	US-08-114-072-1	Sequence 1, Appl
c 880	10	66.7	1168	4	US-09-149-476-79	Sequence 79, Appl	c 953	10	66.7	1365	5	PCT-US94-09361-1	Sequence 1, Appl
c 881	10	66.7	1170	2	US-08-933-750C-76	Sequence 76, Appl	c 954	10	66.7	1371	4	US-09-134-001C-517	Sequence 517, App
c 882	10	66.7	1173	3	US-09-234-613-76	Sequence 76, Appl	c 955	10	66.7	1386	4	US-09-433-248A-1	Sequence 1, Appl
c 883	10	66.7	1173	4	US-09-232-200-50	Sequence 50, Appl	c 956	10	66.7	1401	1	US-07-843-948A-3	Sequence 3, Appl
c 884	10	66.7	1173	4	US-09-232-197-50	Sequence 50, Appl	c 957	10	66.7	1401	2	US-08-218-978-3	Sequence 3, Appl
c 885	10	66.7	1173	4	US-09-232-201-50	Sequence 50, Appl	c 958	10	66.7	1407	1	US-08-218-978-3	Sequence 7, Appl
c 886	10	66.7	1176	4	US-09-142-974B-3	Sequence 3, Appl	c 959	10	66.7	1407	1	US-08-278-630A-7	Sequence 1, Appl
c 887	10	66.7	1188	1	US-08-048-700-1	Sequence 1, Appl	c 960	10	66.7	1409	6	5242798-6	Patent No. 5242798
c 888	10	66.7	1188	3	US-08-839-711-5	Sequence 5, Appl	c 961	10	66.7	1410	3	US-08-147-592A-1	Sequence 1, Appl
c 889	10	66.7	1191	2	US-08-968-751-5	Sequence 5, Appl	c 962	10	66.7	1410	4	US-08-292-694A-1	Sequence 1, Appl
c 890	10	66.7	1196	1	US-08-167-939A-5	Sequence 5, Appl	c 963	10	66.7	1416	1	US-08-236-311-3	Sequence 3, Appl
c 891	10	66.7	1196	1	US-08-567-538-5	Sequence 5, Appl	c 964	10	66.7	1416	3	US-08-457-918-3	Sequence 3, Appl
c 892	10	66.7	1204	4	US-08-861-774B-87	Sequence 87, Appl	c 965	10	66.7	1419	2	US-08-194-981E-4	Sequence 4, Appl
c 893	10	66.7	1213	4	US-08-976-259-7	Sequence 7, Appl	c 966	10	66.7	1419	4	US-09-276-531-1	Sequence 1, Appl
c 894	10	66.7	1215	1	US-08-696-139-1	Sequence 1, Appl	c 967	10	66.7	1425	3	US-08-729-416C-10	Sequence 10, Appl
c 895	10	66.7	1217	4	US-09-610-040-4	Sequence 4, Appl	c 968	10	66.7	1437	4	US-09-296-284-2	Sequence 2, Appl
c 896	10	66.7	1217	4	US-09-610-040-10	Sequence 10, Appl	c 969	10	66.7	1438	4	US-08-821-827C-1	Sequence 1, Appl
c 897	10	66.7	1225	2	US-08-674-149A-1	Sequence 1, Appl	c 970	10	66.7	1438	4	US-09-290-202B-1	Sequence 1, Appl
c 898	10	66.7	1233	4	US-09-276-531-7	Sequence 7, Appl	c 971	10	66.7	1443	1	US-08-443-965B-10	Sequence 10, Appl
c 899	10	66.7	1235	3	US-09-004-171-1	Sequence 1, Appl	c 972	10	66.7	1443	2	US-08-425-989B-10	Sequence 10, Appl
c 900	10	66.7	1245	1	US-07-887-072B-1	Sequence 1, Appl	c 973	10	66.7	1443	2	US-08-443-965B-10	Sequence 10, Appl
c 901	10	66.7	1245	1	US-08-466-444-1	Sequence 1, Appl	c 974	10	66.7	1446	2	US-08-484-126-2	Sequence 2, Appl
c 902	10	66.7	1246	1	US-09-302-769-22	Sequence 22, Appl	c 975	10	66.7	1451	1	US-08-161-286-2	Sequence 2, Appl
c 903	10	66.7	1251	4	US-09-105-537-38	Sequence 38, Appl	c 976	10	66.7	1452	4	US-09-039-982A-36	Sequence 36, Appl

c 977 10 66.7 1452 4 US-09-039-641-36 Sequence 36, Appl  
c 978 10 66.7 1452 4 US-09-039-762A-36 Sequence 36, Appl  
c 979 10 66.7 1452 4 US-09-042-492D-36 Sequence 36, Appl  
c 980 10 66.7 1452 4 US-08-913-612A-36 Sequence 36, Appl  
c 981 10 66.7 1455 1 US-08-446-803-5 Sequence 5, Appl  
c 982 10 66.7 1455 2 US-08-861-837-5 Sequence 5, Appl  
c 983 10 66.7 1455 3 US-08-600-650-5 Sequence 5, Appl  
c 984 10 66.7 1455 4 US-09-170-670-10 Sequence 10, Appl  
c 985 10 66.7 1455 4 US-09-170-670-15 Sequence 15, Appl  
c 986 10 66.7 1455 4 US-09-193-068-10 Sequence 10, Appl  
c 987 10 66.7 1455 4 US-09-193-068-14 Sequence 14, Appl  
c 988 10 66.7 1455 4 US-09-183-412-10 Sequence 10, Appl  
c 989 10 66.7 1455 4 US-09-183-412-14 Sequence 14, Appl  
c 990 10 66.7 1455 4 US-09-354-191A-5 Sequence 5, Appl  
c 991 10 66.7 1455 4 US-09-290-734-10 Sequence 10, Appl  
c 992 10 66.7 1455 4 US-09-290-734-15 Sequence 15, Appl  
c 993 10 66.7 1457 1 US-08-460-512-1 Sequence 1, Appl  
c 994 10 66.7 1462 1 US-08-552-142A-16 Sequence 16, Appl  
c 995 10 66.7 1470 4 US-09-099-041A-27 Sequence 27, Appl  
c 996 10 66.7 1470 4 US-09-245-281-27 Sequence 27, Appl  
c 997 10 66.7 1470 4 US-09-207-359B-27 Sequence 27, Appl  
c 998 10 66.7 1479 1 US-08-644-271-31 Sequence 31, Appl  
c 999 10 66.7 1479 4 US-09-077-955-35 Sequence 35, Appl  
1000 10 66.7 1482 3 US-09-032-365A-16 Sequence 16, Appl

ALIGNMENTS

RESULT 1  
US-09-484-970B-82  
; Sequence 82, Application US/09484970B  
; Patent No. 6426186  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Karen A.  
; APPLICANT: Volkmutch, Wayne  
; APPLICANT: Walker, Michael G.  
; TITLE OF INVENTION: BONE REMODELING GENES  
; FILE REFERENCE: PB-0014 US  
; CURRENT APPLICATION NUMBER: US/09/484, 970B  
; CURRENT FILING DATE: 2000-01-18  
; NUMBER OF SEQ ID NOS: 172  
; SOFTWARE: PERL Program  
; SEQ ID NO 82  
; LENGTH: 776  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No. 6426186 199069.2CB1  
US-09-484-970B-82

Query Match 86.7%; Score 13; DB 4; Length 776;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCCCTGTT 15  
| | | | | | | | | | | | | | | | |  
Db 638 TTCTCCCTGTT 650

RESULT 2  
US-08-619-542B-29/c  
; Sequence 29, Application US/08619542B  
; Patent No. 5830662  
; GENERAL INFORMATION:  
; APPLICANT: The Trustees of Columbia University in the City  
; APPLICANT: of New York  
; TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF NORMALIZED  
; TITLE OF INVENTION: CDNA LIBRARIES  
; NUMBER OF SEQUENCES: 78  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP

; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/619,542B  
; FILING DATE: June 21, 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 42840-A-PCT-US  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1419 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
US-08-619-542B-29  
  
Query Match 86.7%; Score 13; DB 2; Length 1419;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CCTTCTCCCTG 13  
| | | | | | | | | | | | | | | | |  
Db 1020 CCTTCTCCCTG 1008  
  
RESULT 3  
US-09-295-744A-1  
; Sequence 1, Application US/09295744A  
; Patent No. 6355228  
; GENERAL INFORMATION:  
; APPLICANT: Fuglsang, Claus Crone  
; TITLE OF INVENTION: An Oral Care Product Comprising A Mutan  
; Binding Domain  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 6355228o No. 6355228disk of No. 6355228th America, Inc.  
; STREET: 405 Lexington Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10174  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/295,744A  
; FILING DATE: 20-Apr-1999  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Rozek, Carol  
; REGISTRATION NUMBER: 36,993  
; REFERENCE/DOCKET NUMBER: 4735.204-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-867-0123  
; TELEFAX: 212-878-9655  
; INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1905 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
STRAIN: Trichoderma harzianum CBS 243.71  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 1..120  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-295-744A-1

Query Match 86.7%; Score 13; DB 4; Length 1905;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTCTCCCTGT 14  
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Db 1568 CTTCTCCCTGT 1580

## RESULT 4

US-09-221-017B-351/c  
; Sequence 351, Application US/09221017B  
; Patent No. 6444799  
; GENERAL INFORMATION:  
; APPLICANT: Ross, Bruce C.  
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF  
; NUMBER OF SEQUENCES: 1120  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/221,017B  
; FILING DATE: 23-DEC-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: Pp1182  
; FILING DATE: 31-DEC-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: Pp1546  
; FILING DATE: 30-JAN-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: Pp2911  
; FILING DATE: 09-APR-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/AU98/01023  
; FILING DATE: 10-DEC-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Monroy, Gladys H  
; REGISTRATION NUMBER: 32,430  
; REFERENCE/DOCKET NUMBER: 27340-20021.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-813-5600  
; TELEFAX: 650-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 351:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2431 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: UNKNOWN  
; ORIGINAL SOURCE:  
; ORGANISM: PORYPHYROMONAS GINGIVALIS  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 1...2431  
US-09-221-017B-351

Query Match 86.7%; Score 13; DB 4; Length 2431;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCCCTGT 15  
|||||  
Db 655 TTCTCCCTGT 643

## RESULT 5

US-08-149-695-8  
; Sequence 8, Application US/08149695  
; Patent No. 5412085  
; GENERAL INFORMATION:  
; APPLICANT: Allen, Rebecca L.  
; APPLICANT: Lonsdale, David M.  
; TITLE OF INVENTION: A Pollen-Specific Promoter From Maize  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held and Malloy  
; STREET: 500 W. Madison, 34th Floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: U.S.A.  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/149,695  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/911,532  
; FILING DATE: 09-JUL-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pochopien, Donald J.  
; REGISTRATION NUMBER: 32167  
; REFERENCE/DOCKET NUMBER: 92 P139  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312)707-9155  
; TELEFAX: (312)707-8889  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2687 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Zea mays  
; STRAIN: Line W22  
US-08-149-695-8

Query Match 86.7%; Score 13; DB 1; Length 2687;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCCCTGT 15

Db 477 TTCTCCCTGTT 489

## RESULT 6

US-08-377-228-8  
; Sequence 8, Application US/08377228  
; Patent No. 5545546  
; GENERAL INFORMATION:  
; APPLICANT: ALLEN, Rebecca L.  
; APPLICANT: LONSDALE, David M.  
; TITLE OF INVENTION: A Pollen-Specific Promoter From Maize  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/377,228  
; FILING DATE: 24-JAN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/149,695  
; FILING DATE: 09-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/911,532  
; FILING DATE: 09-JUL-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 33229/290/PIHI  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2687 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
US-08-377-228-8

Query Match 86.7%; Score 13; DB 1; Length 2687;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCCCTGTT 15  
Db 477 TTCTCCCTGTT 489

## RESULT 7

US-08-149-695-1  
; Sequence 1, Application US/08149695  
; Patent No. 5412085  
; GENERAL INFORMATION:  
; APPLICANT: ALLEN, Rebecca L.  
; APPLICANT: Lonsdale, David M.  
; TITLE OF INVENTION: A Pollen-Specific Promoter From Maize  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAndrews, Held and Malloy  
; STREET: 500 W. Madison, 34th Floor  
; CITY: Chicago

; STATE: Illinois  
; COUNTRY: U.S.A.  
; ZIP: 60661  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/149,695  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/911,532  
; FILING DATE: 09-JUL-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pochopien, Donald J.  
; REGISTRATION NUMBER: 32167  
; REFERENCE/DOCKET NUMBER: 92 P139  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312)707-8889  
; TELEFAX: (312)707-9155  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2873 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Zea mays  
; STRAIN: Line W22  
; TISSUE TYPE: Pollen  
US-08-149-695-1

Query Match 86.7%; Score 13; DB 1; Length 2873;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCCCTGTT 15  
Db 663 TTCTCCCTGTT 675

## RESULT 8

US-08-377-228-1  
; Sequence 1, Application US/08377228  
; Patent No. 5545546  
; GENERAL INFORMATION:  
; APPLICANT: ALLEN, Rebecca L.  
; APPLICANT: LONSDALE, David M.  
; TITLE OF INVENTION: A Pollen-Specific Promoter From Maize  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/377,228  
; FILING DATE: 24-JAN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/149,695



```
; FILING DATE: 09-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/911,532
; FILING DATE: 09-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 33229/290/PIHI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2873 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-377-228-1

Query Match      86.7%; Score 13; DB 1; Length 2873;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCCCTGTT 15
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Db 663 TTCTCCCTGTT 675

RESULT 9
US-08-244-189-1/c
; Sequence 1, Application US/08244189
; Patent No. 5580727
; GENERAL INFORMATION:
; APPLICANT: Ohki, Misao
; APPLICANT: Kikuchi, Kimiko
; APPLICANT: Miyoshi, Hiroyuki
; APPLICANT: Kozu, Tomoko
; TITLE OF INVENTION: No. 5580727el DNAs, Polypeptides Encoded Thereby
; TITLE OF INVENTION: and Methods for Detecting the DNAs and Polypeptides
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/244,189
; FILING DATE: 15-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 760-183P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4287 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
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; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1579..3834
US-08-244-189-1

Query Match      86.7%; Score 13; DB 1; Length 4287;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCCCTGTT 15
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Db 298 TTCTCCCTGTT 286

RESULT 10
US-08-306-691B-53/c
; Sequence 53, Application US/08306691B
; Patent No. 5734039
; GENERAL INFORMATION:
; APPLICANT: Calabretta, Bruno
; APPLICANT: Skorski, Tomasz
; TITLE OF INVENTION: ANTISENSE
; TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
; STREET: Two Penn Center, Suite 1800
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/306,691B
; FILING DATE: September 15, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 8321-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: No. 5734039e
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4287 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-306-691B-53

Query Match      86.7%; Score 13; DB 1; Length 4287;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCCCTGTT 15
   |||||
Db 298 TTCTCCCTGTT 286

RESULT 11
US-08-770-301A-2/c
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Sequence 2, Application US/08770301A  
Patent No. 5948637  
GENERAL INFORMATION:  
APPLICANT: IKEDA, JUN  
APPLICANT: KANEDA, SUMIKO  
APPLICANT: YANAGI, HIDEKI  
APPLICANT: MATSUMOTO, MASAYASU  
APPLICANT: YURA, TAKASHI  
TITLE OF INVENTION: NOVEL STRESS PROTEINS  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
STREET: PO BOX 747  
CITY: FALLS CHURCH  
STATE: VA  
COUNTRY: USA  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,301A  
FILING DATE: 20-DEC-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MURPHY JR, GERALD M  
REGISTRATION NUMBER: 28,977  
REFERENCE/DOCKET NUMBER: 1422-287  
TELEPHONE: (703)-205-8000  
TELEFAX: (703)-205-8050  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4503 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
IDENTIFICATION METHOD: E  
US-08-770-301A-2

Query Match 86.7%; Score 13; DB 2; Length 4503;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTG 13  
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Db 2923 CCTTCTCCCCCTG 2911

RESULT 12  
US-09-175-581-2/c  
Sequence 2, Application US/09175581  
Patent No. 6034232  
GENERAL INFORMATION:  
APPLICANT: IKEDA, JUN  
APPLICANT: KANEDA, SUMIKO  
APPLICANT: YANAGI, HIDEKI  
APPLICANT: MATSUMOTO, MASAYASU  
APPLICANT: YURA, TAKASHI  
TITLE OF INVENTION: NOVEL STRESS PROTEINS  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
STREET: PO BOX 747  
CITY: FALLS CHURCH  
STATE: VA  
COUNTRY: USA  
ZIP: 22040-0747

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/175,581  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/770,301  
FILING DATE: 20-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: MURPHY JR, GERALD M  
REGISTRATION NUMBER: 28,977  
REFERENCE/DOCKET NUMBER: 1422-287  
TELEPHONE: (703)-205-8000  
TELEFAX: (703)-205-8050  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4503 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
IDENTIFICATION METHOD: E  
US-09-175-581-2

Query Match 86.7%; Score 13; DB 3; Length 4503;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTG 13  
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Db 2923 CCTTCTCCCCCTG 2911

RESULT 13  
US-09-295-744A-12  
Sequence 12, Application US/09295744A  
Patent No. 6355228  
GENERAL INFORMATION:  
APPLICANT: Fudlsang, Claus Crone  
TITLE OF INVENTION: An Oral Care Product Comprising A Mutan Binding Domain  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NO. 6355228o No. 6355228disk of No. 6355228th America, Inc.  
STREET: 405 Lexington Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10174  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/295,744A  
FILING DATE: 20-Apr-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Rozek, Carol  
REGISTRATION NUMBER: 36,993  
REFERENCE/DOCKET NUMBER: 4735,204-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:  
LENGTH: 6032 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
STRAIN: Trichoderma harzianum CBS 243.71  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 3188..5092  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-09-295-744A-12

Query Match 86.7%; Score 13; DB 4; Length 6032;

Best Local Similarity 100.0%; Pred. No. 36; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTCTCCCCCTGT 14

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Db 4755 CTTCTCCCCCTGT 4767

#### RESULT 14

US-09-813-133A-3/c  
; Sequence 3, Application US/09813133A  
; Patent No. 6455294  
; GENERAL INFORMATION:  
; APPLICANT: GAN, Weiniu et al  
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001173  
; CURRENT APPLICATION NUMBER: US/09/813,133A  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 55827  
; TYPE: DNA  
; ORGANISM: Human  
US-09-813-133A-3

Query Match 86.7%; Score 13; DB 4; Length 55827;

Best Local Similarity 100.0%; Pred. No. 36; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTCTCCCCCTGT 14

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Db 48061 CTTCTCCCCCTGT 48049

#### RESULT 15

US-09-103-840A-1  
; Sequence 1, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; TITLE OF INVENTION: TUBERCULOSIS  
; FILE REFERENCE: 24366-20007.00  
; CURRENT APPLICATION NUMBER: US/09/103,840A  
; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 4411529  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; OTHER INFORMATION: H37RV

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Query Match 86.7%; Score 13; DB 4; Length 4411529;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTCTCCCCCTG 13

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Db 2740254 CTTCTCCCCCTG 2740266

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OM nucleic - nucleic search, using sw model

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Perfect score: 15  
Sequence: 1 ccttcccccctgtt 15

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 350425 seqs, 194966369 residues

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14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	14	93.3	482	9	US-10-001-835-84
5	14	93.3	594	10	US-09-864-761-13104
6	14	93.3	8894	10	US-09-764-864-1692
7	14	93.3	8894	10	US-09-764-877-3063
8	14	93.3	16877	10	US-09-764-877-3349
9	13	86.7	209	10	US-09-864-761-23357
10	13	86.7	210	10	US-09-922-217-616
11	13	86.7	210	10	US-09-833-263-616
12	13	86.7	285	10	US-09-867-701-4769
13	13	86.7	315	9	US-09-712-363-96
14	13	86.7	337	10	US-09-867-701-10110
15	13	86.7	383	10	US-09-954-456-892
16	13	86.7	383	10	US-09-880-107-1077
17	13	86.7	444	9	US-10-040-739-1245
18	13	86.7	469	10	US-09-864-761-551
19	13	86.7	494	10	US-09-867-701-6731

Sequence 8112, Ap	500	86.7	13	20	US-09-864-761-8112
Sequence 15376, A	565	86.7	13	21	US-09-864-761-15376
Sequence 8638, Ap	598	86.7	13	22	US-09-864-761-8638
Sequence 5908, Ap	705	86.7	13	23	US-09-974-300-5908
Sequence 5909, Ap	705	86.7	13	24	US-09-974-300-5909
Sequence 96, Appl	957	86.7	13	25	US-09-771-730-96
Sequence 442, App	1059	86.7	13	26	US-09-886-055-442
Sequence 19, Appl	1077	86.7	13	27	US-09-771-730-19
Sequence 1569, Ap	1119	86.7	13	28	US-09-938-842A-1569
Sequence 9217, Ap	1656	86.7	13	29	US-09-815-242-9217
Sequence 5, Appl	2007	86.7	13	30	US-09-974-300-5
Sequence 579, App	2525	86.7	13	31	US-09-925-300-579
Sequence 3, Appl	2902	86.7	13	32	US-09-921-771-3
Sequence 1204, Ap	4254	86.7	13	33	US-09-764-847-1204
Sequence 1203, Ap	4255	86.7	13	34	US-09-764-847-1203
Sequence 93, Appl	4521	86.7	13	35	US-10-002-600-93
Sequence 479, App	5728	86.7	13	36	US-09-917-800A-479
Sequence 1607, Ap	5938	86.7	13	37	US-09-954-456-1607
Sequence 225, App	5938	86.7	13	38	US-09-967-768A-225
Sequence 232, App	14537	86.7	13	39	US-09-962-832-232
Sequence 1768, Ap	30352	86.7	13	40	US-09-764-869-1768
Sequence 6, Appl	180557	86.7	13	41	US-10-003-806-6
Sequence 9, Appl	180557	86.7	13	42	US-10-003-806-9
Sequence 12763, A	68	80.0	12	43	US-09-878-574-12763
Sequence 17945, A	114	80.0	12	44	US-09-864-761-17945
Sequence 29686, A	171	80.0	12	45	US-09-864-761-29686
Sequence 20593, A	174	80.0	12	46	US-09-864-761-20593
Sequence 4063, Ap	198	80.0	12	47	US-09-974-300-4063
Sequence 26180, A	208	80.0	12	48	US-09-864-761-26180
Sequence 23158, A	238	80.0	12	49	US-09-864-761-23158
Sequence 9020, Ap	257	80.0	12	50	US-09-878-574-9020
Sequence 1887, Ap	258	80.0	12	51	US-09-923-876-1887
Sequence 6888, Ap	259	80.0	12	52	US-09-878-574-6888
Sequence 10358, A	261	80.0	12	53	US-09-878-574-10358
Sequence 13106, A	268	80.0	12	54	US-09-878-574-13106
Sequence 1032, Ap	270	80.0	12	55	US-09-954-456-1002
Sequence 2136, Ap	277	80.0	12	56	US-09-764-869-2136
Sequence 2137, Ap	278	80.0	12	57	US-09-764-869-2137
Sequence 11893, A	278	80.0	12	58	US-09-783-590-11893
Sequence 6284, Ap	278	80.0	12	59	US-09-867-701-6284
Sequence 7492, Ap	287	80.0	12	60	US-09-878-574-7492
Sequence 23773, A	294	80.0	12	61	US-09-864-761-23773
Sequence 598, App	303	80.0	12	62	US-09-833-381-598
Sequence 635, App	324	80.0	12	63	US-09-764-864-635
Sequence 1125, Ap	325	80.0	12	64	US-09-920-300A-1125
Sequence 1125, Ap	325	80.0	12	65	US-10-033-528-1125
Sequence 3979, Ap	327	80.0	12	66	US-09-878-574-3979
Sequence 6452, Ap	342	80.0	12	67	US-09-864-761-6452
Sequence 4037, Ap	398	80.0	12	68	US-09-878-574-4037
Sequence 920, App	401	80.0	12	69	US-09-946-807-920
Sequence 920, App	401	80.0	12	70	US-09-795-668-920
Sequence 920, App	401	80.0	12	71	US-09-795-668-920
Sequence 2331, Ap	403	80.0	12	72	US-09-878-574-2331
Sequence 1180, Ap	410	80.0	12	73	US-09-864-761-1180
Sequence 3161, Ap	440	80.0	12	74	US-09-983-965-3161
Sequence 6315, Ap	449	80.0	12	75	US-09-864-761-6315
Sequence 710, App	455	80.0	12	76	US-09-583-817-710
Sequence 5334, Ap	467	80.0	12	77	US-09-864-761-5334
Sequence 6443, Ap	473	80.0	12	78	US-09-864-761-6443
Sequence 701, App	477	80.0	12	79	US-09-917-800A-701
Sequence 663, App	486	80.0	12	80	US-09-919-580-663
Sequence 14683, A	494	80.0	12	81	US-09-864-761-14683
Sequence 10889, A	496	80.0	12	82	US-09-864-761-10689
Sequence 13125, A	506	80.0	12	83	US-09-864-761-13125
Sequence 18121, A	512	80.0	12	84	US-09-864-761-18121
Sequence 208, App	544	80.0	12	85	US-09-728-445-208
Sequence 540, App	546	80.0	12	86	US-09-919-580-540
Sequence 7150, Ap	557	80.0	12	87	US-09-864-761-7150
Sequence 6342, Ap	565	80.0	12	88	US-09-974-300-6342
Sequence 76, Appl	580	80.0	12	89	US-10-001-879-76
Sequence 9824, Ap	582	80.0	12	90	US-09-864-761-9824
Sequence 7042, Ap	595	80.0	12	91	US-09-864-761-7042
Sequence 414, App	621	80.0	12	92	US-09-879-536-414

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c 98	12	80.0	936	10	US-09-974-300-836	Sequence 836, App	171	11	73.3	195	12	US-10-033-528-1847	Sequence 1847, Ap
c 99	12	80.0	970	10	US-09-974-300-1871	Sequence 1871, Ap	172	11	73.3	209	10	US-09-864-761-21470	Sequence 21470, A
c 100	12	80.0	987	10	US-09-978-396-41	Sequence 41, Appl	173	11	73.3	216	10	US-09-974-300-7574	Sequence 7574, Ap
c 101	12	80.0	1012	10	US-09-864-761-17503	Sequence 17503, A	174	11	73.3	233	10	US-09-752-639-3	Sequence 3, Appl
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c 103	12	80.0	1274	9	US-09-981-876-72	Sequence 72, Appl	c 176	11	73.3	234	10	US-09-815-343-84	Sequence 84, Appl
c 104	12	80.0	1296	9	US-09-981-876-126	Sequence 126, App	c 177	11	73.3	235	10	US-09-783-590-2146	Sequence 2146, Ap
c 105	12	80.0	1343	10	US-09-923-300-779	Sequence 779, App	178	11	73.3	235	10	US-09-867-701-8842	Sequence 8842, Ap
c 106	12	80.0	1346	10	US-09-728-932-77	Sequence 77, Appl	179	11	73.3	236	10	US-09-923-876-2115	Sequence 2115, Ap
c 107	12	80.0	1486	10	US-09-925-302-247	Sequence 247, App	180	11	73.3	236	10	US-09-843-856-24	Sequence 24, Appl
c 108	12	80.0	1584	10	US-09-974-300-231	Sequence 231, App	181	11	73.3	240	10	US-09-923-876-5718	Sequence 5718, Ap
c 109	12	80.0	1622	10	US-09-864-864-303	Sequence 303, App	182	11	73.3	242	10	US-09-920-345-23	Sequence 23, Appl
c 110	12	80.0	1652	10	US-09-938-803-23	Sequence 23, Appl	183	11	73.3	254	10	US-09-908-711-44	Sequence 44, Appl
c 111	12	80.0	1657	10	US-09-764-870-28	Sequence 28, Appl	184	11	73.3	254	10	US-09-867-701-8876	Sequence 8876, Ap
c 112	12	80.0	1715	10	US-09-917-800A-1631	Sequence 1631, Ap	185	11	73.3	256	10	US-09-923-876-656	Sequence 656, App
c 113	12	80.0	1756	10	US-09-925-297-221	Sequence 221, App	186	11	73.3	258	10	US-09-923-876-2314	Sequence 2314, Ap
c 114	12	80.0	2100	10	US-09-799-777-94	Sequence 94, Appl	187	11	73.3	260	10	US-09-783-590-2807	Sequence 2807, Ap
c 115	12	80.0	2127	12	US-10-143-002-1	Sequence 1, Appl	188	11	73.3	261	9	US-09-974-300-5852	Sequence 5852, Ap
c 116	12	80.0	2563	10	US-09-782-051-1	Sequence 1, Appl	189	11	73.3	261	9	US-09-736-457-405	Sequence 405, App
c 117	12	80.0	2590	10	US-09-908-988B-3	Sequence 3, Appl	190	11	73.3	261	9	US-09-902-941-405	Sequence 405, App
c 118	12	80.0	2679	10	US-09-880-107-2219	Sequence 20, Appl	191	11	73.3	261	9	US-09-867-701-7801	Sequence 7801, Ap
c 119	12	80.0	2680	10	US-09-782-378A-20	Sequence 20, Appl	192	11	73.3	261	9	US-09-867-701-7801	Sequence 7801, Ap
c 120	12	80.0	2770	10	US-09-977-269-5	Sequence 5, Appl	193	11	73.3	264	10	US-09-878-574-6353	Sequence 6353, Ap
c 121	12	80.0	3394	10	US-09-977-269-5	Sequence 5, Appl	194	11	73.3	265	10	US-09-867-701-1171	Sequence 1171, Ap
c 122	12	80.0	3622	12	US-10-002-600-5	Sequence 5, Appl	195	11	73.3	265	10	US-09-983-965-3168	Sequence 3168, Ap
c 123	12	80.0	4152	10	US-10-004-090-493	Sequence 493, App	196	11	73.3	267	10	US-09-878-574-7886	Sequence 7886, Ap
c 124	12	80.0	4620	10	US-09-925-300-359	Sequence 359, App	197	11	73.3	268	10	US-09-878-574-7148	Sequence 7148, Ap
c 125	12	80.0	5230	10	US-09-880-253A-60	Sequence 60, Appl	198	11	73.3	276	9	US-09-815-343-800	Sequence 800, App
c 126	12	80.0	5770	10	US-09-838-718A-5	Sequence 5, Appl	199	11	73.3	277	9	US-10-040-739-1517	Sequence 1517, Ap
c 127	12	80.0	5870	10	US-09-838-718A-8	Sequence 8, Appl	200	11	73.3	282	10	US-09-294-093B-3162	Sequence 3162, Ap
c 128	12	80.0	5906	10	US-09-838-718A-6	Sequence 6, Appl	201	11	73.3	282	10	US-09-923-876-5496	Sequence 5496, Ap
c 129	12	80.0	6314	10	US-09-838-718A-6	Sequence 6, Appl	202	11	73.3	283	10	US-09-867-701-6226	Sequence 6226, Ap
c 130	12	80.0	6314	10	US-09-838-718A-6	Sequence 6, Appl	203	11	73.3	287	10	US-09-864-761-24815	Sequence 24815, A
c 131	12	80.0	7661	9	US-09-860-670-282	Sequence 282, App	204	11	73.3	289	10	US-09-294-093B-4750	Sequence 4750, Ap
c 132	12	80.0	7911	10	US-09-764-869-1738	Sequence 1738, Ap	205	11	73.3	290	10	US-09-964-824A-160	Sequence 160, App
c 133	12	80.0	9289	10	US-09-764-887-471	Sequence 471, App	206	11	73.3	291	9	US-09-878-574-8247	Sequence 8247, Ap
c 134	12	80.0	9751	10	US-09-946-239-7	Sequence 7, Appl	207	11	73.3	293	10	US-09-440-829-1	Sequence 1, Appl
c 135	12	80.0	12308	10	US-09-738-973-422	Sequence 422, App	208	11	73.3	297	10	US-09-983-965-3208	Sequence 3208, Ap
c 136	12	80.0	17865	10	US-09-764-869-1943	Sequence 472, App	209	11	73.3	297	10	US-09-925-300-82	Sequence 82, Appl
c 137	12	80.0	19334	10	US-09-764-869-1943	Sequence 472, App	210	11	73.3	329	10	US-09-864-761-25189	Sequence 25189, A
c 138	12	80.0	19345	10	US-09-764-869-1944	Sequence 1944, Ap	211	11	73.3	332	10	US-09-974-300-3463	Sequence 3463, Ap
c 139	12	80.0	26668	10	US-09-962-832-222	Sequence 222, App	212	11	73.3	339	10	US-09-983-965-839	Sequence 839, App
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c 141	12	80.0	30352	10	US-09-764-869-1768	Sequence 1768, Ap	214	11	73.3	316	10	US-09-878-574-13656	Sequence 13656, A
c 142	12	80.0	30568	10	US-09-764-877-3851	Sequence 3851, Ap	215	11	73.3	318	10	US-09-960-352-13237	Sequence 13237, A
c 143	12	80.0	32189	10	US-09-764-878-379	Sequence 379, App	216	11	73.3	322	10	US-09-764-877-495	Sequence 495, App
c 144	12	80.0	32221	10	US-09-764-878-377	Sequence 377, App	217	11	73.3	325	10	US-09-783-590-6936	Sequence 6936, Ap
c 145	12	80.0	53332	10	US-09-801-861-3	Sequence 3, Appl	218	11	73.3	326	10	US-09-867-701-4951	Sequence 4951, Ap
c 146	12	80.0	53542	10	US-09-801-861-3	Sequence 3, Appl	219	11	73.3	334	10	US-09-728-445-78	Sequence 78, Appl
c 147	12	80.0	63000	10	US-09-780-172-61	Sequence 18, Appl	220	11	73.3	335	9	US-09-925-299-422	Sequence 422, App
c 148	12	80.0	65608	9	US-09-954-531-180	Sequence 180, App	221	11	73.3	335	9	US-10-040-739-749	Sequence 749, App
c 149	12	80.0	65608	10	US-09-962-436-292	Sequence 292, App	222	11	73.3	335	10	US-09-864-761-22350	Sequence 22350, A
c 150	12	80.0	65608	10	US-09-962-832-119	Sequence 119, App	223	11	73.3	337	10	US-09-099-823-3	Sequence 3, Appl
c 151	12	80.0	11282	9	US-10-094-989-3	Sequence 3, Appl	224	11	73.3	339	10	US-09-867-701-9248	Sequence 9248, Ap
c 152	12	80.0	152331	9	US-10-095-407-16	Sequence 16, Appl	225	11	73.3	345	10	US-09-983-965-4371	Sequence 4371, Ap
c 153	12	80.0	173808	12	US-10-003-806-10	Sequence 10, Appl	226	11	73.3	348	10	US-09-867-701-3917	Sequence 3917, Ap
c 154	12	80.0	302250	10	US-09-962-832-154	Sequence 154, App	227	11	73.3	349	10	US-09-960-352-4856	Sequence 4856, Ap
c 155	12	80.0	659158	9	US-09-711-208-20	Sequence 20, Appl	228	11	73.3	351	9	US-09-974-300-3758	Sequence 3758, Ap
c 156	12	73.3	24	10	US-09-885-441-40	Sequence 40, Appl	229	11	73.3	356	9	US-10-040-739-817	Sequence 817, App
c 157	11	73.3	29	10	US-09-989-441-17	Sequence 17, Appl	230	11	73.3	357	10	US-09-090-672B-22	Sequence 22, Appl
c 158	11	73.3	112	10	US-09-864-761-26478	Sequence 26478, A	231	11	73.3	359	10	US-09-878-574-3336	Sequence 3336, Ap
c 159	11	73.3	114	10	US-09-864-761-25460	Sequence 25460, A	232	11	73.3	361	10	US-09-964-436-216	Sequence 216, App
c 160	11	73.3	115	10	US-09-867-701-1787	Sequence 1787, Ap	233	11	73.3	361	10	US-09-954-456-652	Sequence 652, App
c 161	11	73.3	149	10	US-09-294-093B-4891	Sequence 4891, Ap	234	11	73.3	361	10	US-09-880-107-605	Sequence 685, App
c 162	11	73.3	149	10	US-09-923-876-3663	Sequence 3663, Ap	235	11	73.3	367	10	US-09-867-701-6005	Sequence 6005, App
c 163	11	73.3	153	10	US-09-864-761-19579	Sequence 19579, A	236	11	73.3	370	10	US-09-960-352-4081	Sequence 4081, Ap
c 164	11	73.3	157	10	US-09-864-761-25740	Sequence 25740, A	237	11	73.3	378	9	US-09-954-531-57	Sequence 57, Appl
c 165	11	73.3	158	10	US-09-864-761-23440	Sequence 23440, A	238	11	73.3	378	9	US-09-954-531-236	Sequence 236, App

c 239	11	73.3	378	10	US-09-880-107-833	Sequence 833, App	c 312	11	73.3	501	10	US-09-833-381-803	Sequence 803, App
c 240	11	73.3	381	10	US-09-216-393-44	Sequence 44, Appl	c 313	11	73.3	502	10	US-09-783-590-4163	Sequence 4163, App
c 241	11	73.3	387	10	US-09-878-574-875	Sequence 875, App	c 314	11	73.3	504	10	US-09-864-761-22567	Sequence 22567, A
c 242	11	73.3	390	10	US-09-960-352-4127	Sequence 4127, App	c 315	11	73.3	506	10	US-09-864-761-12223	Sequence 12223, A
c 243	11	73.3	393	10	US-09-783-590-6945	Sequence 6945, App	c 316	11	73.3	509	10	US-09-783-590-3787	Sequence 3787, App
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c 245	11	73.3	408	10	US-09-960-352-2140	Sequence 2140, App	c 318	11	73.3	522	9	US-09-764-868-403	Sequence 403, App
c 246	11	73.3	408	10	US-09-764-877-3003	Sequence 3003, App	c 319	11	73.3	522	9	US-09-964-824A-302	Sequence 302, App
c 247	11	73.3	408	10	US-09-764-877-3004	Sequence 3004, App	c 320	11	73.3	526	10	US-09-917-800A-1156	Sequence 1156, App
c 248	11	73.3	410	10	US-09-864-761-10520	Sequence 10520, A	c 321	11	73.3	529	9	US-09-764-868-126	Sequence 126, App
c 249	11	73.3	410	10	US-09-969-708-543	Sequence 543, App	c 322	11	73.3	529	9	US-09-864-761-8061	Sequence 8061, App
c 250	11	73.3	411	10	US-09-783-590-3737	Sequence 3737, App	c 323	11	73.3	529	10	US-09-864-761-16389	Sequence 16389, A
c 251	11	73.3	415	10	US-09-960-352-14713	Sequence 14713, A	c 324	11	73.3	529	10	US-09-878-574-4302	Sequence 4302, App
c 252	11	73.3	416	10	US-09-960-352-12322	Sequence 12322, A	c 325	11	73.3	531	10	US-09-864-761-8792	Sequence 8792, App
c 253	11	73.3	417	10	US-09-983-965-3464	Sequence 3464, App	c 326	11	73.3	534	10	US-09-893-737-173	Sequence 773, App
c 254	11	73.3	418	10	US-09-960-352-7989	Sequence 7989, App	c 327	11	73.3	539	10	US-09-216-393-52	Sequence 52, Appl
c 255	11	73.3	418	10	US-09-960-352-9491	Sequence 9491, App	c 328	11	73.3	539	10	US-09-864-761-12409	Sequence 12409, A
c 256	11	73.3	419	9	US-09-954-531-332	Sequence 332, App	c 329	11	73.3	540	10	US-09-962-436-7	Sequence 7, Appl
c 257	11	73.3	419	9	US-09-954-531-555	Sequence 555, App	c 330	11	73.3	542	10	US-09-864-761-6706	Sequence 6706, App
c 258	11	73.3	419	10	US-09-864-761-309	Sequence 309, App	c 331	11	73.3	544	10	US-09-864-761-28521	Sequence 28521, A
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c 260	11	73.3	419	10	US-09-954-456-1100	Sequence 1100, App	c 333	11	73.3	546	9	US-09-736-457-936	Sequence 936, App
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c 262	11	73.3	419	10	US-09-880-107-2007	Sequence 2007, App	c 335	11	73.3	546	10	US-09-794-987-3	Sequence 3, Appl
c 263	11	73.3	419	10	US-09-967-768A-134	Sequence 134, App	c 336	11	73.3	547	10	US-09-917-800A-241	Sequence 241, App
c 264	11	73.3	424	10	US-09-960-352-1003	Sequence 1003, App	c 337	11	73.3	550	9	US-09-924-400-235	Sequence 235, App
c 265	11	73.3	425	10	US-09-880-107-465	Sequence 465, App	c 338	11	73.3	550	10	US-09-810-936-235	Sequence 235, App
c 266	11	73.3	426	10	US-09-864-761-4730	Sequence 4730, App	c 339	11	73.3	550	10	US-09-429-755-235	Sequence 235, App
c 267	11	73.3	426	10	US-09-960-352-3166	Sequence 3166, App	c 340	11	73.3	551	9	US-09-954-531-566	Sequence 566, App
c 268	11	73.3	432	10	US-09-216-393-46	Sequence 46, Appl	c 341	11	73.3	555	10	US-09-864-761-9540	Sequence 9540, App
c 269	11	73.3	437	10	US-09-925-297-388	Sequence 388, App	c 342	11	73.3	555	10	US-09-864-761-26450	Sequence 26450, A
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c 273	11	73.3	440	10	US-09-764-868-770	Sequence 770, App	c 346	11	73.3	556	10	US-09-864-761-8462	Sequence 8462, App
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c 275	11	73.3	445	10	US-09-864-761-4914	Sequence 4914, App	c 348	11	73.3	566	10	US-09-864-761-5207	Sequence 5207, App
c 276	11	73.3	447	10	US-09-960-352-11683	Sequence 11683, A	c 349	11	73.3	567	10	US-09-998-598-1064	Sequence 1064, App
c 277	11	73.3	452	10	US-09-983-965-4219	Sequence 4219, App	c 350	11	73.3	575	9	US-09-764-868-518	Sequence 518, App
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c 284	11	73.3	463	10	US-09-864-761-2604	Sequence 2604, App	c 357	11	73.3	587	10	US-09-864-761-12666	Sequence 12666, A
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c 293	11	73.3	471	10	US-09-864-761-6481	Sequence 6481, App	c 366	11	73.3	632	10	US-09-749-225-4	Sequence 4, Appl
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c 295	11	73.3	474	10	US-09-998-598-1749	Sequence 1749, App	c 368	11	73.3	641	10	US-09-764-877-918	Sequence 918, App
c 296	11	73.3	475	10	US-09-864-761-1361	Sequence 1361, App	c 369	11	73.3	642	10	US-09-216-393-42	Sequence 42, Appl
c 297	11	73.3	478	10	US-09-864-761-1968	Sequence 1968, App	c 370	11	73.3	673	10	US-09-917-800A-1258	Sequence 1258, App
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c 299	11	73.3	479	10	US-09-864-761-33103	Sequence 33103, A	c 372	11	73.3	692	10	US-09-099-823-5	Sequence 5, Appl
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c 302	11	73.3	485	10	US-09-864-761-16562	Sequence 16562, A	c 375	11	73.3	740	10	US-09-764-869-381	Sequence 381, App
c 303	11	73.3	486	10	US-09-764-869-2144	Sequence 2144, App	c 376	11	73.3	742	10	US-09-772-134B-96	Sequence 96, Appl
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c 310	11	73.3	497	10	US-09-864-761-6060	Sequence 6060, App	c 383	11	73.3	820	10	US-09-833-381-1325	Sequence 1325, App
c 311	11	73.3	500	10	US-09-879-536-5	Sequence 5, Appl	c 384	11	73.3	822	12	US-10-001-870-79	Sequence 79, Appl

c 385	11	73.3	829	9	US-09-924-400-317	Sequence 317, App	458	11	73.3	1575	10	US-09-735-171A-4	Sequence 4, Appli
c 386	11	73.3	829	10	US-09-810-936-317	Sequence 317, App	459	11	73.3	1626	10	US-09-881-401-3	Sequence 3, Appli
c 387	11	73.3	858	10	US-09-764-869-1984	Sequence 1984, Ap	c 460	11	73.3	1633	10	US-09-967-552A-1	Sequence 1, Appli
c 388	11	73.3	871	10	US-09-770-445-560	Sequence 560, App	c 461	11	73.3	1660	9	US-09-764-868-244	Sequence 244, App
c 389	11	73.3	900	10	US-09-974-300-2377	Sequence 2377, Ap	c 462	11	73.3	1682	10	US-09-925-297-129	Sequence 129, App
c 390	11	73.3	945	9	US-09-938-842A-1526	Sequence 1526, Ap	c 463	11	73.3	1700	10	US-09-967-552A-29	Sequence 29, Appl
c 391	11	73.3	951	10	US-09-875-338-1096	Sequence 10, Appl	c 464	11	73.3	1759	12	US-10-044-090-402	Sequence 1, Appli
c 392	11	73.3	954	10	US-09-815-242-6066	Sequence 6066, Ap	c 465	11	73.3	1789	10	US-09-840-704-1	Sequence 401, App
c 393	11	73.3	955	10	US-09-770-445-326	Sequence 326, App	c 466	11	73.3	1803	10	US-09-822-830A-401	Sequence 25, Appl
c 394	11	73.3	959	10	US-09-917-800A-1381	Sequence 1381, Ap	c 467	11	73.3	1802	10	US-09-967-552A-25	Sequence 52, Appl
c 395	11	73.3	970	10	US-09-925-299-232	Sequence 232, App	c 468	11	73.3	1842	10	US-09-822-830A-55	Sequence 88, Appl
c 396	11	73.3	1016	10	US-09-925-301-438	Sequence 438, App	c 469	11	73.3	1844	10	US-09-735-705-88	Sequence 88, Appl
c 397	11	73.3	1024	10	US-09-835-992A-78	Sequence 78, Appl	c 470	11	73.3	1844	10	US-09-850-716A-88	Sequence 88, Appl
c 398	11	73.3	1027	10	US-09-919-344-31	Sequence 31, Appl	c 471	11	73.3	1844	10	US-09-897-778-88	Sequence 218, App
c 399	11	73.3	1046	10	US-09-925-301-390	Sequence 390, App	c 472	11	73.3	1853	10	US-09-925-301-218	Sequence 19708, A
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c 401	11	73.3	1048	10	US-09-764-853-51	Sequence 51, Appl	c 474	11	73.3	1859	10	US-09-925-300-26	Sequence 542, App
c 402	11	73.3	1052	10	US-09-917-800A-1437	Sequence 1437, Ap	c 475	11	73.3	1866	12	US-10-044-090-542	Sequence 115, App
c 403	11	73.3	1052	10	US-09-917-800A-1515	Sequence 1515, Ap	c 476	11	73.3	1867	9	US-09-967-768A-115	Sequence 1348, Ap
c 404	11	73.3	1057	10	US-09-834-975-1044	Sequence 1044, Ap	c 477	11	73.3	1918	9	US-09-764-868-1348	Sequence 83, Appl
c 405	11	73.3	1064	10	US-09-804-682-29	Sequence 29, Appl	c 478	11	73.3	1933	9	US-09-989-920-83	Sequence 189, App
c 406	11	73.3	1065	10	US-09-804-682-33	Sequence 33, Appl	c 479	11	73.3	1945	9	US-09-974-298-189	Sequence 2927, Ap
c 407	11	73.3	1067	10	US-09-822-849A-179	Sequence 179, App	c 480	11	73.3	1958	10	US-09-864-761-2927	Sequence 355, App
c 408	11	73.3	1076	9	US-09-764-884-13	Sequence 13, Appl	c 481	11	73.3	1960	10	US-09-764-864-355	Sequence 3198, Ap
c 409	11	73.3	1086	10	US-09-880-192-40	Sequence 40, Appl	c 482	11	73.3	1979	10	US-09-864-761-3198	Sequence 10553, A
c 410	11	73.3	1095	10	US-09-728-628-2	Sequence 2, Appli	c 483	11	73.3	1979	10	US-09-864-761-10553	Sequence 49, Appl
c 411	11	73.3	1101	10	US-09-771-161A-3	Sequence 3, Appli	c 484	11	73.3	2020	9	US-09-984-245-49	Sequence 1, Appli
c 412	11	73.3	1117	10	US-09-925-302-152	Sequence 152, App	c 485	11	73.3	2046	10	US-09-749-225-1	Sequence 5, Appli
c 413	11	73.3	1128	10	US-09-815-242-9216	Sequence 9216, Ap	c 486	11	73.3	2046	10	US-09-822-849A-232	Sequence 232, App
c 414	11	73.3	1129	10	US-09-917-800A-1438	Sequence 1438, Ap	c 487	11	73.3	2091	9	US-10-136-573A-22	Sequence 22, Appl
c 415	11	73.3	1132	10	US-09-925-301-187	Sequence 187, App	c 488	11	73.3	2091	9	US-09-877-665-22	Sequence 22, Appl
c 416	11	73.3	1132	10	US-09-808-457-3	Sequence 3, Appli	c 489	11	73.3	2091	9	US-09-817-647-22	Sequence 22, Appl
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c 419	11	73.3	1175	10	US-09-823-356-31	Sequence 31, Appl	c 492	11	73.3	2097	10	US-09-920-552-12	Sequence 12, Appl
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c 421	11	73.3	1193	10	US-09-826-507-1	Sequence 1, Appli	c 494	11	73.3	2100	10	US-09-842-552-87	Sequence 87, Appl
c 422	11	73.3	1205	10	US-09-925-297-166	Sequence 166, App	c 495	11	73.3	2146	10	US-09-925-299-160	Sequence 160, App
c 423	11	73.3	1231	10	US-09-808-457-1	Sequence 1, Appli	c 496	11	73.3	2160	10	US-09-822-830A-551	Sequence 551, App
c 424	11	73.3	1243	9	US-10-001-835-5	Sequence 5, Appli	c 497	11	73.3	2163	10	US-09-802-669-94	Sequence 94, Appl
c 425	11	73.3	1248	10	US-09-880-107-3744	Sequence 3744, Ap	c 498	11	73.3	2165	10	US-09-822-849A-239	Sequence 239, App
c 426	11	73.3	1274	10	US-09-917-800A-1440	Sequence 1440, Ap	c 499	11	73.3	2193	10	US-09-012-135A-2	Sequence 2, Appli
c 427	11	73.3	1291	12	US-10-044-090-454	Sequence 454, App	c 500	11	73.3	2198	10	US-09-800-908-2	Sequence 2, Appli
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c 429	11	73.3	1332	9	US-09-952-598-269	Sequence 269, App	c 504	11	73.3	2272	10	US-09-944-944-82	Sequence 82, Appl
c 430	11	73.3	1332	9	US-09-989-293A-269	Sequence 269, App	c 505	11	73.3	2284	9	US-09-989-293A-514	Sequence 514, App
c 431	11	73.3	1332	10	US-09-989-722-269	Sequence 269, App	c 506	11	73.3	2284	10	US-09-866-028-82	Sequence 82, Appl
c 432	11	73.3	1332	10	US-09-989-723-269	Sequence 269, App	c 507	11	73.3	2284	9	US-09-989-722-514	Sequence 514, App
c 433	11	73.3	1332	10	US-09-989-279-269	Sequence 269, App	c 508	11	73.3	2284	9	US-09-989-723-514	Sequence 514, App
c 434	11	73.3	1332	10	US-09-989-727-269	Sequence 269, App	c 509	11	73.3	2284	10	US-09-989-279-514	Sequence 514, App
c 435	11	73.3	1332	10	US-09-989-731-269	Sequence 269, App	c 510	11	73.3	2284	10	US-09-989-727-514	Sequence 514, App
c 436	11	73.3	1332	10	US-09-989-732-269	Sequence 269, App	c 511	11	73.3	2284	10	US-09-944-449-82	Sequence 82, Appl
c 437	11	73.3	1332	10	US-09-991-073-269	Sequence 269, App	c 512	11	73.3	2284	10	US-09-989-731-514	Sequence 514, App
c 438	11	73.3	1332	10	US-09-991-073-269	Sequence 269, App	c 513	11	73.3	2284	10	US-09-989-073-514	Sequence 514, App
c 439	11	73.3	1332	10	US-09-990-442-269	Sequence 269, App	c 514	11	73.3	2284	10	US-09-945-587-82	Sequence 82, Appl
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c 441	11	73.3	1332	10	US-09-993-604-269	Sequence 269, App	c 516	11	73.3	2284	10	US-09-991-163-514	Sequence 514, App
c 442	11	73.3	1332	10	US-09-990-456-269	Sequence 269, App	c 517	11	73.3	2284	10	US-09-991-163-514	Sequence 514, App
c 443	11	73.3	1332	10	US-09-989-721-269	Sequence 269, App	c 518	11	73.3	2284	10	US-09-944-403-82	Sequence 82, Appl
c 444	11	73.3	1364	10	US-09-822-830A-363	Sequence 363, App	c 519	11	73.3	2284	9	US-09-944-896-82	Sequence 82, Appl
c 445	11	73.3	1365	10	US-09-815-242-9347	Sequence 9347, Ap	c 520	11	73.3	2284	9	US-09-944-944-82	Sequence 82, Appl
c 446	11	73.3	1367	9	US-09-764-884-21	Sequence 21, Appl	c 521	11	73.3	2284	9	US-09-989-293A-514	Sequence 514, App
c 447	11	73.3	1367	10	US-09-925-299-53	Sequence 53, Appl	c 522	11	73.3	2284	10	US-09-866-028-82	Sequence 82, Appl
c 448	11	73.3	1374	10	US-09-191-724-9	Sequence 9, Appli	c 523	11	73.3	2284	10	US-09-989-722-514	Sequence 514, App
c 449	11	73.3	1399	9	US-09-938-842A-4490	Sequence 4490, Ap	c 524	11	73.3	2284	10	US-09-989-723-514	Sequence 514, App
c 450	11	73.3	1441	9	US-10-001-887-24	Sequence 24, Appl	c 525	11	73.3	2284	10	US-09-945-015-82	Sequence 82, Appl
c 451	11	73.3	1444	10	US-09-801-574-37	Sequence 37, Appl	c 526	11	73.3	2284	10	US-09-944-396-82	Sequence 82, Appl
c 452	11	73.3	1494	10	US-09-728-952-80	Sequence 80, Appl	c 527	11	73.3	2284	10	US-09-944-097-82	Sequence 82, Appl
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c 454	11	73.3	1514	10	US-09-881-401-1	Sequence 1, Appli	c 529	11	73.3	2284	10	US-09-990-456-514	Sequence 514, App
c 455	11	73.3	1545	10	US-09-925-301-392	Sequence 392, App	c 530	11	73.3	2284	10	US-09-944-432-82	Sequence 82, Appl
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			1575	10	US-09-735-169A-4	Sequence 4, Appli							



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c 532	11	73.3	2284	10	US-09-989-721-514	Sequence 514, App	605	11	73.3	3402	10	US-09-989-727-118	Sequence 118, App
c 533	11	73.3	2284	10	US-09-943-851A-82	Sequence 82, Appl	606	11	73.3	3402	10	US-09-989-727-118	Sequence 118, App
c 534	11	73.3	2297	10	US-09-934-332-1	Sequence 1, Appli	607	11	73.3	3402	10	US-09-989-731-118	Sequence 118, App
c 535	11	73.3	2311	10	US-09-764-870-583	Sequence 583, App	608	11	73.3	3402	10	US-09-989-732-118	Sequence 118, App
c 536	11	73.3	2311	10	US-09-764-853-865	Sequence 865, App	609	11	73.3	3402	10	US-09-991-073-118	Sequence 118, App
c 537	11	73.3	2314	10	US-09-764-870-584	Sequence 584, App	610	11	73.3	3402	10	US-09-990-442-118	Sequence 118, App
c 538	11	73.3	2314	10	US-09-764-870-585	Sequence 585, App	611	11	73.3	3402	10	US-09-991-163-118	Sequence 118, App
c 539	11	73.3	2314	10	US-09-764-853-864	Sequence 864, App	612	11	73.3	3402	10	US-09-993-604-118	Sequence 118, App
c 540	11	73.3	2314	10	US-09-764-853-866	Sequence 866, App	613	11	73.3	3402	10	US-09-990-456-118	Sequence 118, App
c 541	11	73.3	2333	10	US-09-726-643-33	Sequence 33, Appl	614	11	73.3	3402	10	US-09-989-721-118	Sequence 118, App
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c 544	11	73.3	2434	10	US-09-764-877-3336	Sequence 3336, Ap	617	11	73.3	3436	10	US-09-789-561-12	Sequence 12, Appl
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c 546	11	73.3	2482	10	US-09-742-201-1	Sequence 1, Appli	c 619	11	73.3	3474	10	US-09-993-811-11	Sequence 11, Appl
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c 549	11	73.3	2533	10	US-09-817-647-5	Sequence 5, Appli	c 622	11	73.3	3517	12	US-10-044-090-186	Sequence 186, App
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c 555	11	73.3	2539	10	US-09-919-172-53	Sequence 53, Appl	c 628	11	73.3	3932	10	US-09-764-847-1927	Sequence 1927, Ap
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c 560	11	73.3	2599	10	US-09-822-849A-416	Sequence 416, App	c 633	11	73.3	4152	10	US-09-925-300-359	Sequence 359, App
c 561	11	73.3	2617	10	US-09-853-386-123	Sequence 123, App	c 634	11	73.3	4160	10	US-09-920-552-19	Sequence 19, Appl
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c 563	11	73.3	2791	10	US-09-729-674-51	Sequence 51, Appl	c 636	11	73.3	4188	10	US-09-920-552-20	Sequence 20, Appl
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c 567	11	73.3	2827	10	US-09-834-291-4	Sequence 4, Appli	c 640	11	73.3	4396	10	US-09-880-107-2329	Sequence 107, App
c 568	11	73.3	2867	10	US-09-954-456-1227	Sequence 1227, Ap	c 641	11	73.3	4540	10	US-09-917-800A-1684	Sequence 1684, Ap
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c 570	11	73.3	2901	12	US-10-044-090-528	Sequence 528, App	c 643	11	73.3	4600	9	US-09-736-457-1797	Sequence 1797, Ap
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c 574	11	73.3	3035	9	US-09-992-598-5	Sequence 5, Appli	c 647	11	73.3	4859	10	US-09-880-107-1647	Sequence 1647, Ap
c 575	11	73.3	3033	9	US-09-989-293A-5	Sequence 5, Appli	c 648	11	73.3	4901	10	US-09-764-864-1710	Sequence 1710, Ap
c 576	11	73.3	3033	10	US-09-989-722-5	Sequence 5, Appli	c 649	11	73.3	4961	10	US-09-920-552-15	Sequence 15, Appl
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c 582	11	73.3	3033	10	US-09-991-073-5	Sequence 5, Appli	c 655	11	73.3	5344	12	US-10-014-070-4	Sequence 4, Appli
c 583	11	73.3	3033	10	US-09-990-442-5	Sequence 5, Appli	c 656	11	73.3	5433	10	US-09-954-456-315	Sequence 315, App
c 584	11	73.3	3033	10	US-09-991-163-5	Sequence 5, Appli	c 657	11	73.3	5444	10	US-09-996-617-1	Sequence 1, Appli
c 585	11	73.3	3033	10	US-09-993-604-5	Sequence 5, Appli	c 658	11	73.3	5444	10	US-09-931-071-1	Sequence 1, Appli
c 586	11	73.3	3033	10	US-09-990-456-5	Sequence 5, Appli	c 659	11	73.3	5450	12	US-10-044-090-504	Sequence 504, App
c 587	11	73.3	3033	10	US-09-989-721-5	Sequence 5, Appli	c 660	11	73.3	5503	12	US-10-044-090-7	Sequence 7, Appli
c 588	11	73.3	3033	12	US-10-052-586-1	Sequence 1, Appli	c 661	11	73.3	5511	9	US-09-974-298-13	Sequence 13, Appl
c 589	11	73.3	3080	10	US-09-815-108-18	Sequence 18, Appl	c 662	11	73.3	5511	12	US-10-044-090-285	Sequence 285, App
c 590	11	73.3	3112	10	US-09-758-386-1	Sequence 1, Appli	c 663	11	73.3	5551	10	US-09-905-129-17	Sequence 17, Appl
c 591	11	73.3	3112	10	US-09-815-108-16	Sequence 16, Appl	c 664	11	73.3	5551	10	US-09-991-630-17	Sequence 17, Appl
c 592	11	73.3	3129	10	US-09-815-242-9247	Sequence 9247, Ap	c 665	11	73.3	5557	10	US-09-764-869-1473	Sequence 1473, Ap
c 593	11	73.3	3129	10	US-09-925-697-1	Sequence 1, Appli	c 666	11	73.3	5557	10	US-09-764-869-2252	Sequence 2252, Ap
c 594	11	73.3	3160	9	US-09-860-670-286	Sequence 286, App	c 667	11	73.3	5701	12	US-10-014-070-1	Sequence 1, Appli
c 595	11	73.3	3160	9	US-09-860-670-287	Sequence 287, App	c 668	11	73.3	5763	12	US-10-002-600-79	Sequence 79, Appl
c 596	11	73.3	3197	10	US-09-875-338-6	Sequence 6, Appli	c 669	11	73.3	6065	10	US-09-764-877-3627	Sequence 3627, Ap
c 597	11	73.3	3197	10	US-09-875-338-19	Sequence 19, Appl	c 670	11	73.3	6083	9	US-10-029-413A-21	Sequence 21, Appl
c 598	11	73.3	3212	10	US-09-834-291-1	Sequence 1, Appli	c 671	11	73.3	6250	10	US-09-205-658-158	Sequence 158, App
c 599	11	73.3	3266	10	US-09-814-777A-33	Sequence 33, Appl	c 672	11	73.3	6385	10	US-09-764-847-1049	Sequence 1049, Ap
c 600	11	73.3	3353	10	US-09-963-159-1	Sequence 1, Appli	c 673	11	73.3	6408	10	US-09-967-552A-74	Sequence 74, Appl
c 601	11	73.3	3402	9	US-09-992-598-118	Sequence 118, App	c 674	11	73.3	6440	10	US-09-920-552-127	Sequence 127, App
c 602	11	73.3	3402	9	US-09-989-293A-118	Sequence 118, App	c 675	11	73.3	6660	10	US-09-764-877-2529	Sequence 2529, Ap
c 603	11	73.3	3402	10	US-09-989-722-118	Sequence 118, App	c 676	11	73.3	6746	10	US-09-919-497-18	Sequence 18, Appl

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678	11	73.3	6802	12	US-10-002-600-68	Sequence 68, Appl	c 751	11	73.3	167343	10	US-09-962-436-281	Sequence 281, App
679	11	73.3	7011	10	US-09-954-456-964	Sequence 964, App	c 752	11	73.3	167343	10	US-09-964-824A-273	Sequence 273, App
680	11	73.3	7301	9	US-09-956-993-3	Sequence 3, Appli	753	11	73.3	170834	10	US-09-835-232-7	Sequence 7, Appli
681	11	73.3	7301	10	US-09-764-887-415	Sequence 415, App	754	11	73.3	176373	9	US-10-095-407-17	Sequence 17, Appli
682	11	73.3	7703	10	US-09-764-887-456	Sequence 456, App	755	11	73.3	249487	9	US-10-026-188-3	Sequence 3, Appli
683	11	73.3	7736	10	US-09-764-846-333	Sequence 333, App	756	11	73.3	302250	10	US-09-962-832-154	Sequence 154, App
684	11	73.3	7934	9	US-09-764-868-1389	Sequence 1389, Ap	757	11	73.3	326014	10	US-09-933-267A-1	Sequence 1, Appli
685	11	73.3	7934	9	US-09-764-868-1390	Sequence 1390, Ap	758	11	73.3	326014	10	US-09-731-231A-3	Sequence 1, Appli
686	11	73.3	8746	10	US-09-764-860-1022	Sequence 1022, Ap	759	11	73.3	452237	10	US-09-933-267A-1	Sequence 1, Appli
687	11	73.3	9121	10	US-09-070-927A-221	Sequence 221, App	c 760	11	73.3	452237	10	US-09-933-267A-1	Sequence 1, Appli
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689	11	73.3	9914	10	US-09-764-847-1558	Sequence 1558, Ap	c 762	11	73.3	684973	10	US-09-263-959-1	Sequence 1, Appli
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691	11	73.3	10062	10	US-09-888-615-5	Sequence 5, Appli	764	10	66.7	20	12	US-10-033-145-1427	Sequence 1427, Ap
692	11	73.3	10144	10	US-09-880-107-2168	Sequence 2168, Ap	c 765	10	66.7	20	12	US-09-426-548-53	Sequence 53, Appli
693	11	73.3	10432	10	US-09-919-172-97	Sequence 97, Appli	c 766	10	66.7	24	9	US-09-935-371-53	Sequence 53, Appli
694	11	73.3	11230	10	US-09-911-842-3	Sequence 3, Appli	c 767	10	66.7	31	10	US-09-801-274-1700	Sequence 1700, Ap
695	11	73.3	11282	10	US-09-764-847-1747	Sequence 1747, Ap	c 768	10	66.7	37	9	US-09-864-785-1997	Sequence 1997, Ap
696	11	73.3	11316	9	US-09-764-868-1391	Sequence 1391, Ap	c 769	10	66.7	50	10	US-09-504-231A-3107	Sequence 3107, Ap
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699	11	73.3	11962	10	US-09-905-129-20	Sequence 20, Appl	c 772	10	66.7	50	10	US-09-274-553B-3122	Sequence 3122, Ap
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704	11	73.3	14918	10	US-09-764-864-1766	Sequence 1766, Ap	c 777	10	66.7	83	10	US-09-777-564-1269	Sequence 1269, Ap
705	11	73.3	15266	10	US-09-764-877-3797	Sequence 3797, Ap	c 778	10	66.7	88	10	US-09-319-580-792	Sequence 792, App
706	11	73.3	15271	10	US-09-764-877-3798	Sequence 3798, Ap	c 779	10	66.7	91	10	US-09-842-628-19	Sequence 19, Appl
707	11	73.3	15425	10	US-09-764-869-1654	Sequence 1654, Ap	c 780	10	66.7	91	10	US-09-842-628-20	Sequence 20, Appl
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711	11	73.3	17217	10	US-09-764-877-3566	Sequence 3566, Ap	c 784	10	66.7	104	10	US-09-864-761-23405	Sequence 23405, A
712	11	73.3	17509	10	US-09-880-107-2097	Sequence 2097, Ap	c 785	10	66.7	106	10	US-09-789-836-33	Sequence 33, Appl
713	11	73.3	17581	10	US-09-764-869-2170	Sequence 2170, Ap	c 786	10	66.7	108	10	US-09-783-590-8630	Sequence 8630, Ap
714	11	73.3	18871	10	US-09-764-847-1317	Sequence 1317, Ap	c 787	10	66.7	109	10	US-09-878-574-15429	Sequence 15429, A
715	11	73.3	20222	10	US-09-764-877-3774	Sequence 3774, Ap	c 788	10	66.7	112	10	US-09-864-761-30526	Sequence 30526, A
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718	11	73.3	26668	10	US-09-962-832-222	Sequence 222, App	c 791	10	66.7	117	10	US-09-983-965-284	Sequence 284, App
719	11	73.3	27483	10	US-09-764-877-2928	Sequence 2928, Ap	c 792	10	66.7	121	10	US-09-764-877-392	Sequence 392, App
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724	11	73.3	31871	10	US-09-764-847-1403	Sequence 1403, Ap	c 797	10	66.7	135	9	US-10-079-623-234	Sequence 234, App
725	11	73.3	32035	10	US-09-764-847-1611	Sequence 1611, Ap	c 798	10	66.7	135	10	US-09-864-761-31834	Sequence 31834, A
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727	11	73.3	32189	10	US-09-764-877-3291	Sequence 3291, Ap	c 800	10	66.7	143	10	US-09-817-607-12	Sequence 12, Appl
728	11	73.3	32190	10	US-09-764-877-338	Sequence 338, App	c 801	10	66.7	143	10	US-09-864-761-26391	Sequence 26391, A
729	11	73.3	32193	9	US-09-764-868-1508	Sequence 1508, Ap	c 802	10	66.7	146	10	US-09-864-761-17351	Sequence 17351, A
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744	11	73.3	53226	10	US-09-818-264-3	Sequence 3, Appli	c 817	10	66.7	176	10	US-09-874-300-5425	Sequence 5425, Ap
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c 826	10	66.7	191	10	US-09-867-701-4632	Sequence 4632, Ap	899	10	66.7	260	10	US-09-878-574-7830	Sequence 7830, Ap
c 827	10	66.7	193	10	US-09-878-574-14136	Sequence 14136, A	900	10	66.7	261	10	US-09-923-876-1682	Sequence 1682, Ap
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c 829	10	66.7	194	10	US-09-783-590-5058	Sequence 5058, Ap	902	10	66.7	261	10	US-09-974-300-3982	Sequence 3982, Ap
c 830	10	66.7	196	10	US-09-867-701-10861	Sequence 10861, A	c 903	10	66.7	262	9	US-09-946-807-115	Sequence 115, App
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c 832	10	66.7	197	10	US-09-878-574-10118	Sequence 10118, A	c 905	10	66.7	262	10	US-09-923-876-5765	Sequence 5765, Ap
c 833	10	66.7	198	10	US-09-783-590-96	Sequence 96, Appl	c 906	10	66.7	262	10	US-09-795-668-115	Sequence 115, App
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c 835	10	66.7	199	10	US-09-864-761-31815	Sequence 31815, A	c 908	10	66.7	262	10	US-09-795-686-115	Sequence 115, App
c 836	10	66.7	200	10	US-09-864-761-16964	Sequence 16964, A	c 909	10	66.7	263	9	US-09-920-455-41	Sequence 41, Appl
c 837	10	66.7	201	10	US-09-783-590-4958	Sequence 4958, Ap	c 910	10	66.7	263	10	US-09-878-574-10546	Sequence 10546, A
c 838	10	66.7	204	9	US-09-924-400-23	Sequence 23, Appl	c 911	10	66.7	263	10	US-09-783-590-10753	Sequence 9932, Ap
c 839	10	66.7	204	10	US-09-864-761-21109	Sequence 21109, A	c 912	10	66.7	264	10	US-09-878-574-9932	Sequence 9932, Ap
c 840	10	66.7	204	10	US-09-810-936-23	Sequence 23, Appl	c 913	10	66.7	264	10	US-09-783-590-10753	Sequence 10753, A
c 841	10	66.7	204	10	US-09-429-753-23	Sequence 23, Appl	c 914	10	66.7	265	10	US-09-923-876-1861	Sequence 1861, Ap
c 842	10	66.7	207	10	US-09-783-590-1369	Sequence 1369, Ap	c 915	10	66.7	267	10	US-09-983-965-1916	Sequence 1916, Ap
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c 844	10	66.7	214	10	US-09-783-590-4487	Sequence 4487, Ap	c 917	10	66.7	269	10	US-09-864-761-28336	Sequence 28336, A
c 845	10	66.7	216	10	US-09-960-352-12269	Sequence 12269, A	c 918	10	66.7	269	10	US-09-764-860-815	Sequence 815, App
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c 847	10	66.7	218	10	US-09-867-701-9494	Sequence 9494, Ap	c 920	10	66.7	270	10	US-09-783-590-10960	Sequence 10960, A
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c 850	10	66.7	222	10	US-09-974-300-6198	Sequence 6198, Ap	c 923	10	66.7	276	10	US-09-998-598-1516	Sequence 1516, Ap
c 851	10	66.7	223	10	US-09-969-708-251	Sequence 251, App	c 924	10	66.7	277	10	US-09-878-574-8021	Sequence 8021, Ap
c 852	10	66.7	223	10	US-09-880-107-3092	Sequence 3092, Ap	c 925	10	66.7	277	10	US-09-853-386-118	Sequence 118, App
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c 854	10	66.7	228	10	US-09-923-876-21	Sequence 21, Appl	c 927	10	66.7	279	10	US-09-983-965-3460	Sequence 3460, Ap
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c 856	10	66.7	229	10	US-09-783-590-573	Sequence 573, App	c 929	10	66.7	281	10	US-09-843-856-22	Sequence 22, Appl
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c 859	10	66.7	231	10	US-09-867-701-8998	Sequence 8998, Ap	c 932	10	66.7	284	10	US-09-867-701-9424	Sequence 9424, Ap
c 860	10	66.7	231	10	US-09-974-300-3901	Sequence 3901, Ap	c 933	10	66.7	285	10	US-09-294-093B-1810	Sequence 1810, Ap
c 861	10	66.7	231	10	US-09-998-598-591	Sequence 591, App	c 934	10	66.7	285	10	US-09-974-300-8295	Sequence 8295, Ap
c 862	10	66.7	232	10	US-09-923-876-3393	Sequence 3393, Ap	c 935	10	66.7	286	10	US-09-294-093B-2055	Sequence 2055, Ap
c 863	10	66.7	232	10	US-09-923-876-3404	Sequence 3404, Ap	c 936	10	66.7	288	10	US-09-878-574-13617	Sequence 13617, A
c 864	10	66.7	233	10	US-09-923-876-2746	Sequence 2746, Ap	c 937	10	66.7	289	10	US-09-777-564-1354	Sequence 1354, Ap
c 865	10	66.7	233	10	US-09-923-876-3501	Sequence 3501, Ap	c 938	10	66.7	289	10	US-09-777-564-1416	Sequence 1416, Ap
c 866	10	66.7	233	10	US-09-960-352-1831	Sequence 1831, Ap	c 939	10	66.7	289	10	US-09-853-386-126	Sequence 126, App
c 867	10	66.7	235	10	US-09-864-761-28318	Sequence 28318, A	c 940	10	66.7	289	10	US-09-783-590-9747	Sequence 9747, Ap
c 868	10	66.7	238	10	US-09-867-701-1663	Sequence 1663, Ap	c 941	10	66.7	289	12	US-09-920-300A-877	Sequence 877, App
c 869	10	66.7	239	9	US-10-002-3448-72	Sequence 72, Appl	c 942	10	66.7	289	10	US-10-033-528-877	Sequence 877, App
c 870	10	66.7	240	10	US-09-764-877-43	Sequence 43, Appl	c 943	10	66.7	290	10	US-09-835-932A-18	Sequence 18, Appl
c 871	10	66.7	240	10	US-09-923-876-3261	Sequence 3261, Ap	c 944	10	66.7	290	10	US-09-864-761-26148	Sequence 26148, A
c 872	10	66.7	245	9	US-09-920-455-71	Sequence 71, Appl	c 945	10	66.7	290	10	US-09-920-300A-208	Sequence 208, App
c 873	10	66.7	246	10	US-09-878-574-10785	Sequence 10785, A	c 946	10	66.7	290	12	US-10-033-528-208	Sequence 208, App
c 874	10	66.7	246	10	US-09-960-352-3963	Sequence 3963, Ap	c 947	10	66.7	292	10	US-09-294-093B-5999	Sequence 5999, Ap
c 875	10	66.7	247	10	US-09-864-761-27981	Sequence 27981, A	c 948	10	66.7	293	10	US-09-783-590-2110	Sequence 2110, Ap
c 876	10	66.7	247	10	US-09-867-701-9096	Sequence 9096, Ap	c 949	10	66.7	294	10	US-09-864-761-27669	Sequence 27669, A
c 877	10	66.7	250	10	US-09-759-143-409	Sequence 409, App	c 950	10	66.7	294	10	US-09-853-386-113	Sequence 113, App
c 878	10	66.7	250	10	US-09-780-669-409	Sequence 409, App	c 951	10	66.7	295	10	US-09-867-701-5004	Sequence 5004, Ap
c 879	10	66.7	250	10	US-09-822-827-409	Sequence 409, App	c 952	10	66.7	297	10	US-09-294-093B-5897	Sequence 5897, Ap
c 880	10	66.7	252	10	US-09-783-590-11720	Sequence 11720, A	c 953	10	66.7	299	9	US-10-040-733-324	Sequence 324, App
c 881	10	66.7	253	10	US-09-923-876-4628	Sequence 4628, Ap	c 954	10	66.7	300	10	US-09-294-093B-227	Sequence 227, App
c 882	10	66.7	253	10	US-09-878-574-5715	Sequence 5715, Ap	c 955	10	66.7	300	10	US-09-777-564-598	Sequence 598, App
c 883	10	66.7	254	10	US-09-923-876-1884	Sequence 1884, Ap	c 956	10	66.7	300	10	US-09-878-574-14582	Sequence 14582, A
c 884	10	66.7	254	10	US-09-923-876-4631	Sequence 4631, Ap	c 957	10	66.7	301	9	US-09-938-842A-3278	Sequence 3278, Ap
c 885	10	66.7	254	10	US-09-878-574-8879	Sequence 8879, Ap	c 958	10	66.7	301	10	US-09-604-287A-8	Sequence 8, Appl
c 886	10	66.7	255	10	US-09-923-876-963	Sequence 963, App	c 959	10	66.7	301	10	US-09-339-338-8	Sequence 8, Appl
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c 888	10	66.7	256	9	US-09-736-457-423	Sequence 423, App	c 961	10	66.7	302	9	US-10-040-733-691	Sequence 691, App
c 889	10	66.7	256	9	US-09-902-941-423	Sequence 941, App	c 962	10	66.7	302	10	US-09-925-301-579	Sequence 579, App
c 890	10	66.7	256	10	US-09-777-564-1167	Sequence 1167, Ap	c 963	10	66.7	302	10	US-09-783-590-4807	Sequence 4807, Ap
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c 892	10	66.7	256	10	US-09-974-300-80218	Sequence 80218, Ap	c 965	10	66.7	305	10	US-09-960-352-459	Sequence 459, App
c 893	10	66.7	256	12	US-10-033-528-902	Sequence 902, App	c 966	10	66.7	306	10	US-09-294-093B-5954	Sequence 5954, Ap
c 894	10	66.7	258	10	US-09-923-876-1832	Sequence 1832, Ap	c 967	10	66.7	308	9	US-09-933-797-457	Sequence 457, App
c 895	10	66.7	259	10	US-09-923-876-5658	Sequence 5658, Ap	c 968	10	66.7	309	10	US-09-960-352-7042	Sequence 7042, Ap
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c 969      10 66.7 310 10 US-09-880-107-195      Sequence 195, App
c 970      10 66.7 311 10 US-09-294-093B-3446      Sequence 3446, Ap
c 971      10 66.7 311 10 US-09-867-701-3021      Sequence 3021, Ap
c 972      10 66.7 311 10 US-09-764-877-2603      Sequence 2603, Ap
c 973      10 66.7 311 10 US-09-764-877-2604      Sequence 2604, Ap
c 974      10 66.7 312 10 US-09-294-093B-4427      Sequence 4427, Ap
c 975      10 66.7 312 10 US-09-864-761-18515      Sequence 18515, A
c 976      10 66.7 312 10 US-09-974-300-4869      Sequence 4869, Ap
c 977      10 66.7 313 10 US-09-764-877-2606      Sequence 2606, Ap
c 978      10 66.7 313 10 US-09-853-386-119      Sequence 119, App
c 979      10 66.7 315 10 US-09-563-817-639      Sequence 639, App
c 980      10 66.7 317 10 US-09-920-300A-323      Sequence 323, App
c 981      10 66.7 317 12 US-10-033-528-323      Sequence 323, App
c 982      10 66.7 318 10 US-09-976-787-27      Sequence 27, Appl
c 983      10 66.7 318 10 US-09-865-198-26      Sequence 26, Appl
c 984      10 66.7 318 10 US-09-894-018-102      Sequence 102, App
c 985      10 66.7 318 10 US-09-965-098-104      Sequence 104, App
c 986      10 66.7 318 12 US-10-051-852-104      Sequence 104, App
c 987      10 66.7 320 9 US-09-954-531-889      Sequence 889, App
c 988      10 66.7 321 10 US-09-960-253-46      Sequence 46, Appl
c 989      10 66.7 321 10 US-09-965-099-6      Sequence 6, Appli
c 990      10 66.7 321 12 US-10-051-852-6      Sequence 11, Appli
c 991      10 66.7 322 9 US-09-982-107-11      Sequence 2126, Ap
c 992      10 66.7 322 10 US-09-974-300-2126      Sequence 947, App
c 993      10 66.7 323 10 US-09-560-863-947      Sequence 947, App
c 994      10 66.7 324 10 US-09-976-787-16      Sequence 16, Appl
c 995      10 66.7 324 10 US-09-865-198-16      Sequence 16, Appl
c 996      10 66.7 324 10 US-09-974-300-4470      Sequence 4470, Ap
c 997      10 66.7 326 10 US-09-783-590-742      Sequence 742, App
c 998      10 66.7 327 10 US-09-960-352-4630      Sequence 4630, Ap
c 999      10 66.7 329 9 US-09-954-531-543      Sequence 543, App
c1000     10 66.7 329 10 US-09-878-574-3214      Sequence 3214, Ap

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## ALIGNMENTS

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RESULT 1
US-09-764-864-1704
; Sequence 1704, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; CURRENT APPLICATION NUMBER: US/09/764.864
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1704
; LENGTH: 15857
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-864-1704

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Query Match      100.0%; Score 15; DB 10; Length 15857;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CCTTCTCCCTCTGT 15
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Db 13094 CCTTCTCCCTCTGT 13108

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RESULT 2
US-09-954-456-1577/c
; Sequence 1577, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
; TITLE OF INVENTION: Sets

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; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954.456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1577
; LENGTH: 389
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: n-a,t,g or c
US-09-954-456-1577

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Query Match      93.3%; Score 14; DB 10; Length 389;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CCTTCTCCCTCTGT 14
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Db 296 CCTTCTCCCTCTGT 283

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RESULT 3
US-09-880-107-3234/c
; Sequence 3234, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3234
; LENGTH: 389
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 T84491
; NAME/KEY: unsure
; LOCATION: (1)..(389)
; OTHER INFORMATION: n = a or c or g or t
US-09-880-107-3234

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Query Match 93.3%; Score 14; DB 10; Length 389;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGT 14  
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DB 296 CCTTCTCCCTGT 283

## RESULT 4

US-10-001-835-84/c  
; Sequence 84, Application US/10001835  
; Patent No. US20020160387A1  
; GENERAL INFORMATION:  
; APPLICANT: Salceda, Susana  
; APPLICANT: Macina, Roberto  
; APPLICANT: Recipon, Herve  
; APPLICANT: Caiferey, Robert  
; APPLICANT: Sun, Yongming  
; APPLICANT: Liu, Chenghua  
; TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Pro  
; FILE REFERENCE: DEX-0277  
; CURRENT APPLICATION NUMBER: US/10/001,835  
; CURRENT FILING DATE: 2001-11-20  
; PRIOR APPLICATION NUMBER: 60/249,997  
; PRIOR FILING DATE: 2000-11-20  
; NUMBER OF SEQ ID NOS: 228  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 84  
; LENGTH: 482  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-001-835-84

Query Match 93.3%; Score 14; DB 9; Length 482;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTCTCCCTGT 15  
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DB 188 CTCTCCCTGT 175

## RESULT 5

US-09-864-761-13104  
; Sequence 13104, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aeonica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 13104  
; LENGTH: 594  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO ALL36968.3  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.5  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.76  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.68  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.82  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.7  
US-09-864-761-13104

Query Match 93.3%; Score 14; DB 10; Length 594;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGT 14  
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DB 192 CCTTCTCCCTGT 205

## RESULT 6

US-09-764-864-1692/c  
; Sequence 1692, Application US/09764864  
; Patent No. US20020132753A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT223  
; CURRENT APPLICATION NUMBER: US/09/764,864  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1792  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1692  
; LENGTH: 8894  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-764-864-1692

Query Match 93.3%; Score 14; DB 10; Length 8894;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGT 14  
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DB 4843 CCTTCTCCCTGT 4830

## RESULT 7

US-09-764-877-3063  
; Sequence 3063, Application US/09764877  
; Patent No. US20020147140A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; FILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC005  
; CURRENT APPLICATION NUMBER: US/09/764,877  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 4031  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3063  
; LENGTH: 8894  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-764-877-3063

Query Match 93.3%; Score 14; DB 10; Length 8894;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGT 14  
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Db 4052 CCTTCTCCCCCTGT 4065

## RESULT 8

US-09-764-877-3349/c  
; Sequence 3349, Application US/09764877  
; Patent No. US20020147140A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC005  
; CURRENT APPLICATION NUMBER: US/09/764,877  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 4031  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3349  
; LENGTH: 16877  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-764-877-3349

Query Match 93.3%; Score 14; DB 10; Length 16877;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGT 14  
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Db 1269 CCTTCTCCCCCTGT 1256

## RESULT 9

US-09-864-761-25357  
; Sequence 25357, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Acomica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; Prior application data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 864  
; LENGTH: 1256  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-864-761-25357

Query Match 93.3%; Score 14; DB 10; Length 1256;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGT 14  
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Db 1269 CCTTCTCCCCCTGT 1256

US-09-864-761-25357  
; Sequence 25357, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Acomica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; Prior application data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 864  
; LENGTH: 1256  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-864-761-25357

Query Match 86.7%; Score 13; DB 10; Length 209;  
Best Local Similarity 100.0%; Pred. No. 53;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTTCTCCCCCTGT 14  
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Db 41 CTTCTCCCCCTGT 53

## RESULT 10

US-09-922-217-616/c  
; Sequence 616, Application US/09922217  
; Patent No. US20020076414A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Secrist, Heather  
; APPLICANT: Benson, Darin R.  
; APPLICANT: Mesgher, Madeleine Joy  
; APPLICANT: Stolk, John A.  
; APPLICANT: Wang, Tongtong

APPLICANT: Jiang, Yuqiu  
APPLICANT: Smith, Carole Lynn  
APPLICANT: King, Gordon E.  
APPLICANT: Wang, Aijun  
APPLICANT: Clapper, Jonathan D.  
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS  
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE  
FILE REFERENCE: 210121.471C13  
CURRENT APPLICATION NUMBER: US/09/922.217  
CURRENT FILING DATE: 2001-08-03  
NUMBER OF SEQ ID NOS: 1124  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 616  
LENGTH: 210  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 156, 181, 194  
OTHER INFORMATION: n = A,T,C or G  
US-09-922-217-616

Query Match 86.7%; Score 13; DB 10; Length 210;  
Best Local Similarity 100.0%; Pred. No. 53;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTG 13  
Db 173 CCTTCTCCCCCTG 161

## RESULT 11

US-09-833-263-616/c  
Sequence 616, Application US/09833263  
Patent No. US20020110547A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Aijun  
APPLICANT: Clapper, Jonathan D.  
APPLICANT: Stolk, John A.  
APPLICANT: Meagher, Madeleine J.  
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE  
FILE REFERENCE: 210121.471C12  
CURRENT APPLICATION NUMBER: US/09/833,263  
CURRENT FILING DATE: 2001-04-10  
NUMBER OF SEQ ID NOS: 1093  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 616  
LENGTH: 210  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(210)  
OTHER INFORMATION: n = A,T,C or G  
US-09-833-263-616

Query Match 86.7%; Score 13; DB 10; Length 210;  
Best Local Similarity 100.0%; Pred. No. 53;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTG 13  
Db 173 CCTTCTCCCCCTG 161

## RESULT 12

US-09-867-701-4769/c  
Sequence 4769, Application US/09867701  
Patent No. US20020132237A1  
GENERAL INFORMATION:  
APPLICANT: Aglate, Paul A.  
APPLICANT: Jones, Robert

APPLICANT: Harlocker, Susan L.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
FILE REFERENCE: 210121.497  
CURRENT APPLICATION NUMBER: US/09/867,701  
CURRENT FILING DATE: 2001-05-29  
NUMBER OF SEQ ID NOS: 10912  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4769  
LENGTH: 285  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-867-701-4769

Query Match 86.7%; Score 13; DB 10; Length 285;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTG 13  
Db 23 CCTTCTCCCCCTG 11

## RESULT 13

US-09-712-363-96/c  
Sequence 96, Application US/09712363  
Patent No. US20020164588A1  
GENERAL INFORMATION:  
APPLICANT: Eisenberg, David  
APPLICANT: Rotstein, Sergio H.  
APPLICANT: Marcotte, Edward M.  
TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND  
TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS  
FILE REFERENCE: 07419-032001  
CURRENT APPLICATION NUMBER: US/09/712,363  
CURRENT FILING DATE: 2000-11-13  
PRIOR APPLICATION NUMBER: PCT/US00/02246  
PRIOR FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: 60/179,531  
PRIOR FILING DATE: 2000-02-01  
PRIOR APPLICATION NUMBER: 60/117,844  
PRIOR FILING DATE: 1999-01-29  
PRIOR APPLICATION NUMBER: 60/118,206,  
PRIOR FILING DATE: 1999-02-01  
PRIOR APPLICATION NUMBER: 60/126,593  
PRIOR FILING DATE: 1999-03-26  
PRIOR APPLICATION NUMBER: 60/134,093  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 60/134,092  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 60/165,124  
PRIOR FILING DATE: 1999-11-12  
PRIOR APPLICATION NUMBER: 60/165,086  
PRIOR FILING DATE: 1999-11-12  
NUMBER OF SEQ ID NOS: 292  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 96  
LENGTH: 315  
TYPE: DNA  
ORGANISM: Mycobacterium tuberculosis  
US-09-712-363-96

Query Match 86.7%; Score 13; DB 9; Length 315;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTG 13  
Db 106 CCTTCTCCCCCTG 94

## RESULT 14

US-09-867-701-10110/c

; Sequence 10110, Application US/09867701  
; Patent No. US20020132237A1  
; GENERAL INFORMATION:  
; APPLICANT: Aglate, Paul A.  
; APPLICANT: Jones, Robert  
; APPLICANT: Harlocker, Susan L.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.497  
; CURRENT APPLICATION NUMBER: US/09/867,701  
; CURRENT FILING DATE: 2001-05-29  
; NUMBER OF SEQ ID NOS: 10912  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10110  
; LENGTH: 337  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(337)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-867-701-10110

Query Match 86.7%; Score 13; DB 10; Length 337;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCCCTGTT 15  
|||||  
DB 130 TTCTCCCTGTT 118

## RESULT 15

US-09-954-456-892/c  
; Sequence 892, Application US/09954456  
; Patent No. US20020115057A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, Paul  
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc  
; TITLE OF INVENTION: Sets  
; FILE REFERENCE: 689290-76  
; CURRENT APPLICATION NUMBER: US/09/954,456  
; CURRENT FILING DATE: 2001-09-18  
; PRIOR APPLICATION NUMBER: US/60/233,617  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: US/60/234,052  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: US/60/234,923  
; PRIOR FILING DATE: 2000-09-25  
; PRIOR APPLICATION NUMBER: US/60/235,134  
; PRIOR FILING DATE: 2000-09-25  
; PRIOR APPLICATION NUMBER: US/60/235,637  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US/60/235,638  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US/60/235,711  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: US/60/235,720  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: US/60/235,840  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: US/60/235,863  
; PRIOR FILING DATE: 2000-09-27  
; NUMBER OF SEQ ID NOS: 2276  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 892  
; LENGTH: 383  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-954-456-892

Query Match 86.7%; Score 13; DB 10; Length 383;  
Best Local Similarity 100.0%; Pred. No. 52;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCTTCTCCCTG 13  
|||||  
DB 287 CCTTCTCCCTG 275

Search completed: December 11, 2002, 20:32:36  
Job time : 75.5 secs



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OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 16:56:23 ; Search time 1655.5 Seconds  
(without alignments)  
146.743 Million cell updates/sec

Title: US-09-750-609-10

Perfect score: 15

Sequence: 1 cctctcccccgttt 15

Scoring table: OLIGO\_NUC

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Searched: 16154066 seqs, 8097743376 residues

Word size : 0

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

EST:\*

1: em\_estba:\*  
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6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
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12: gb\_est3:\*  
13: gb\_est4:\*  
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17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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c 4	15	100.0	297	9	AV067076
5	15	100.0	378	14	F07213
6	15	100.0	393	14	T08889
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c 7	15	100.0	399	9	AJ449549
8	15	100.0	401	17	TA8E07P
c 9	15	100.0	403	13	BI706542
c 10	15	100.0	410	10	AW139708
c 11	15	100.0	420	10	AW504644
c 12	15	100.0	421	12	BF514910
c 13	15	100.0	430	13	BG961625
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c 19	15	100.0	452	12	BF926997
c 20	15	100.0	458	9	AI629376
c 21	15	100.0	469	17	BH635764
c 22	15	100.0	471	17	TA295E02P
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c 31	15	100.0	557	9	AL700490
c 32	15	100.0	575	9	AJ397416
33	15	100.0	580	10	BE265171
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c 41	15	100.0	649	10	AW956920
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c 63	15	100.0	743	9	AJ452402
c 64	15	100.0	748	12	BE781551
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c 79	15	100.0	866	9	AJ456352

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AL452614	T. brucei
BI706542	fq07c03.y
AW139708	UI-H-BII-
AW504644	UI-HF-BNO
BF514910	UI-H-BW1-
BG961625	PMO-CT064
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BF926997	CM2-NT019
AI629376	fc05g01.y
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R24819	yg29a01.r1
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R87939	yo47c09.r1
BH622683	1007090G0
AL495313	T. brucei
AJ266559	zq51602.f
AJ446382	AJ446382
AL490520	T. brucei
AL700490	DRF2p686B
AJ397416	AJ397416
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AJ447956	AJ447956
AJ398497	AJ398497
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BF962681	PM4-NN120
AQ661274	Sheared D
BE875768	601487226
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AJ448372	AJ448372
BE250288	600943424
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AJ446776	AJ446776
AJ451509	AJ451509
AJ445545	AJ445545
BI952476	HVSMEM000
BI758440	603022555
AU119633	AU119633
AJ456352	AJ456352

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c 82	15	100.0	911	13	BF116925	602867677	155	14	93.3	372	12	BF803420	QV1-CI017
c 83	15	100.0	919	17	CNS0408B	AL297092	156	14	93.3	372	12	BF805878	CM1-CI009
c 84	15	100.0	920	12	BG028087	Tetraodon	c 157	14	93.3	374	12	BF845773	CM0-EN004
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c 86	15	100.0	935	10	BE250545	AGENCOURT	159	14	93.3	378	12	BF803021	CM1-CI009
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c 88	15	100.0	937	9	AJ455128	AGENCOURT	161	14	93.3	379	12	BF850310	CM3-NN118
c 89	15	100.0	983	13	BI524272	AJ455128	c 162	14	93.3	381	12	BF850709	CM0-EN004
c 90	15	100.0	992	17	CNS037BW	BI524272	163	14	93.3	382	14	T81121	yq24303.r1
c 91	15	100.0	1024	17	CNS04QEC	AL231125	c 164	14	93.3	383	9	AI243320	qn7e08.x
c 92	15	100.0	1042	10	BE250477	Tetraodon	165	14	93.3	384	12	BF805833	CM1-CI001
c 93	15	100.0	1045	14	BM803241	BE250477	166	14	93.3	385	12	BF805832	CM1-CI001
c 94	15	100.0	1056	17	CNS05F31	BM803241	167	14	93.3	386	12	BF805864	CM1-CI009
c 95	15	100.0	1075	12	BF676401	Tetraodon	168	14	93.3	388	12	BF847001	CM0-EN004
c 96	15	100.0	1083	17	CNS05F32	BF676401	169	14	93.3	388	12	BF807456	QV2-HT054
c 97	15	100.0	1099	17	AG052686	AL334487	170	14	93.3	388	12	BF372412	QV3-FT003
c 98	15	100.0	1101	17	CNS05D5A	AG052686	171	14	93.3	389	9	AI918458	ts31c06.x
c 99	15	100.0	1105	12	BG776955	AL331975	c 172	14	93.3	389	14	T84491	yd47g10.s1
c 100	15	100.0	1152	14	BM925445	BG776955	173	14	93.3	391	12	BF803010	CM1-CI009
c 101	15	100.0	1360	12	BE729544	BM925445	174	14	93.3	392	14	H19733	yn60f08.r1
c 102	15	100.0	1530	14	BM921681	BE729544	175	14	93.3	393	12	BF802019	CM1-CI009
c 103	15	100.0	1708	11	BC016738	BM921681	c 176	14	93.3	393	14	BQ329285	CM0-EN004
c 104	15	100.0	4427	11	BC034038	BC016738	177	14	93.3	395	12	BF805843	CM1-CI001
c 105	14	93.3	137	9	AI352379	BC034038	178	14	93.3	397	12	BF801614	CM1-CI009
c 106	14	93.3	151	12	BF950314	AI352379	c 179	14	93.3	397	12	BF845769	CM0-EN004
c 107	14	93.3	174	9	AA212165	BF950314	180	14	93.3	398	12	BF846988	CM0-EN004
c 108	14	93.3	193	12	BF512918	AA212165	c 181	14	93.3	398	17	AZ711196	RPC1-24-8
c 109	14	93.3	217	12	BF950238	BF512918	c 182	14	93.3	399	12	BF845770	CM0-EN004
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c 111	14	93.3	228	12	BB408677	BF950256	184	14	93.3	399	13	BI917611	603183764
c 112	14	93.3	228	10	BB149305	BB408677	185	14	93.3	400	12	BF805842	CM1-CI001
c 113	14	93.3	232	12	BF950328	BB149305	c 186	14	93.3	400	12	BF850712	CM0-EN004
c 114	14	93.3	235	12	BF950252	BF950328	c 187	14	93.3	404	12	BF848311	CM0-EN004
c 115	14	93.3	235	12	BF950252	BF950252	c 188	14	93.3	405	12	BF958566	QV2-NN004
c 116	14	93.3	236	10	AV380926	BF950252	c 189	14	93.3	408	12	BF802043	CM1-CI009
c 117	14	93.3	237	12	BF950323	AV380926	c 190	14	93.3	408	13	BI030787	IL5-MT026
c 118	14	93.3	237	12	AZ455812	BF950323	c 191	14	93.3	409	12	BF802065	CM1-CI009
c 119	14	93.3	249	12	BF950246	AZ455812	c 192	14	93.3	409	12	BF848294	CM0-EN004
c 120	14	93.3	251	12	BF950315	BF950246	c 193	14	93.3	410	13	BJ071292	BJ071292
c 121	14	93.3	252	10	AW753137	BF950315	c 194	14	93.3	411	12	BF808569	CM1-CI009
c 122	14	93.3	254	12	BF950239	AW753137	c 195	14	93.3	412	12	BF801583	CM1-CI009
c 123	14	93.3	256	12	BF950264	BF950239	c 196	14	93.3	412	12	BF801592	CM1-CI009
c 124	14	93.3	257	12	BF950303	BF950264	c 197	14	93.3	412	12	BF848303	CM0-EN004
c 125	14	93.3	258	12	BF950241	BF950303	c 198	14	93.3	413	12	BF848304	CM0-EN004
c 126	14	93.3	258	12	BF950311	BF950241	c 199	14	93.3	413	14	BQ312529	RC1-BN041
c 127	14	93.3	262	9	AV269236	BF950311	c 200	14	93.3	413	14	BQ373132	QV3-FT003
c 128	14	93.3	262	12	BF950261	AV269236	c 201	14	93.3	414	12	BF803014	CM1-CI009
c 129	14	93.3	264	9	AA101092	BF950261	c 202	14	93.3	417	10	AW215073	up06b11.y
c 130	14	93.3	264	12	BF950263	AA101092	c 203	14	93.3	417	12	BF801633	CM1-CI009
c 131	14	93.3	266	14	BQ637029	BF950263	c 204	14	93.3	418	9	AI751952	cn12q10.x
c 132	14	93.3	272	10	BQ606731	BQ637029	c 205	14	93.3	418	12	BF802016	CM1-CI009
c 133	14	93.3	284	14	BQ575469	BQ606731	c 206	14	93.3	418	12	BF802039	CM1-CI009
c 134	14	93.3	287	10	BB722558	BQ575469	c 207	14	93.3	418	12	BF848306	CM0-EN004
c 135	14	93.3	288	10	AW377774	BB722558	c 208	14	93.3	418	12	BF850710	CM0-EN004
c 136	14	93.3	288	14	F02779	AW377774	c 209	14	93.3	419	12	BF803030	CM1-CI009
c 137	14	93.3	290	10	BB133038	F02779	c 210	14	93.3	419	12	BF848301	CM0-EN004
c 138	14	93.3	290	10	BB443106	BB133038	c 211	14	93.3	421	12	BF848309	CM0-EN004
c 139	14	93.3	307	10	BB260972	BB443106	c 212	14	93.3	422	12	BF802257	CM1-CI009
c 140	14	93.3	308	10	BB215312	BB260972	c 213	14	93.3	423	10	AW822429	uq0f12.x
c 141	14	93.3	308	12	BF845775	BB215312	c 214	14	93.3	423	12	BF845768	CM0-EN004
c 142	14	93.3	316	10	BE507352	BF845775	c 215	14	93.3	424	12	BF808551	CM1-CI009
c 143	14	93.3	316	10	BE507362	BE507352	c 216	14	93.3	425	12	BF846991	CM0-EN004
c 144	14	93.3	327	14	H41711	BE507362	c 217	14	93.3	425	14	BU022123	QHE5P19.y
c 145	14	93.3	333	12	BF845771	H41711	c 218	14	93.3	425	17	AQ113334	CITP-HSP-2
c 146	14	93.3	350	14	H23897	BF845771	c 219	14	93.3	426	12	BF802002	CM1-CI009
c 147	14	93.3	355	12	BF848315	H23897	c 220	14	93.3	426	14	BQ340311	QV2-NN200
c 148	14	93.3	357	12	BF805845	BF848315	c 221	14	93.3	427	10	AW751856	QV2-CT012
c 149	14	93.3	364	14	BQ324261	BF805845	c 222	14	93.3	427	12	BF801988	CM1-CI009
c 150	14	93.3	365	12	BF808577	BQ324261	c 223	14	93.3	428	9	AI124748	am61e12.x
c 151	14	93.3	365	12	BF808575	BF808577	c 224	14	93.3	428	12	BF801995	CM1-CI009
c 152	14	93.3	367	12	BF805875	BF808575	c 225	14	93.3	429	9	AI270694	qu90f12.x

226	14	93.3	430	12	BF802018	BF802018	CM1-CI009	299	14	93.3	586	10	AW365203	AW365203	MR0-HT006
227	14	93.3	430	12	BF802024	BF802024	CM1-CI009	300	14	93.3	587	10	AW177882	AW177882	IL3-HT005
228	14	93.3	430	12	BF802260	BF802260	CM1-CI009	301	14	93.3	587	10	BF618307	BF618307	HVSMEC000
229	14	93.3	430	12	BF848298	BF848298	CM0-EN004	302	14	93.3	588	10	BE614114	BE614114	601503857
230	14	93.3	431	12	BF808544	BF808544	CM1-CI009	303	14	93.3	588	10	BQ182579	BQ182579	UI-H-EU0-
231	14	93.3	432	12	BF803013	BF803013	CM1-CI009	c 304	14	93.3	595	13	B1908590	B1908590	603069993
232	14	93.3	432	12	BF808581	BF808581	CM1-CI009	305	14	93.3	599	10	AW177833	AW177833	IL3-HT005
233	14	93.3	434	12	BF846978	BF846978	CM0-EN004	306	14	93.3	599	10	AW177881	AW177881	IL3-HT005
234	14	93.3	434	12	BG897595	BG897595	HOA15-1-G	307	14	93.3	599	10	AW177881	AW177881	IL3-HT005
235	14	93.3	434	17	BH169414	BH169414	SALK_0013	308	14	93.3	600	13	B1986622	B1986622	3174-14 M
236	14	93.3	435	12	BF802261	BF802261	CM1-CI009	309	14	93.3	600	13	B1986645	B1986645	3174-44 M
237	14	93.3	436	12	BF931083	BF931083	CM1-NF027	c 310	14	93.3	601	12	BE747858	BE747858	601578641
238	14	93.3	437	12	BF803008	BF803008	CM1-CI009	311	14	93.3	602	14	BQ180978	BQ180978	UI-H-EU0-
239	14	93.3	437	12	BF848312	BF848312	CM0-EN004	312	14	93.3	602	14	BQ181939	BQ181939	UI-H-EU0-
240	14	93.3	439	12	BF801998	BF801998	CM1-CI009	c 313	14	93.3	603	13	BG924790	BG924790	HNC36-1-G
241	14	93.3	440	9	AI744681	AI744681	wg02g02.x	c 314	14	93.3	605	17	B16174	B16174	347C19-TP C
242	14	93.3	440	12	BF802020	BF802020	CM1-CI009	c 315	14	93.3	605	17	AQ525566	AQ525566	HS-5227-B
243	14	93.3	440	12	BF802069	BF802069	CM1-CI009	316	14	93.3	609	17	BQ390929	BQ390929	NISC_mq15
244	14	93.3	441	12	BF802256	BF802256	CM1-CI009	317	14	93.3	610	14	BQ396664	BQ396664	NISC_nq22
245	14	93.3	442	12	BF802010	BF802010	CM1-CI009	318	14	93.3	612	9	AL646235	AL646235	AL646235
246	14	93.3	443	12	BF808572	BF808572	CM1-CI009	c 319	14	93.3	612	17	BH083105	BH083105	RPCI-24-3
247	14	93.3	444	12	BF846989	BF846989	CM0-EN004	c 320	14	93.3	614	14	BQ183139	BQ183139	UI-H-EU0-
248	14	93.3	445	13	BG927815	BG927815	HNC45-1-B	c 321	14	93.3	615	12	BG898807	BG898807	HOA4-1-C-
249	14	93.3	445	14	BQ329284	BQ329284	CM0-EN004	c 322	14	93.3	615	12	BF031013	BF031013	601558879
250	14	93.3	446	12	BF847000	BF847000	CM0-EN004	c 323	14	93.3	617	10	BE542024	BE542024	601066932
251	14	93.3	447	12	BF848316	BF848316	CM0-EN004	324	14	93.3	623	9	AJ398773	AJ398773	AJ398773
252	14	93.3	447	12	BF850711	BF850711	CM0-EN004	325	14	93.3	628	14	BQ392790	BQ392790	NISC_mq26
253	14	93.3	449	9	AA670642	AA670642	v107a05.r	326	14	93.3	630	10	BB657487	BB657487	BB657487
254	14	93.3	449	12	BF801585	BF801585	CM1-CI009	327	14	93.3	634	14	BQ181814	BQ181814	UI-H-EU0-
255	14	93.3	450	10	AA03106	AA03106	UI-HF-BK0	328	14	93.3	634	14	BQ183943	BQ183943	UI-H-EU0-
256	14	93.3	450	12	BF847003	BF847003	CM0-EN004	329	14	93.3	638	14	BQ182672	BQ182672	UI-H-EU0-
257	14	93.3	451	17	AZ883987	AZ883987	RPCI-23-1	330	14	93.3	639	13	BM120815	BM120815	L0944D13-
258	14	93.3	453	12	BF802265	BF802265	CM1-CI009	c 331	14	93.3	642	17	AG050166	AG050166	Pan trogl
259	14	93.3	453	12	BF850717	BF850717	CM0-EN004	c 332	14	93.3	649	9	AL659701	AL659701	AL659701
260	14	93.3	453	17	AZ816990	AZ816990	2M0085P19	333	14	93.3	650	14	BQ182475	BQ182475	UI-H-EU0-
261	14	93.3	454	12	BF802017	BF802017	CM1-CI009	334	14	93.3	651	10	BQ004619	BQ004619	UI-H-EI0-
262	14	93.3	456	12	BF801999	BF801999	CM1-CI009	c 335	14	93.3	653	10	AW365204	AW365204	MR0-HT006
263	14	93.3	460	14	R94700	R94700	Yq43c03.s1	c 336	14	93.3	653	12	BG789292	BG789292	SEAUMC009
264	14	93.3	461	17	BH212045	BH212045	SALK_0070	337	14	93.3	656	17	AZ753211	AZ753211	RPCI-24-8
265	14	93.3	470	12	BF802021	BF802021	CM1-CI009	c 338	14	93.3	660	10	BE514784	BE514784	601316712
266	14	93.3	471	13	BM254681	BM254681	S16196.MA	c 339	14	93.3	662	12	BQ324914	BQ324914	602423553
267	14	93.3	474	17	AQ954581	AQ954581	nbe00071A	340	14	93.3	664	14	BQ004652	BQ004652	UI-H-EI0-
268	14	93.3	476	9	AA043301	AA043301	zk55d09.s	341	14	93.3	664	14	BQ004652	BQ004652	UI-H-EI0-
269	14	93.3	478	14	BQ339938	BQ339938	QV2-NN004	342	14	93.3	668	14	BQ181085	BQ181085	UI-H-EU0-
270	14	93.3	481	13	BM308641	BM308641	sak48f11	343	14	93.3	674	17	BH335850	BH335850	CH230-169
271	14	93.3	489	12	BF953694	BF953694	RC4-NN117	c 344	14	93.3	677	14	BG975859	BG975859	602842179
272	14	93.3	500	12	BF019465	BF019465	uxi0e10.y	c 345	14	93.3	677	14	BQ045396	BQ045396	GA_Ed008
273	14	93.3	503	14	BE557334	BE557334	H4045D12-	346	14	93.3	679	12	BF445084	BF445084	naD23b04
274	14	93.3	504	12	BE705850	BE705850	IL3-HT005	347	14	93.3	680	14	BQ044975	BQ044975	UI-H-EU0-
275	14	93.3	505	14	T84490	T84490	Yd47g10.r1	c 348	14	93.3	685	10	AW604437	AW604437	RC3-CT025
276	14	93.3	513	10	BE584979	BE584979	2-6B-20 P	c 349	14	93.3	688	13	BG928689	BG928689	HNC72-1-G
277	14	93.3	519	13	BF791283	BF791283	i0d4b01.y	c 350	14	93.3	688	13	BM041978	BM041978	603615856
278	14	93.3	519	17	AZ654173	AZ654173	IM0528009	351	14	93.3	688	14	BQ045399	BQ045399	GA_Ed008
279	14	93.3	523	17	AZ650645	AZ650645	IM0520M22	c 352	14	93.3	691	12	BG680572	BG680572	602629006
280	14	93.3	525	14	BQ074021	BQ074021	fz34c12.x	353	14	93.3	693	17	AG077385	AG077385	Pan trogl
281	14	93.3	533	13	BI465317	BI465317	603206638	c 354	14	93.3	695	12	BE747221	BE747221	601580938
282	14	93.3	535	9	AI949103	AI949103	wq19e09.x	c 355	14	93.3	701	12	BG428158	BG428158	602498808
283	14	93.3	536	12	BE705855	BE705855	IL3-HT005	c 356	14	93.3	712	12	BM726822	BM726822	UI-E-EJ0-
284	14	93.3	536	12	R21046	R21046	Yg52a04.r1	357	14	93.3	721	17	AG122350	AG122350	Pan trogl
285	14	93.3	542	12	BG898084	BG898084	HOA38-1-F	c 358	14	93.3	723	17	CNS034JM	CNS034JM	Tetraodon
286	14	93.3	553	10	AW365206	AW365206	MR0-HT006	c 359	14	93.3	727	12	BG472445	BG472445	602514136
287	14	93.3	555	17	AZ818736	AZ818736	2M0088M19	360	14	93.3	729	14	BQ183753	BQ183753	UI-H-EU0-
288	14	93.3	556	10	AV702592	AV702592	AV702592	c 361	14	93.3	732	14	BQ182050	BQ182050	UI-H-EU0-
289	14	93.3	556	13	BQ035372	BQ035372	EJ035372	c 362	14	93.3	733	12	BG473938	BG473938	602516428
290	14	93.3	560	12	BF792066	BF792066	602252473	c 363	14	93.3	739	13	BE741013	BE741013	601595387
291	14	93.3	567	14	BQ182258	BQ182258	UI-H-EU0-	c 364	14	93.3	739	13	BI684772	BI684772	603307140
292	14	93.3	567	14	BQ334034	BQ334034	MR0-MT012	c 365	14	93.3	743	13	BI890095	BI890095	2F637-2-0
293	14	93.3	568	12	BE705849	BE705849	IL3-HT005	c 366	14	93.3	746	17	AQ368213	AQ368213	tox00001N
294	14	93.3	577	17	AZ344936	AZ344936	IM0079D16	c 367	14	93.3	751	12	BG327445	BG327445	602426427
295	14	93.3	583	14	BQ419281	BQ419281	faa36h04	c 368	14	93.3	752	14	BQ007885	BQ007885	UI-H-EI0-
296	14	93.3	584	14	BQ004253	BQ004253	UI-H-EI0-	c 369	14	93.3	755	10	BE130672	BE130672	L48-873T3
297	14	93.3	585	10	AV764095	AV764095	AV764095	c 370	14	93.3	758	14	BQ181926	BQ181926	UI-H-EU0-
298	14	93.3	585	14	BQ285725	BQ285725	faa29b10	c 371	14	93.3	762	12	BG860360	BG860360	1024070A0

372	14	93.3	762	17	AG180802	Pan trogl	c 445	13	86.7	114	17	BH607467
373	14	93.3	779	12	BG548733	602576352	446	13	86.7	122	17	BH639659
374	14	93.3	779	14	BM718964	UI-E-E01-	447	13	86.7	126	17	AZ342525
375	14	93.3	788	17	BH588802	BOHT002TR	448	13	86.7	144	10	AW391528
376	14	93.3	786	13	BI143705	602307352	449	13	86.7	144	10	AW391528
377	14	93.3	797	13	BI868694	603392022	450	13	86.7	148	9	AL714822
378	14	93.3	801	17	BI9622	F612-Sp6 I	451	13	86.7	150	14	H48109
379	14	93.3	804	12	BF974470	602243566	452	13	86.7	151	9	AV130769
380	14	93.3	814	12	BG583044	EST484786	453	13	86.7	151	9	AQ267724
381	14	93.3	825	12	BF248204	601821203	454	13	86.7	151	17	FR0024607
382	14	93.3	827	13	BI079126	602873417	455	13	86.7	157	17	AZ716683
383	14	93.3	839	17	AQ741331	HS_5570.B	456	13	86.7	158	9	AI071619
384	14	93.3	850	12	BF029076	601764573	457	13	86.7	161	17	AZ737405
385	14	93.3	854	12	BG853922	1024038E0	458	13	86.7	161	17	AZ746018
386	14	93.3	855	17	AQ329452	nbxb0045C	459	13	86.7	164	12	BF805837
387	14	93.3	862	14	BQ224734	AGENCOURT	460	13	86.7	175	9	AI213318
388	14	93.3	865	12	BF246979	601854369	461	13	86.7	178	10	AW779636
389	14	93.3	869	12	BF979683	602288532	462	13	86.7	183	17	AZ019037
390	14	93.3	872	14	BQ898530	AGENCOURT	463	13	86.7	189	9	AL079975
391	14	93.3	878	14	BQ215741	AGENCOURT	464	13	86.7	190	10	AW815589
392	14	93.3	881	12	BF036952	601459183	465	13	86.7	190	14	C01728
393	14	93.3	890	12	BF668633	602123688	466	13	86.7	194	17	BH777251
394	14	93.3	894	12	BF672581	602152157	467	13	86.7	194	17	BH889400
395	14	93.3	895	17	CNS01TLD	Tetraodon	468	13	86.7	202	17	AZ652917
396	14	93.3	906	13	BM008669	603618339	469	13	86.7	213	9	AV097028
397	14	93.3	915	9	AI524687	th12a07.x	470	13	86.7	213	10	BE011550
398	14	93.3	929	12	BF182768	601809275	471	13	86.7	214	9	AI906075
399	14	93.3	940	14	BQ691486	AGENCOURT	472	13	86.7	214	9	BE152676
400	14	93.3	948	17	AQ901536	HS_3233.B	473	13	86.7	214	9	AV287420
401	14	93.3	959	12	BQ24674	602275481	474	13	86.7	214	10	BB429038
402	14	93.3	964	14	BQ711308	AGENCOURT	475	13	86.7	215	10	BB269976
403	14	93.3	965	14	BQ958755	AGENCOURT	476	13	86.7	216	12	BE700178
404	14	93.3	972	17	CNS055QD	Tetraodon	477	13	86.7	216	17	BM62670
405	14	93.3	976	17	AQ743771	HS_5501.A	478	13	86.7	217	17	BH642291
406	14	93.3	978	12	BG257353	602377878	479	13	86.7	218	10	BB591677
407	14	93.3	984	17	CNS055VJ	Tetraodon	480	13	86.7	218	10	BB600484
408	14	93.3	987	17	CNS042VD	Tetraodon	481	13	86.7	218	10	BE326565
409	14	93.3	992	12	BF308416	601890733	482	13	86.7	219	10	BB435389
410	14	93.3	1001	17	CNS04VKF	AGENCOURT	483	13	86.7	220	10	BB435389
411	14	93.3	1010	13	BQ044425	603621780	484	13	86.7	220	10	BB435389
412	14	93.3	1027	14	BQ059568	AGENCOURT	485	13	86.7	220	10	BB435937
413	14	93.3	1041	17	CNS03DDE	Tetraodon	486	13	86.7	221	9	AV096817
414	14	93.3	1047	13	BI255744	602977157	487	13	86.7	223	9	AZ277728
415	14	93.3	1052	12	BE745033	601576127	488	13	86.7	224	9	AI986006
416	14	93.3	1067	14	BQ052391	AGENCOURT	489	13	86.7	224	10	BB573977
417	14	93.3	1074	14	BM917151	AGENCOURT	490	13	86.7	224	14	BQ761694
418	14	93.3	1098	17	CNS04WXE	AGENCOURT	491	13	86.7	224	17	AZ759964
419	14	93.3	1106	12	BE962757	601656153	492	13	86.7	228	10	BB431706
420	14	93.3	1111	13	BM551502	AGENCOURT	493	13	86.7	229	17	BH780156
421	14	93.3	1119	14	BQ051343	AGENCOURT	494	13	86.7	232	10	BB010620
422	14	93.3	1120	13	BM477118	AGENCOURT	495	13	86.7	232	12	BG816697
423	14	93.3	1122	13	BM454475	AGENCOURT	496	13	86.7	233	10	BB581505
424	14	93.3	1123	12	BF143187	601788085	497	13	86.7	235	17	BH771436
425	14	93.3	1128	12	BG831422	602766345	498	13	86.7	236	9	AB030425
426	14	93.3	1129	14	BM805290	AGENCOURT	499	13	86.7	236	10	AW320415
427	14	93.3	1196	14	BQ948502	AGENCOURT	500	13	86.7	236	17	AZ426618
428	14	93.3	1203	12	BG845061	1024008F0	501	13	86.7	237	9	AI471025
429	14	93.3	1212	14	BQ650647	AGENCOURT	502	13	86.7	237	10	BB112151
430	14	93.3	1232	13	BM461098	AGENCOURT	503	13	86.7	237	10	BB558253
431	14	93.3	1247	17	AG073214	Pan trogl	504	13	86.7	237	17	BH110722
432	14	93.3	1277	12	BG843851	6024004C1	505	13	86.7	238	9	AV054336
433	14	93.3	1350	12	BE747035	601580783	506	13	86.7	238	13	BI035026
434	14	93.3	1484	12	BG111620	602282659	507	13	86.7	239	14	AQ274667
435	14	93.3	1501	12	BF694757	602080846	508	13	86.7	239	9	AV277865
436	14	93.3	1541	12	BE964119	601657803	509	13	86.7	239	13	BI027975
437	14	93.3	1626	12	BG171210	602321410	510	13	86.7	240	9	AA016724
438	14	93.3	1739	14	BM924739	AGENCOURT	511	13	86.7	240	10	BB029874
439	14	93.3	1806	12	BF163541	601809843	512	13	86.7	241	9	AI688865
440	14	93.3	1998	11	AK018387	Mus muscu	513	13	86.7	242	17	BH771488
441	14	93.3	6320	11	AF161390	Homo sapi	514	13	86.7	243	10	AV364197
442	13	86.7	39	17	AZ405991	1M0175L05	515	13	86.7	243	17	BH620099
443	13	86.7	87	9	AI869477	tw41f12.x	516	13	86.7	244	10	BB318509
444	13	86.7	113	12	BG274355	WHE2227_F	517	13	86.7	245	9	AV028813

c 518	13	86.7	246	9	AI683289	AT1683289	tw50b04.x	591	13	86.7	289	17	BH873402	BH873402	hp44g05.b
519	13	86.7	246	10	BF3398012	BF3398012	BF3398012	592	13	86.7	290	10	BB053804	BB053804	BB053804
520	13	86.7	246	12	BF332977	BF332977	MR1-BT079	c 593	13	86.7	290	10	BB070371	BB070371	BB070371
c 521	13	86.7	246	17	AG019279	AG019279	Homo sapi	594	13	86.7	290	10	BB163034	BB163034	BB163034
522	13	86.7	248	9	AI695589	AI695589	we51f08.x	595	13	86.7	290	10	BB163469	BB163469	BB163469
523	13	86.7	248	13	BI803042	BI803042	H098F07.E	596	13	86.7	290	10	BB338926	BB338926	BB338926
c 524	13	86.7	248	13	BM544141	BM544141	AGENCOURT	c 597	13	86.7	290	14	BQ750100	BQ750100	SnEST4a68
c 525	13	86.7	249	9	AI963337	AI963337	wt61h04.x	c 598	13	86.7	290	14	T32268	ES745993	Hu
c 526	13	86.7	249	9	AA491947	AA491947	ng16f10.s	c 599	13	86.7	291	9	AA482059	zv41f12.r	AA482059
527	13	86.7	251	9	AA481877	AA481877	zv41f12.s	600	13	86.7	291	9	AA487189	BB487189	BB487189
528	13	86.7	253	9	AT000537	AT000537	AT000537	601	13	86.7	292	9	AI006401	ua71f05.f	AI006401
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c 530	13	86.7	254	12	BG320136	BG320136	Zm03.04c1	603	13	86.7	292	13	BM279763	zah5425.z	BM279763
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532	13	86.7	255	9	AA464195	AA464195	zx83h03.s	605	13	86.7	295	10	BB351351	BB351351	BB351351
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535	13	86.7	257	12	BF804130	BF804130	CM2-C1013	608	13	86.7	296	9	AA252217	zr63g09.s	AA252217
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540	13	86.7	261	9	AA989735	AA989735	am71h09.s	c 613	13	86.7	297	13	BM444856	EBem09_SO	BM444856
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545	13	86.7	266	9	AI220015	AI220015	qg78f03.x	618	13	86.7	299	13	BM055337	le93e08.y	BM055337
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548	13	86.7	268	10	BB394149	BB394149	BB394149	621	13	86.7	302	10	BB082086	BB082086	BB082086
c 549	13	86.7	268	10	BB595252	BB595252	BB595252	622	13	86.7	304	10	BB090072	BB090072	BB090072
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551	13	86.7	268	17	BF771664	BF771664	hg35h02.g	624	13	86.7	305	10	BB111799	BB111799	BB111799
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554	13	86.7	269	13	BM286435	BM286435	5265h08.MA	c 627	13	86.7	306	10	AW261976	xg29g03.x	AW261976
555	13	86.7	270	9	AI537021	AI537021	to15a12.x	c 628	13	86.7	307	9	AI174421	aa46a08.s	AI174421
556	13	86.7	271	9	AV267711	AV267711	AV267711	c 629	13	86.7	308	9	AI125316	qg88c12.x	AI125316
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560	13	86.7	274	10	AV372754	AV372754	AV372754	633	13	86.7	313	10	BB492349	BB492349	BB492349
561	13	86.7	274	10	BB329366	BB329366	BB329366	634	13	86.7	314	10	AW121317	UI-M-BH2	AW121317
c 562	13	86.7	274	10	BB561701	BB561701	BB561701	635	13	86.7	314	10	BB255595	BB255595	BB255595
c 563	13	86.7	275	9	AI476509	AI476509	tm22d03.x	636	13	86.7	315	9	AA809592	AA809592	AA809592
c 564	13	86.7	275	9	AA464790	AA464790	zx83h03.r	637	13	86.7	315	9	AV101685	AV101685	AV101685
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c 566	13	86.7	276	12	BF928076	BF928076	IL5-NT022	639	13	86.7	315	12	BF843172	MR2-MT104	BF843172
c 567	13	86.7	277	12	BF509374	BF509374	UI-H-BI4-	640	13	86.7	315	14	FI3867	ATTS4789.Ve	FI3867
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570	13	86.7	280	17	BBH80065	BBH80065	fzmb014f0	643	13	86.7	317	10	BB093270	BB093270	BB093270
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c 573	13	86.7	282	12	BE862910	BE862910	UI-M-BG1-	646	13	86.7	318	9	AV211282	AV211282	AV211282
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c 578	13	86.7	284	10	BB361253	BB361253	BB361253	651	13	86.7	320	17	BH778661	fzmb013f0	BH778661
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c 580	13	86.7	285	9	AA428416	AA428416	zr62d05.f	653	13	86.7	322	14	BQ005821	UI-H-EDO-	BQ005821
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582	13	86.7	286	10	BB330111	BB330111	BB330111	655	13	86.7	324	10	BB459722	BB459722	BB459722
583	13	86.7	286	10	BB439644	BB439644	BB439644	656	13	86.7	324	10	BB093093	BB093093	BB093093
c 584	13	86.7	286	13	BI440693	BI440693	lb93g03.x	c 657	13	86.7	325	17	BH877593	hr39c10.g	BH877593
c 585	13	86.7	287	9	AA429183	AA429183	zv49f06.r	658	13	86.7	325	9	AA559093	nj33b06.s	AA559093
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c 589	13	86.7	287	17	BH128332	BH128332	G-3b16.f	c 662	13	86.7	325	14	BQ161052	WHE1077.E	BQ161052
c 590	13	86.7	289	10	BB113081	BB113081	BB113081	c 663	13	86.7	326	12	BF890915	PM2-MT010	BF890915

c 664	13	86.7	326	12	B995814	UI-M-B21-	B995814	737	13	86.7	359	10	B847677	BB847677
c 665	13	86.7	326	12	Bf197918	7p8e09.x	Bf197918	738	13	86.7	360	9	A1422524	A1422524
c 666	13	86.7	327	14	BM709300	UI-E-CQ1-	BM709300	739	13	86.7	360	9	AJ473628	AJ473628
c 667	13	86.7	328	9	AI033641	ow14d10.x	AI033641	740	13	86.7	360	17	BH782688	BH782688
c 668	13	86.7	328	10	BE489020	WHEI1061.E	BE489020	741	13	86.7	361	12	BF022915	BF022915
c 669	13	86.7	328	17	AQ001238	CIT-HSP-2	AQ001238	742	13	86.7	361	13	BF135305	BF135305
c 670	13	86.7	329	12	BE765167	IL2-NT009	BE765167	743	13	86.7	362	9	AI415262	AI415262
c 671	13	86.7	330	9	AUI68814	AUI68814	AUI68814	744	13	86.7	362	10	AV740084	AV740084
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c 674	13	86.7	331	9	AI152630	ud93a03.r	AI152630	747	13	86.7	362	17	AQ908392	AQ908392
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c 677	13	86.7	332	14	BQ027478	UI-H-C00-	BQ027478	750	13	86.7	364	9	AI376555	AI376555
c 678	13	86.7	332	14	BQ662007	HR01C24u	BQ662007	751	13	86.7	364	12	BF458128	BF458128
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c 682	13	86.7	334	9	AI040367	ox16b02.x	AI040367	755	13	86.7	369	12	BF525271	BF525271
c 683	13	86.7	334	14	R75256	MDB1263 Mou	R75256	756	13	86.7	370	10	BB841297	BB841297
c 684	13	86.7	335	9	AA621224	zbU1q03.s	AA621224	757	13	86.7	370	12	BG878712	BG878712
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c 686	13	86.7	335	17	A2932917	zb50g08 J	A2932917	759	13	86.7	370	17	BH866687	BH866687
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## ALIGNMENTS

RESULT 1  
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 ACCESSION AZ284882  
 VERSION GI:9526668  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 181)  
 Z hao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret  
 B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.  
 and Fraser,C.M.  
 Mouse BAC End Sequences from Library RPCI-23  
 Unpublished (1999)  
 TITLE Other GSSs: RPCI-23-442E20.TJ  
 JOURNAL Contact: Shaying Zhao  
 COMMENT Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA

BH876695 hr32g07.b  
 BB840417 BB840417  
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 BB836778 BB836778  
 BF291788 WHE2204.A  
 C22356 C22356 RICE  
 BH785148 fzm013f0  
 AI424915 tg38d07.x  
 AV668547 AV668547  
 W23819 zb79d06.r1

Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: szhao@tigr.Org  
 Clones are derived from the mouse BAC library RPCI-23. For BAC  
 library availability, please contact Pieter de Jong  
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from  
 BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)  
 or from Resea ch Genetics (info@resgen.com). BAC end page:  
 http://www.tigr.org/tdb/bac\_ends/mouse/bac\_end\_intro.html  
 Plate: 442 row: E column: 20  
 Seq primer: T7  
 Class: BAC ends.

FEATURES  
 source

Location/Qualifiers  
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 /clone\_lib="RPCI-23"  
 /sex="Female"  
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 /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site:1:  
 EcoRI; Site:2: EcoRI; Female C57BL/6J mouse kidney and/or  
 brain genomic DNA was isolated and partially digested  
 with a combination of EcoRI and EcoRI Methylase. Size  
 selected DNA was cloned into the pBACe3.6 vector at the  
 EcoRI sites. The ligation products were transformed into  
 DH10B electrocompetent cells (BRL Life Technologies)."  
 BASE COUNT 54 a 54 c 26 g 47 t  
 ORIGIN

Query Match 100.0%; Score 15; DB 17; Length 181;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGTT 15  
 |||||  
 Db 165 CCTTCTCCCTGTT 179

RESULT 2  
 AV335397

LOCUS AV335397 226 bp mRNA linear EST 11-NOV-1999  
 DEFINITION Mus musculus cDNA clone 630571M18 3' similar to AF006196 Mus  
 musculus metalloprotease-disintegrin MDC15 mRNA, mRNA sequence.

ACCESSION AV335397.1 GI:6375449  
 VERSION AV335397  
 KEYWORDS EST.  
 SOURCE house mouse.

## ORGANISM

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 226)

## REFERENCE

## AUTHORS

Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T.,  
 Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F.,  
 Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai  
 C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M.,  
 Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,  
 Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K., Shibata  
 Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H.,  
 Suzuki,H., Takahashi,F., Tateno,M., Tomimaga,N., Tsunoda,Y.,  
 Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A., Yokota,T.,  
 Yoshiki,A., Yoshino,M., Muramatsu,M., and Hayashizaki,Y.  
 RIKEN Mouse ESTs (Konno,H., et al. 1999)  
 Unpublished (1999)

## TITLE

## JOURNAL

## COMMENT

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 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216





## further details.

```

FEATURES
  source
    Location/Qualifiers
      1..297
        /organism="Mus musculus"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone_lib="Mus musculus small intestine C57BL/6J adult"
        /sex="male"
        /tissue_type="small intestine"
        /dev_stage="adult"
        /note="Organ: mammary gland; Vector: p7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTACCAATCGAAGTGGAGCGCGAATGGTTTTTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."
BASE COUNT      95 a      62 c      79 g      61 t
ORIGIN
Query Match      100.0%; Score 15; DB 9; Length 297;
Best Local Similarity 100.0%; Pred. NO. 5.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
    |||||||
Db 45 CCTTCTCCCCCTGTT 31

RESULT 5
LOCUS      F07213
DEFINITION HSC1ZB021 normalized infant brain cDNA Homo sapiens EST 20-FEB-1995
VERSION    c-1zb02, mRNA sequence.
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 378)
AUTHORS   Aufray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C., Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y., Sebastiani-Kabatchis,C. and Tessier,A.
TITLE     IMAGE: molecular integration of the analysis of the human genome and its expression
JOURNAL   C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
MEDLINE   95277534
COMMENT   Contact: Genethon
            Genexpress-Genethon
            Genethon Centre de recherche sur le Genome Humain
            1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
            Tel: 33169472800
            Fax: 33160778698
            Email: genexpress@genethon.fr
            Single read.
            Genexpress_library_id: C; Genexpress_sequence_id: y1c-1zb02
            Seq primer: (-21)MI3_universal.
            Location/Qualifiers
              1..378
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="c-1zb02"
                /clone_lib="normalized infant brain cDNA"
                /sex="Female"
                /tissue_type="total brain"

FEATURES
  source
    Location/Qualifiers
      1..393
        /organism="Homo sapiens"
        /db_xref="ATCC (inhost):85383"
        /db_xref="taxon:9606"
        /clone="HIBBL71"
        /clone_lib="Infant Brain, Bento Soares"
        /note="Vector: Lafmid; The IB library was constructed by directional cloning and oligo(dT)-priming in the Lafmid vector, utilizing a three month old infant human brain (total brain)."
BASE COUNT      78 a     114 c     101 g     99 t     1 others
ORIGIN
Query Match      100.0%; Score 15; DB 14; Length 393;
Best Local Similarity 100.0%; Pred. NO. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
    |||||||
Db 130 CCTTCTCCCCCTGTT 144

RESULT 7
LOCUS      AJ449549/C
DEFINITION AJ449549 riken1 Gallus gallus cDNA clone 22gllr1, mRNA sequence.

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```

/dev_stage="3 months old"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII; Site_2: NotI; sex=Female; dev_stage=3 months old; isolate=muscular atrophy patient; tissue_type=total brain; total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA vector. Clone library from B.Souares, Psychiatry Dept. Columbia University, USA. Normalization_method: Bento Soares, P.N.A.S in press"
BASE COUNT      68 a     111 c     99 g     98 t     2 others
ORIGIN

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Query Match      100.0%; Score 15; DB 14; Length 378;
Best Local Similarity 100.0%; Pred. NO. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CCTTCTCCCCCTGTT 15
    |||||||
Db 193 CCTTCTCCCCCTGTT 207

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RESULT 6
T08889
LOCUS      T08889
DEFINITION EST06781 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBL71 5' end similar to p87 transporter-like protein, mRNA sequence.
ACCESSION  T08889
VERSION    T08889.1 GI:389917
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 393)
AUTHORS   Adams,M.D., Soares,M.B., Kerlavage,A.R., Fields,C. and Venter,J.C.
TITLE     Rapid cDNA sequencing (expressed sequence tags) from a directionally cloned human infant brain cDNA library
JOURNAL   Nat. Genet. 4, 373-380 (1993)
MEDLINE   94004965
COMMENT   Contact: Adams, MD
            The Institute for Genomic Research
            932 Clopper Road, Gaithersburg, MD 20878
            Tel: 3018699056
            Fax: 3018699423
            Email: mdadams@tigr.org
            Seq primer: MI3 Reverse.
            Location/Qualifiers
              1..393
                /organism="Homo sapiens"
                /db_xref="ATCC (inhost):85383"
                /db_xref="taxon:9606"
                /clone="HIBBL71"
                /clone_lib="Infant Brain, Bento Soares"
                /note="Vector: Lafmid; The IB library was constructed by directional cloning and oligo(dT)-priming in the Lafmid vector, utilizing a three month old infant human brain (total brain)."
BASE COUNT      78 a     114 c     101 g     99 t     1 others
ORIGIN

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Query Match      100.0%; Score 15; DB 14; Length 393;
Best Local Similarity 100.0%; Pred. NO. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CCTTCTCCCCCTGTT 15
    |||||||
Db 130 CCTTCTCCCCCTGTT 144

```

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RESULT 7
LOCUS      AJ449549/C
DEFINITION AJ449549 riken1 Gallus gallus cDNA clone 22gllr1, mRNA sequence.

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ACCESSION      AJ449549
VERSION        AJ449549.1  GI:20216770
KEYWORDS       EST.
SOURCE         chicken.
ORGANISM       Gallus gallus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
               Phasianinae; Gallus.
REFERENCE      1 (bases 1 to 399)
AUTHORS        Buerstedde, J.M.
TITLE          Gallus gallus bursal lymphocyte EST
JOURNAL        Unpublished (2002)
COMMENT        Contact: Buerstedde JM
               Cellular Immunology
               Heinrich-Pette-Institute
               Martinistr. 52, 20251 Hamburg, Germany
               Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
               Location/Qualifiers
               1..399
               /organism="Gallus gallus"
               /db_xref="taxon:9031"
               /clone="22g1lrl"
               /clone_lib="rikeni"
               /cell_type="bursal lymphocyte"
               /dev_stage="2-3 weeks old"
               /note="CB inbred strain"

BASE COUNT    120 a 78 c 103 g 97 t 1 others
ORIGIN

Query Match   100.0%; Score 15; DB 9; Length 399;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
    |||||||
DB 107 CCTTCTCCCCCTGTT 93

RESULT 8
TABE07P
LOCUS          T. brucei sheared genomic DNA clone 8e07, forward sequence, genomic
DEFINITION     survey sequence.
ACCESSION      AL452614
VERSION        AL452614.1  GI:11861158
KEYWORDS       GSS.
SOURCE         Trypanosoma brucei.
ORGANISM       Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
               Trypanosoma.
REFERENCE      1 (bases 1 to 401)
AUTHORS        Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
               Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
               Melville, S.E., Rajadream, M.A. and Barrell, B.G.
TITLE          Direct Submission
JOURNAL        Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
               project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
               Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
               nh@sanger.ac.uk
COMMENT        Constructed at the Institute for Genomic Research (TIGR),
               Rockville, MD. Genomic DNA isolated from a cloned population of
               Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
               to give a tight size distribution (
               4 kb). The v + i method used for the library construction is
               described in detail in Smith, H. and Venter, J.C. (Making small
               insert libraries for whole genome shotgun sequencing projects. In
               Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
               Barrell, Oxford University Press, 1999).
               Email: nelsayed@tigr.org
               Details of T. brucei sequencing at the Sanger Centre are available
               at http://www.sanger.ac.uk/projects/T_brucei/.
               Location/Qualifiers
               1....401

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/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="8e07"

BASE COUNT    81 a 91 c 118 g 111 t
ORIGIN

Query Match   100.0%; Score 15; DB 17; Length 401;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
    |||||||
DB 67 CCTTCTCCCCCTGTT 81

RESULT 9
BI706542/c
LOCUS          BI706542
DEFINITION     fq07c03.y1 Zebrafish adult retina cDNA Danio rerio cDNA clone
               4790765.5, similar to TR:Q9UH03 Q9UH03 BK250D10.3; mRNA sequence.
ACCESSION      BI706542
VERSION        BI706542.1  GI:15682237
KEYWORDS       EST.
SOURCE         zebrafish.
ORGANISM       Danio rerio
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
               Cyprinidae; Danio.
REFERENCE      1 (bases 1 to 403)
AUTHORS        Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy,
               S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood,
               K., Steptoe, M., Theising, B., Allen, M., Bowers, T., Person, B.,
               Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E.,
               Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.,
               and Willson, R.
TITLE          WashU Zebrafish EST Project 1998
JOURNAL        Unpublished (1998)
COMMENT        Contact: Stephen L. Johnson
               Washington University School of Medicine
               4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
               Tel: 314 286 1800
               Fax: 314 286 1810
               Email: zbrafish@wustl.edu
               Library constructed by: Chandra Tucker and Gregory Niemi DNA
               Sequencing by: Washington University Genome Sequencing Center Clone
               distribution: RessourcenzentrumPrimatDatenbank, Berlin, Germany
               (web address: www.rzpd.de)
               Seq primer: T3 ET from Amersham
               High quality sequence stop: 396.
               Location/Qualifiers
               1..403
               /organism="Danio rerio"
               /strain="wild-type"
               /db_xref="taxon:7955"
               /clone="4790765"
               /clone_lib="Zebrafish adult retina cDNA"
               /sex="mixed"
               /dev_stage="1-2 years"
               /lab_host="E.Coli XL1-Blue MRF' (XL1-Blue MRF')"
               /note="vector: Lambda ZAP II (pBluescript SK-); Site_1:
               EcoRI; Site_2: SalI; This Zebrafish library was
               constructed by Dr. Susan E. Brockerhoff (email:
               sbrocker@u.washington.edu) RZPD library number: 760"

BASE COUNT    105 a 89 c 116 g 93 t
ORIGIN

Query Match   100.0%; Score 15; DB 13; Length 403;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
    |||||||

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Db 114 CCTTCTCCCCCTGTT 100
      TAG_SEQ=AATGC"
      110 a 124 c 91 g 85 t

RESULT 10
AW139708/c
LOCUS      410 bp mRNA linear EST 30-OCT-1999
DEFINITION UI-H-B11-aeb-a-03-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone
IMAGE:2718605 3', mRNA sequence.
ACCESSION  AW139708
VERSION     AW139708.1 GI:6144426
KEYWORDS    human.
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 410)
AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Oligo-dT track not found. Not 1 site shown in beginning of sequence
            is likely internal to the message. cDNA Library Preparation: M.B.
            Soares Lab Clone distribution: NCI-CGAP clone distribution
            information can be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html The following repetitive
            elements were found in this cDNA sequence: 151-216, >(GGGA
            )n$Simple_repeat
            Seq primer: M13 Forward
            POLYA-No.

FEATURES             Location/Qualifiers
     source           1..410
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2718605"
                     /clone_lib="NCI_CGAP_Sub3"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3-Pac (Pharmacia) with a modified
                     polylinker. Site.1: Not 1; Site.2: Eco RI; The
                     NCI_CGAP_Sub3 library is a subtracted library derived from
                     the NCI_CGAP_Sub1 library, which is a subtracted library
                     derived from B1. B1 constitutes a mixture of 21
                     normalized or subtracted NCI_CGAP libraries: NCI_CGAP_Co4
                     , NCI_CGAP_Pr22, NCI_CGAP_Pr28, NCI_CGAP_Co10,
                     NCI_CGAP_Co16, NCI_CGAP_Kid5, NCI_CGAP_Kid12,
                     NCI_CGAP_Kid3, NCI_CGAP_Kid11, NCI_CGAP_Lym2,
                     NCI_CGAP_Br2, NCI_CGAP_Co8, NCI_CGAP_C11L1, NCI_CGAP_Lei2,
                     NCI_CGAP_Brn23, NCI_CGAP_Lu5, NCI_CGAP_Bu24,
                     NCI_CGAP_Lu19, NCI_CGAP_GC4, NCI_CGAP_GC6,
                     NCI_CGAP_Brn25. These 21 libraries were pooled and a
                     single-stranded DNA preparation of the resulting mixture
                     was used as a tracer in a subtractive hybridization with
                     a driver whose composition is detailed below:
                     NCI_CGAP_Kid3 pool 1 LLAM 3334-3337, 3682-3683,
                     3798-3803 (IMAGE Clonoids 1322376-1323911, 1456008-1456775
                     , 1500552-1502855); NCI_CGAP_Kid5 pool 1 LLAM 3338-3342
                     , 3722-3725, 3776-3778 (IMAGE Clonoids 1323912-1325831,
                     1471368-1472903, 1492104-1493255); NCI_CGAP_Lu5 pool 1
                     LLAM 3375-3582, 3851-3854 (IMAGE Clonoids 1414920-1417991,
                     1520904-1522439); NCI_CGAP_GC4 pool 1 LLAM 3164-3167,
                     3716-3720, 3733-3735 (IMAGE Clonoids 1257096-1258631,
                     1469064-1470983, 1475592-1476743); NCI_CGAP_Pr22 pool 1
                     LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clonoids
                     985608-986759, 1101192-1101959, 1217928-1220615);
                     NCI_CGAP_Co10 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE
                     Clonoids 1057416-1061255, 1144584-1145351). Subtraction
                     was performed as previously described [Bonaldo, Lennon &
                     Soares (1996): Normalization and Subtraction: Two
                     Approaches To Facilitate Gene Discovery. Genome Research
                     6, 791-806.
                     TAG_LIB=NCI_CGAP_Kid3
                     TAG_TISSUE=Kidney

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BASE COUNT      110 a 124 c 91 g 85 t
ORIGIN
Query Match      100.0%; Score 15; DB 10; Length 410;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
      |||
Db 396 CCTTCTCCCCCTGTT 382
      |||

RESULT 11
AW504644/c
LOCUS      420 bp mRNA linear EST 02-MAR-2000
DEFINITION UI-HF-BN0-alk-h-12-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone
IMAGE:3079943 5', mRNA sequence.
ACCESSION  AW504644
VERSION     AW504644.1 GI:7142311
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 420)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: M.B. Soares Lab
            cDNA Library Arrayed by: M.B. Soares Lab
            DNA Sequencing by: M.B. Soares Lab
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.

FEATURES             Location/Qualifiers
     source           1..420
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3079943"
                     /clone_lib="NIH_MGC_50"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /note="Vector: pT7T3-Pac; Site.1: Not1; Site.2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (3.5-4.4Kb). Directionally cloned. Cells provided by
                     Louis M. Staudt, Ph.D. Library preparation by Maria de
                     Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT      124 a 72 c 126 g 98 t
ORIGIN
Query Match      100.0%; Score 15; DB 10; Length 420;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15
      |||
Db 159 CCTTCTCCCCCTGTT 145
      |||

RESULT 12
BF514910/c
LOCUS      421 bp mRNA linear EST 07-DEC-2000
DEFINITION UI-H-BM1-app-a-11-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone
IMAGE:3083036 3', mRNA sequence.
ACCESSION  BF514910

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BF514910.1 GI:11600078  
EST.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 421)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)  
The sequence contained an oligo-dT track that was present in the  
oligonucleotide that was used to prime the synthesis of first  
strand cDNA and therefore this may represent a bonafide poly A  
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:  
NCI-CGAP clone distribution information can be found through the  
I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
Seq primer: M13 Forward  
POLYA=Yes.

FEATURES  
Location/Qualifiers  
1..421  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3083036"  
/clone\_lib="NCI\_CGAP\_Sub7"  
/lab\_host="DHIOB (Life Technologies)"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; NCI\_CGAP\_Sub7  
is a substracted library derived from NCI\_CGAP\_Sub6. The  
NCI\_CGAP\_Sub7 library had 12 million recombinants. A  
single-stranded DNA preparation of NCI\_CGAP\_Sub6 was used  
as a tracer in a subtractive hybridization with a driver  
comprising: the IMAGE pool (NCI\_CGAP\_Kid3 pool 1 LLAM  
3334-3337, 3682-3683, 3798-3803 (IMAGE Clonoids  
132376-132391), 1456008-1456775, 1500552-1502855);  
NCI\_CGAP\_Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778  
(IMAGE Clonoids 1323912-1325831, 1471368-1472903,  
1492104-1493255); NCI\_CGAP\_Lu5 pool 1 LLAM 3575-3582,  
3851-3854 (IMAGE Clonoids 1414920-1417991, 1520904-1522439  
); NCI\_CGAP\_GC4 pool 1 LLAM 3164-3167, 3716-3720,  
3733-3735 (IMAGE Clonoids 1257096-1258631, 1469064-1470983  
), 1475592-1476743); NCI\_CGAP\_Pr22 pool 1 LLAM 2457-2459,  
2758-2759, 3062-3068 (IMAGE Clonoids 985608-986739,  
1101192-1101959, 1217928-1220615); NCI\_CGAP\_Co10 pool 1  
LLAM 2644-2653, 2871-2872 (IMAGE Clonoids 1057416-1061255  
, 1144584-1145351). (6% of the driver population), plus a  
pool of 3,840 arrayed clones from NCI\_CGAP\_Sub1 (IMAGE  
Clonoids 2708616-2710535) and NCI\_CGAP\_Sub2 (IMAGE  
Clonoids 2710536-2712455) (4% of the driver population  
), plus a pool of 11,436 clones from NCI\_CGAP\_Sub3 (IMAGE  
Clonoids 2712456-2723591) (10% of the driver population),  
plus a pool of 5,472 clones from NCI\_CGAP\_Sub4 (IMAGE  
Clonoids 2723592-2729326) (40% of the driver population),  
plus a pool of 4032 clones from NCI\_CGAP\_Sub6 (IMAGE  
Clonoids 2729869-2733190) (40% of the driver population).  
Subtraction was performed as previously described [Bonaldo  
, Lennon & Soares (1996): Normalization and Subtraction:  
Two Approaches To Facilitate Gene Discovery. Gene  
Research 6, 791-806].  
TAG\_LIB=NCI\_CGAP\_Brn50  
TAG\_TISSUE=brain  
TAG\_SEQ=TTTCG"

BASE COUNT 114 a 95 c 111 g 101 t  
ORIGIN  
Query Match 100.0%; Score 15; DB 12; Length 421;  
Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 CCTTCTCCCTGTT 15

BF514910.1 GI:11600078  
EST.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 421)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)  
The sequence contained an oligo-dT track that was present in the  
oligonucleotide that was used to prime the synthesis of first  
strand cDNA and therefore this may represent a bonafide poly A  
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:  
NCI-CGAP clone distribution information can be found through the  
I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
Seq primer: M13 Forward  
POLYA=Yes.

FEATURES  
Location/Qualifiers  
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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3083036"  
/clone\_lib="NCI\_CGAP\_Sub7"  
/lab\_host="DHIOB (Life Technologies)"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; NCI\_CGAP\_Sub7  
is a substracted library derived from NCI\_CGAP\_Sub6. The  
NCI\_CGAP\_Sub7 library had 12 million recombinants. A  
single-stranded DNA preparation of NCI\_CGAP\_Sub6 was used  
as a tracer in a subtractive hybridization with a driver  
comprising: the IMAGE pool (NCI\_CGAP\_Kid3 pool 1 LLAM  
3334-3337, 3682-3683, 3798-3803 (IMAGE Clonoids  
132376-132391), 1456008-1456775, 1500552-1502855);  
NCI\_CGAP\_Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778  
(IMAGE Clonoids 1323912-1325831, 1471368-1472903,  
1492104-1493255); NCI\_CGAP\_Lu5 pool 1 LLAM 3575-3582,  
3851-3854 (IMAGE Clonoids 1414920-1417991, 1520904-1522439  
); NCI\_CGAP\_GC4 pool 1 LLAM 3164-3167, 3716-3720,  
3733-3735 (IMAGE Clonoids 1257096-1258631, 1469064-1470983  
), 1475592-1476743); NCI\_CGAP\_Pr22 pool 1 LLAM 2457-2459,  
2758-2759, 3062-3068 (IMAGE Clonoids 985608-986739,  
1101192-1101959, 1217928-1220615); NCI\_CGAP\_Co10 pool 1  
LLAM 2644-2653, 2871-2872 (IMAGE Clonoids 1057416-1061255  
, 1144584-1145351). (6% of the driver population), plus a  
pool of 3,840 arrayed clones from NCI\_CGAP\_Sub1 (IMAGE  
Clonoids 2708616-2710535) and NCI\_CGAP\_Sub2 (IMAGE  
Clonoids 2710536-2712455) (4% of the driver population  
), plus a pool of 11,436 clones from NCI\_CGAP\_Sub3 (IMAGE  
Clonoids 2712456-2723591) (10% of the driver population),  
plus a pool of 5,472 clones from NCI\_CGAP\_Sub4 (IMAGE  
Clonoids 2723592-2729326) (40% of the driver population),  
plus a pool of 4032 clones from NCI\_CGAP\_Sub6 (IMAGE  
Clonoids 2729869-2733190) (40% of the driver population).  
Subtraction was performed as previously described [Bonaldo  
, Lennon & Soares (1996): Normalization and Subtraction:  
Two Approaches To Facilitate Gene Discovery. Gene  
Research 6, 791-806].  
TAG\_LIB=NCI\_CGAP\_Brn50  
TAG\_TISSUE=brain  
TAG\_SEQ=TTTCG"

BASE COUNT 114 a 95 c 111 g 101 t  
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Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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BF514910.1 GI:11600078  
EST.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 421)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)  
The sequence contained an oligo-dT track that was present in the  
oligonucleotide that was used to prime the synthesis of first  
strand cDNA and therefore this may represent a bonafide poly A  
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:  
NCI-CGAP clone distribution information can be found through the  
I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
Seq primer: M13 Forward  
POLYA=Yes.

FEATURES  
Location/Qualifiers  
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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3083036"  
/clone\_lib="NCI\_CGAP\_Sub7"  
/lab\_host="DHIOB (Life Technologies)"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; NCI\_CGAP\_Sub7  
is a substracted library derived from NCI\_CGAP\_Sub6. The  
NCI\_CGAP\_Sub7 library had 12 million recombinants. A  
single-stranded DNA preparation of NCI\_CGAP\_Sub6 was used  
as a tracer in a subtractive hybridization with a driver  
comprising: the IMAGE pool (NCI\_CGAP\_Kid3 pool 1 LLAM  
3334-3337, 3682-3683, 3798-3803 (IMAGE Clonoids  
132376-132391), 1456008-1456775, 1500552-1502855);  
NCI\_CGAP\_Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778  
(IMAGE Clonoids 1323912-1325831, 1471368-1472903,  
1492104-1493255); NCI\_CGAP\_Lu5 pool 1 LLAM 3575-3582,  
3851-3854 (IMAGE Clonoids 1414920-1417991, 1520904-1522439  
); NCI

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KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
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1. 430
/organism="Populus balsamifera subsp. trichocarpa"
/db_xref="taxon:3694"
/clone_lib="Populus flower cDNA library"
/note="organ: flower"
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Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCGCTGTT 15
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Db 220 CCTTCTCCCGCTGTT 234

RESULT 15
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LOCUS      BQ339760              431 bp      mRNA      linear      EST 20-MAY-2002
DEFINITION QV2-NN0045-211100-494-c07 NN0045 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BQ339760
VERSION    BQ339760.1  GI:20999826
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 431)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-NN0045-
211100-494-c07&t3=2000-11-21&t4=1)
Seq primer: puc 18 forward

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FEATURES
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/dev_stage="Adult"
/note="Organ: nervous normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      75 a 138 c 108 g 110 t
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Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCGCTGTT 15
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Db 399 CCTTCTCCCGCTGTT 413

Search completed: December 11, 2002, 19:01:29
Job time : 1715.5 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 12:26:07 ; Search time 1657 Seconds  
(without alignments)  
263.453 Million cell updates/sec

Title: US-09-750-609-10  
Perfect score: 15  
Sequence: 1 ccttctccccctgtt 15

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: gb\_ba: \*  
2: gb\_htg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_pro: \*  
11: gb\_sts: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vi: \*  
15: em\_ba: \*  
16: em\_fun: \*  
17: em\_hum: \*  
18: em\_in: \*  
19: em\_mu: \*  
20: em\_om: \*  
21: em\_or: \*  
22: em\_ov: \*  
23: em\_pat: \*  
24: em\_ph: \*  
25: em\_pl: \*  
26: em\_ro: \*  
27: em\_sts: \*  
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29: em\_vi: \*  
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31: em\_htg\_inv: \*  
32: em\_htg\_other: \*  
33: em\_htg\_mus: \*  
34: em\_htg\_pin: \*  
35: em\_htg\_rod: \*  
36: em\_htg\_mam: \*  
37: em\_htg\_vrt: \*  
38: em\_sy: \*  
39: em\_htgo\_hum: \*  
40: em\_htgo\_mus: \*  
41: em\_htgo\_other: \*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
C 1	15	100.0	190	9	HS288489	AJ288489 Homo sapi
C 2	15	100.0	600	5	AF506010	AF506010 Gallus ga
C 3	15	100.0	1689	9	AK021867	AK021867 Homo sapi
C 4	15	100.0	1721	4	AF232676	AF232676 Sus scro
C 5	15	100.0	3190	9	BC000776	BC000776 Homo sapi
C 6	15	100.0	3347	5	CHKTGFA	L01121 Gallus gall
C 7	15	100.0	3752	9	AF312211	AF312211 Homo sapi
C 8	15	100.0	4353	9	AB018279	AB018279 Homo sapi
C 9	15	100.0	11001	5	FR092H06	AL035357 Fugu rubr
C 10	15	100.0	11896	1	AE009810	AE009810 Pyrobacul
C 11	15	100.0	12602	14	AF144617	AF144617 Pestivirus
C 12	15	100.0	32802	1	BSSRFAP	X70356 B. subtilis
C 13	15	100.0	34578	9	AC107069	AC107069 Homo sapi
C 14	15	100.0	43347	9	AL138734	AL138734 Human DNA
C 15	15	100.0	56701	9	AL583852	AL583852 Human DNA
C 16	15	100.0	61720	2	AC131033	AC131033 Mus muscu
C 17	15	100.0	62755	2	AC097798	AC097798 Rattus no
C 18	15	100.0	64209	2	AC120156	AC120156 Mus muscu
C 19	15	100.0	65377	9	AL391356	AL391356 Human DNA
C 20	15	100.0	65421	2	AC129736	AC129736 Rattus no
C 21	15	100.0	66283	2	AC108314	AC108314 Rattus no
C 22	15	100.0	68171	9	AL158205	AL158205 Human DNA
C 23	15	100.0	71117	9	HSJ132F21	AL079335 Human DNA
C 24	15	100.0	88502	2	AC021967	AC021967 Homo sapi
C 25	15	100.0	99752	2	AC111526	AC111526 Rattus no
C 26	15	100.0	102853	2	AC116184	AC116184 Rattus no
C 27	15	100.0	106186	2	AC105876	AC105876 Rattus no
C 28	15	100.0	110000	2	AC103237_2	Continuation (3 of
C 29	15	100.0	110000	2	AC125066_2	Continuation (2 of
C 30	15	100.0	110000	2	AC125102_1	Continuation (2 of
C 31	15	100.0	113370	9	AL591493	AL591493 Human DNA
C 32	15	100.0	126392	2	AC018785	AC018785 Homo sapi
C 33	15	100.0	132526	2	AC120946	AC120946 Rattus no
C 34	15	100.0	141105	2	AC117134	AC117134 Rattus no
C 35	15	100.0	141289	9	AL449363	AL449363 Human DNA
C 36	15	100.0	142059	2	AC121163	AC121163 Rattus no
C 37	15	100.0	142662	2	AC118810	AC118810 Rattus no
C 38	15	100.0	142882	2	AC128133	AC128133 Rattus no
C 39	15	100.0	144201	9	HS230119	Z93942 Human DNA s
C 40	15	100.0	146191	1	D50453	D50453 Bacillus su
C 41	15	100.0	146427	2	AC124033	AC124033 Rattus no
C 42	15	100.0	148500	2	AC094249	AC094249 Rattus no
C 43	15	100.0	151514	2	AC113827	AC113827 Rattus no
C 44	15	100.0	154023	2	AC112466	AC112466 Rattus no
C 45	15	100.0	154888	2	AC114830	AC114830 Rattus no

ALIGNMENTS

RESULT 1  
HSA288489/c  
LOCUS HSA288489 Homo sapiens partial COL4A3 gene for alpha3 type IV collagen, exon  
DEFINITION 3.  
ACCESSION AJ288489  
VERSION AJ288489.1 GI:13559182  
KEYWORDS alpha3 type IV collagen; col4a3 gene.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 190)  
AUTHORS Heidet.L., Arrondel.C., Forestier.L., Cohen-Solal.L., Mollet.G.,  
Gutierrez.B., Stavrou.C., Gubler.M.C. and Antignac.C.

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES

Structure of the human type IV collagen gene COL4A3 and mutations in autosomal Alport syndrome  
J. Am. Soc. Nephrol. 12 (1), 97-106 (2001)  
21064696  
11134255  
2 (bases 1 to 190)  
Antignac C.  
Direct Submission  
Submitted (28-MAR-2000) Antignac C., U423, INSERM, Hopital Necker-Enfants malades 149 rue de Sevres, 75015 Paris, FRANCE  
Location/Qualifiers  
1..190  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
51..140  
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCTCCCTCGTGT 15  
|||||  
Db 60 CCTCTCCCTCGTGT 46

RESULT 2  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AF506010/c  
Gallus gallus TNF family B cell activation factor (BAFF) mRNA, partial cds.  
AF506010  
AF506010.1 GI:22087370  
chicken.  
Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
1 (bases 1 to 600)  
Schneider,K., Kolthow,S., Schneider,P., Goebel,T., Kaspers,B. and Staeheli,P.  
A chicken homolog of the B cell activating factor of the TNF family (BAFF)  
Unpublished  
2 (bases 1 to 600)  
Schneider,K., Kolthow,S., Schneider,P., Goebel,T., Kaspers,B. and Staeheli,P.  
Direct Submission  
Submitted (24-APR-2002) Virology, University of Freiburg, Hermann-Herder-Str.11, Freiburg 79104, Germany  
Location/Qualifiers  
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BASE COUNT  
ORIGIN

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QY 1 CCTTCTCCCTCGTGT 15  
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Db 75 CCTTCTCCCTCGTGT 61

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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AK021867  
Homo sapiens cDNA FLJ11805 fis, clone HEMBA1006278, moderately similar to POLY(A) POLYMERASE (EC 2.7.7.19).  
AK021867  
AK021867.1 GI:10433146  
oligo capping; fis (full insert sequence).  
Homo sapiens embryo, 10 weeks whole embryo, mainly head cDNA to mRNA, clone\_lib:HEMBAL clone:HEMBAL1006278.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1  
Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahara,K., Masuno,Y. and Oshima,A.  
NEDO human cDNA sequencing project  
Unpublished  
2 (bases 1 to 1689)  
Isogai,T. and Otsuki,T.  
Direct Submission  
Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)  
NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection; Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.  
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BASE COUNT  
ORIGIN



Query Match 100.0%; Score 15; DB 9; Length 1689;  
 Best Local Similarity 100.0%; Pred. No. 1.le+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15  
 Db 123 CCTTCTCCCCCTGTT 109

RESULT 4  
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 DEFINITION Sus scrofa prophet of pit-1 (Prop-1) mRNA, complete cds.  
 ACCESSION AF232676  
 VERSION AF232676.1 GI:11275672  
 KEYWORDS Sus scrofa.  
 SOURCE Sus scrofa  
 ORGANISM Sus scrofa

REFERENCE 1 (bases 1 to 1721)  
 AUTHORS Sloop,K.W., McCutchan Schiller,A., Smith,T.P., Blanton,J.R. Jr.,  
 Rohrer,G.A., Meier,B.C. and Rhodes,S.J.  
 TITLE Biochemical and genetic characterization of the porcine Prophet of  
 pit-1 pituitary transcription factor  
 JOURNAL Mol. Cell. Endocrinol. 168 (1-2), 77-87 (2000)  
 MEDLINE 20519384  
 PUBMED 11064154

REFERENCE 2 (bases 1 to 1721)  
 AUTHORS McCutchan Schiller,A.L., Sloop,K.W., Blanton,J.R. Jr., Meier,B.C.  
 and Rhodes,S.J.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-FEB-2000) Biology, Indiana University Purdue  
 University Indianapolis, 723 West Michigan Street, Indianapolis, IN  
 46202-5132, USA

FEATURES  
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 PPMWCFPPHYNHLPSPSTGSGSFARHQSESDWYPTLHTPTGHLPCPPAPPVLPUS  
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BASE COUNT 457 a 460 c 469 g 333 t 2 others  
 ORIGIN

Query Match 100.0%; Score 15; DB 4; Length 1721;  
 Best Local Similarity 100.0%; Pred. No. 1.le+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15  
 Db 236 CCTTCTCCCCCTGTT 222

RESULT 5  
 BC000776

LOCUS BC000776 3190 bp mRNA linear PRI 12-JUL-2001  
 DEFINITION Homo sapiens, Similar to KIAA0736 gene product, clone  
 IMAGE:3509807, mRNA, partial cds.  
 ACCESSION BC000776  
 VERSION BC000776.1 GI:12653962  
 KEYWORDS

SOURCE Homo sapiens.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 3190)  
 AUTHORS Strausberg,R.  
 JOURNAL Direct Submission  
 Submitted (15-NOV-2000) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
 REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov  
 COMMENT Contact: MGC help desk  
 Email: cgapbs-re@mail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Rubin Laboratory  
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
 http://www.systemsbio.org  
 Contact: amadan@systemsbiology.org  
 Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia  
 Greene, Mark Kettman and Anuradha Madan

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
 Series: IRAL Plate: 7 Row: 1 Column: 18  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: Hexamer frequency ORF  
 analysis.

FEATURES  
 source  
 Location/Qualifiers  
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BASE COUNT 662 a 850 c 868 g 810 t  
 ORIGIN

Query Match 100.0%; Score 15; DB 9; Length 3190;  
 Best Local Similarity 100.0%; Pred. No. 1.le+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15  
 Db 2096 CCTTCTCCCCCTGTT 2110

RESULT 6  
 CHKTGFBA/c

LOCUS CHKTGFBA 3347 bp mRNA linear VRT 21-JUL-1994  
 DEFINITION Gallus gallus transforming growth factor-beta type III receptor  
 mRNA, complete cds.  
 ACCESSION L01121  
 VERSION L01121.1 GI:511842

KEYWORDS TGF-beta; betaglycan; plasma membrane; transforming growth factor-beta receptor; transforming growth factor-beta type III

SOURCE Gallus gallus (library: lambda zap) embryonic brain cDNA to mRNA.

ORGANISM Gallus gallus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

AUTHORS Barnett,J.V., Moustakas,A., Lin,W., Wang,X.F., Lin,H.Y., Galper,J.B. and Maas,R.L.

TITLE Cloning and developmental expression of the chick type II and type III TGF beta receptors

JOURNAL Dev. Dyn. 199 (1), 12-27 (1994)

MEDLINE 94220749

PUBMED 8167376

FEATURES source Location/Qualifiers 1..3347 /organism="Gallus gallus" /db\_xref="taxon:9031" /tissue\_type="brain" /dev\_stage="embryonic" /germline /tissue\_lib="lambda zap" 152..2677 /codon\_start=1 /product="transforming growth factor-beta type III receptor" /protein\_id="AAA49090.1" /db\_xref="GI:511843" /translation="MSSSCVTPVFMILCFADAGVPVRECVLSPVNSHPVHALLE SFTVLGGASRTTGLPOEVHVLNRNDEGLDHHREVTLLTPISSVHIHQKPLVF LNSPLPLWKLTERLAPIRRVFVSGSIWFEKNGFSLSAETEKNFPERNEHL LWAQKEYGAVTSFTELKISRNIYIKVGEDQVPTCNTEKFLSLNLAGVLPKRA ECLMSNIVOEREVHIELITPNSNPYSAFQVDIIVDKPSQPGAKLERNVLLKCK KSNVWIKSHDQGVLEVTNSIGFGETERSMTWSKVIPIFSSHSLIKWAYEH KYPSVTSYKAPVANRFLQLEHTEEMDEEDHSLPELTELHGAKNPALSGLTFF PHNGHGTGEGIFPSPRSVDTLINHDHFEHLSKHKEPEVOGSADVALSIKDDK VINTAVEKDSQASQYTRTELSDHSCARMNGTHFIEISLPNKGTYRSTVILDKIV YFNSIVLIQSSPAEGSFDDDDMESGNGFCGDADGVDVTFNSWPEIAFNCVLPQPEK DFNPMFEPWPEPHITNTVFNMEYKTDLEFLAPSGOLFSENGPIYEVSVTKADIS LGFAIQTCFVSPSPNDRMSDYTIENICPKDESVKFYSTEKLNFPPIAHQAQDKRFS FVEKPIFNISLLFLHCLTLCNTDKDQRLPKCPVPDEACTSLNVDMLAMHNRKT FTKPLVITHEGKPEPSSLPKSNVRQPSVFGDITLVVGIAPFAAEVIGALLTGALWFI YSHGGEAGRKQVPTRSPASENSSAAHSIGSTQSTPCSSSAT"

BASE COUNT 996 a 712 c 708 g 931 t

ORIGIN

Query Match 100.0%; Score 15; DB 5; Length 3347; Best Local Similarity 100.0%; Pred. No. 1.1e+03; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCGCTGTT 15

Db 1368 CCTTCTCCCGCTGTT 1354

RESULT 7

AF312211/c

LOCUS AF312211 3752 bp mRNA linear PRI 04-AUG-2001

DEFINITION Homo sapiens neo-poly(A) polymerase mRNA, complete cds.

ACCESSION AF312211

VERSION AF312211.1 GI:15080910

KEYWORDS

SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Topalian,S.L., Kaneko,S., Gonzales,M.I., Bond,G.L., Ward,Y. and Manley,J.L.

TITLE Identification and functional characterization of neo-poly(A) polymerase, an RNA processing enzyme overexpressed in human tumors

JOURNAL Mol. Cell. Biol. 21 (16), 5614-5623 (2001)

MEDLINE 21356984

PUBMED 11463842

REFERENCE 2 (bases 1 to 3752)

AUTHORS Topalian,S.L., Gonzales,M.I., Wang,X. and Wang,R.-F.

TITLE Direct Submission

JOURNAL Submitted (09-OCT-2000) Surgery Branch, NCI, National Institutes of Health, Building 10, Room 2B47, Bethesda, MD 20892, USA

FEATURES source Location/Qualifiers 1..3752 /organism="Homo sapiens" /db\_xref="taxon:9606" /cell\_type="malignant melanoma" 232..2442 /note="similar to Homo sapiens poly(A) polymerase protein (PAP) encoded by GenBank Accession Number X76770" /codon\_start=1 /product="neo-poly(A) polymerase" /protein\_id="AAK83701.1" /db\_xref="GI:15080911" /translation="MKEMSANTVLDQRQOKHYGITSPIASLSPKEIDHIYVTKLIDA MKPFGVFDEEELNHLRVLVGLKLNVLKWEISDVSESKNLPSPVAVGKIFTFGSY RLGHTKGAIDALCVAPRIVERSDFQFSEKLKHODGRNLRAVDAFVPVTKFEF DGIEDLVFARLAIQITSDNLDLDDSLRSLDIRCIRSLNGCVTDDELHLVPNKET FRLLRAVKLWAKERGIIYNWGLGVSWMALVARTCQLYPNAASATLVHKKFLVFS KWEPNPVLLKQEEENLNPVMDPRVNSDRYHLMDIITPAPQOONSTYVSTSTRT VVVEEFKGLAVTDEILQGGSKSLEPPNFQKYRHYIVLTASASTEENHLEWVGL VESKIRLVGNLNERFEITLAHVNPQSPFGNKEHKDNNYVSMWFLGIIFRRVENAES VINDTLYIQSFDTVYRQANNIMLKEGMEIATHVKKOLHLYLPAEILOKKKKOS LSDVNRSSGSGLOSKRLSDSSCLDSRDTNGTTPNSPASKSDSPSGVETERNASERA AVIVEKPLVPPAAGLSIPVIGAKVDSTVYKTPVPTVCTIPTVVGVRNVIPRTYHPN AGOQHLNGSNITKVTYKRSHPSDIGTPKRLKQVEKFIRESLTFKDPRTAEKRK KSDVALGGESMPTIDTTSRKLPSKLPDPDSSSPVANNIRVIKNSIRLTNR"

BASE COUNT 1175 a 709 c 738 g 1130 t

ORIGIN

Query Match 100.0%; Score 15; DB 9; Length 3752; Best Local Similarity 100.0%; Pred. No. 1.1e+03; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCGCTGTT 15

Db 169 CCTTCTCCCGCTGTT 155

RESULT 8

AB018279

LOCUS AB018279 4353 bp mRNA linear PRI 16-JUN-1999

DEFINITION Homo sapiens mRNA for KIAA0736 protein, complete cds.

ACCESSION AB018279

VERSION AB018279.1 GI:3882192

KEYWORDS

SOURCE Homo sapiens adult male brain cDNA to mRNA, clone\_lib:pBluescriptII SK plus clone:hk03846.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Nagase,T., Ishikawa,K., Suyama,M., Kikuno,R., Miyaajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.

TITLE Prediction of the coding sequences of unidentified human genes. XI. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro

JOURNAL DNA Res. 5 (5), 277-286 (1998)

MEDLINE 99087487

REFERENCE 2 (bases 1 to 4353)

AUTHORS Ohara,O., Suyama,M., Nagase,T., Ishikawa,K. and Kikuno,R.

TITLE Direct Submission

JOURNAL Submitted (08-OCT-1998) Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913, Fax:+81-438-52-3914)

FEATURES source Location/Qualifiers



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BASE COUNT 3155 a 2199 c 2486 g 3161 t  
ORIGIN  
Query Match 100.0%; Score 15; DB 5; Length 11001;  
Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCTTCTCCCTGTT 15  
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Db 6409 CCTTCTCCCTGTT 6395  
RESULT 10  
AE009810/c  
LOCUS  
DEFINITION Pyrobaculum aerophilum strain IM2 section 65 of 201 of the complete genome. linear BCT 16-JAN-2002  
ACCESSION AE009810 AE009441  
VERSION AE009810.1 GI:18159943  
KEYWORDS Pyrobaculum aerophilum.  
SOURCE Pyrobaculum aerophilum  
ORGANISM Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;  
REFERENCE 1 (bases 1 to 11896)  
AUTHORS Fitz-Gibbon,S.T., Ladner,H., Kim,U.J., Stetter,K.O., Simon,M.I. and Miller,J.H.  
TITLE Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (2), 984-989 (2002)  
PUBMED 11792869  
REFERENCE 2 (bases 1 to 11896)  
AUTHORS Fitz-Gibbon,S.T., Ladner,H., Kim,U.-J., Stetter,K.O., Simon,M.I. and Miller,J.H.  
TITLE Direct Submission  
JOURNAL Submitted (12-DEC-2001) Microbiology and Molecular Genetics, University of California, Los Angeles, 405 Hilgard Ave, Los Angeles, CA 90095-1489; USA  
FEATURES  
source  
1..11896  
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gene	5401. .6453 /gene="PAE1226" /note="DNA metabolism; DNA replication, recombination, and repair" /codon_start=1 /transl_table=11 /product="DNA endonuclease, conjectural" /protein_id="AAL63338.1" /db_xref="GI:18159950"
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CDS	/translation="MIHLVDYALLKPKLYLVDEAVAGARAEELGVAAVCVNIYAPVV RPLLRKVKLCVVADFPALPTASRIALYSRLAEVADEIDVAPIGLVSRRAEYVRR DLISVVGAGRGVVKVITEPYLRDEERTYLDVIAEAGAHFKTSSTGFAEAYAAARQ GNPVHSTPERAAAIARYIKEKGYRLGVKNAGGIRTREQAKAIVDAIGWGEDPARVRLG TSTPEALL" 7987. .8274 /gene="PAE1232" 7987. .8274 /gene="PAE1232" /note="Fatty acid and phospholipid metabolism; Other" /codon_start=1 /transl_table=11 /product="acylphosphatase, putative" /protein_id="AAL63341.1" /db_xref="GI:18159953"
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Query Match 100.0%; Score 15; DB 1; Length 11896;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+02; Indels 0; Gaps 0;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGTT 15  
 Db 6661 CCTTCTCCCCCTGTT 6647

RESULT 11  
 AF144617  
 LOCUS 12602 bp RNA linear VRL 23-AUG-2001  
 DEFINITION Pestivirus giraffe-1 H138 complete genome.  
 ACCESSION AF144617  
 VERSION AF144617.2 GI:15282441  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 pestivirus giraffe-1 H138.  
 Pestivirus giraffe-1 H138  
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 pestivirus;  
 1 (bases 1 to 12602)  
 Becher,P., Orlich,M., Kosmidou,A., Konig,M., Baroth,M. and  
 Thiel,H.J.  
 Genetic diversity of pestiviruses: identification of novel groups  
 and implications for classification  
 Virology 262 (1), 64-71 (1999)  
 99420379  
 10489341  
 2 (bases 1 to 12602)  
 Avalos-Ramirez,R., Orlich,M., Thiel,H.J. and Becher,P.  
 Evidence for the presence of two novel pestivirus species  
 Virology 286 (2), 456-465 (2001)  
 21378881  
 11485413  
 3 (bases 1 to 12602)  
 Avalos-Ramirez,R., Orlich,M., Thiel,H.J. and Becher,P.  
 Complete genomic sequences of pestiviruses from giraffe and  
 reinder: evidence for the presence of two novel species within the  
 genus pestivirus  
 Unpublished  
 4 (bases 1 to 12602)  
 Becher,P. and Orlich,M.  
 Direct Submission  
 Submitted (21-APR-1999) Justus-Liebig-Universitaet Giessen,  
 Institut fuer Virologie (Fachbereich Veterinaermedizin),  
 Frankfurt Str. 107, Giessen D-35392, Germany  
 5 (bases 1 to 12602)  
 Avalos-Ramirez,R., Orlich,M. and Becher,P.  
 Direct Submission  
 Submitted (26-MAR-2001) Justus-Liebig-Universitaet Giessen,  
 Institut fuer Virologie (Fachbereich Veterinaermedizin),  
 Frankfurt Str. 107, Giessen D-35392, Germany  
 Sequence update by submitter  
 On Aug 23, 2001 this sequence version replaced gi:6049239.  
 Location/Qualifiers  
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 /isolate="giraffe-1 H138"  
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 383. 12352  
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 CPLWLTSCDEGAKKQVAPDRVEGRMQIKPKSEKSDRTKPPDATIVLDGVKYQV  
 KKKGVKYSADGLYHNKPKPSKKLEKALLAWAILAVLPQFVAGENITQNLSD  
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CDS  
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 BASE COUNT 4053 a 2545 c 3288 g 2716 t  
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 Best Local Similarity 100.0%; Pred. No. 9.7e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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MEETIAQIWEVLGRKQIGHDDFFALGCHSLKAMTAVPHQOELGIDILPVLKLFAPT  
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Query Match 100.0%; Score 15; DB 1; Length 32802;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CCTTCTCCCCCTGTT 15  
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Db 29177 CCTTCTCCCCCTGTT 29163

RESULT 13  
AC107069/c

LOCUS AC107069 34578 bp DNA linear PRI 29-MAY-2002  
DEFINITION Homo sapiens BAC clone RP11-249A8 from 2, complete sequence.  
ACCESSION AC107069  
VERSION AC107069.5 GI:20146820  
KEYWORDS HTG.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 34578)  
Sulston,J.E. and Waterston,R.  
Toward a complete human genome sequence  
Genome Res. 8 (11), 1097-1108 (1998)  
PUBMED 99063792  
9847074  
REFERENCE 2 (bases 1 to 34578)  
Scott,K., Kozlowicz,A., Spalding,L. and Trani,L.  
The sequence of Homo sapiens BAC clone RP11-249A8  
Unpublished (2001)  
REFERENCE 3 (bases 1 to 34578)  
Waterston,R.H.  
Direct Submission  
Submitted (15-JAN-2002) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
REFERENCE 4 (bases 1 to 34578)  
Waterston,R.H.  
Direct Submission  
Submitted (04-APR-2002) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
REFERENCE 5 (bases 1 to 34578)  
Waterston,R.H.  
Direct Submission  
Submitted (13-APR-2002) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
REFERENCE 6 (bases 1 to 34578)  
Waterston,R.H.  
Direct Submission  
Submitted (29-MAY-2002) Department of Genetics, Washington  
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
On Apr 13, 2002 this sequence version replaced gi:19924179.  
----- Genome Center  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: http://genome.wustl.edu/gsc  
Contact: sapiens@wustl.edu  
----- Summary Statistics  
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Center project name: H\_NH0249A08  
-----

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:  
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:  
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:  
The RPCI-11 human BAC library was made from the blood of one male



donor, as described by Osogawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanesi, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>  
VECTOR: pBACe3.6

# NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-495023, 2000 bp overlap;  
the clone sequenced to the right is RP11-56365, 2000 bp overlap.  
Actual start of this clone is at base position 126621 of  
RP11-495023.

## FEATURES

source

Location/Qualifiers

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/clone\_lib="RPC1-11"

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565..616

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3664..4328

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4372..4459

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6872..6897

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6917..7221

/rpt\_family="MER2\_type"

7240..7267

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8517..9128

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9623..9918

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10230..10311

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10910..11214

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11616..11700

/rpt\_family="L2"

11711..11996

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11997..12065

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12723..12743

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12930..12965

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repeat\_region 14255..14316  
/rpt\_family="(CA)n"  
repeat\_region 14609..14696  
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repeat\_region 15519..15572  
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repeat\_region 15951..15997  
/rpt\_family="ERV1"  
repeat\_region 16430..16390  
/rpt\_family="MaLR"  
repeat\_region 18201..18343  
/rpt\_family="CR1"  
repeat\_region 18517..18822  
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repeat\_region 19992..20085  
/rpt\_family="MER1\_type"  
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/rpt\_family="MER1\_type"  
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Query Match 100.0%; Score 15; DB 9; Length 34578;  
Best Local Similarity 100.0%; Pred. No. 8.9e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTCTCCCCCTGTT 15  
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Db 1831 CCTCTCCCCCTGTT 1817

RESULT 14  
AL138734/c

LOCUS AL138734

DEFINITION Human DNA sequence from clone RP1-310P17 on chromosome 6. Contains  
GSSs, complete sequence.

ACCESSION AL138734

VERSION AL138734.6 GI:8388469

KEYWORDS HTG.

SOURCE human.

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 43347)  
 Tromans,A.  
 Direct Submission  
 Submitted (21-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
 requests: clonerequest@sanger.ac.uk  
 On Jun 8, 2000 this sequence version replaced gi:8247412.  
 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.  
 This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.  
 The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at [http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr6>  
 RPI-310P17 is from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see <http://bacpac.med.buffalo.edu/VECTOR:pcYPAC2>  
 IMPORTANT: This sequence is not the entire insert of clone RPI-310P17 it may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.  
 The true left end of clone RPI-310P17 is at 1 in this sequence. The true left end of clone RPI-413H6 is at 43244 in this sequence.

FEATURES  
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 complement(428..891)  
 /note="match: GSS: Em:B53078"  
 complement(580..878)  
 /note="match: GSS: Em:AQ269829"  
 1740..1867  
 /note="MIR repeat: matches 20..146 of consensus"  
 1924..2090  
 /note="L1MB8 repeat: matches 6005..6171 of consensus"  
 2151..2266  
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 2281..2431  
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 2432..2878  
 /note="L1MB8 repeat: matches 5429..5879 of consensus"  
 2879..3641  
 /note="LTR17 repeat: matches 1..780 of consensus"  
 3516..4013  
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 3642..3924  
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 4063..4518  
 /note="match: GSS: Em:AQ508138"  
 complement(4129..4662)  
 /note="match: GSS: Em:AQ316392"

misc\_feature  
 4657..5169  
 /note="match: GSS: Em:AQ484379"  
 4665..5178  
 /note="match: GSS: Em:AQ432756"  
 5449..5596  
 /note="L2 repeat: matches 2580..2750 of consensus"  
 6304..6577  
 /note="AluX repeat: matches 9..282 of consensus"  
 6589..6721  
 /note="AluSq/x repeat: matches 1..133 of consensus"  
 6732..7036  
 /note="AluSp repeat: matches 1..305 of consensus"  
 7164..7253  
 /note="MIR repeat: matches 47..147 of consensus"  
 7584..7643  
 /note="30 copies 2 mer gt 96% conserved"  
 7969..8079  
 /note="MIR repeat: matches 28..143 of consensus"  
 8265..8544  
 /note="AluJo repeat: matches 2..289 of consensus"  
 8711..8799  
 /note="MIR repeat: matches 59..145 of consensus"  
 9753..9893  
 /note="AluY repeat: matches 168..311 of consensus"  
 10697..11158  
 /note="L2 repeat: matches 2290..2750 of consensus"  
 11255..11286  
 /note="16 copies 2 mer ac 100% conserved"  
 11352..11558  
 /note="HERVL repeat: matches 1757..1969 of consensus"  
 12998..13299  
 /note="AluX repeat: matches 1..311 of consensus"  
 14005..14200  
 /note="MIR repeat: matches 1..208 of consensus"  
 14674..14748  
 /note="L1ME3 repeat: matches 5872..5956 of consensus"  
 15052..15480  
 /note="L1M4 repeat: matches 3375..3822 of consensus"  
 15481..15498  
 /note="AluS repeat: matches 152..170 of consensus"  
 15499..15731  
 /note="AluSq/x repeat: matches 71..308 of consensus"  
 15732..15790  
 /note="AluS repeat: matches 1..152 of consensus"  
 15822..16105  
 /note="L1PA16 repeat: matches 5830..6110 of consensus"  
 16106..16416  
 /note="AluSp repeat: matches 1..313 of consensus"  
 16417..17711  
 /note="L1PA16 repeat: matches 4517..5830 of consensus"  
 17737..18032  
 /note="MER61A repeat: matches 7..314 of consensus"  
 18038..18426  
 /note="L1PA16 repeat: matches 4125..4510 of consensus"  
 18427..18706  
 /note="L1M4 repeat: matches 3826..4124 of consensus"  
 18703..19271  
 /note="L1MD2 repeat: matches 5774..6331 of consensus"  
 19272..19892  
 /note="L2 repeat: matches 1452..2147 of consensus"  
 19893..19948  
 /note="MADE1 repeat: matches 5..80 of consensus"  
 19949..20211  
 /note="L2 repeat: matches 1194..1452 of consensus"  
 20944..21113  
 /note="AluSq/x repeat: matches 129..299 of consensus"  
 21140..21264  
 /note="AluSc repeat: matches 1..125 of consensus"  
 21581..21650  
 /note="35 copies 2 mer tt 68% conserved"  
 21747..21896  
 /note="L1MD3 repeat: matches 7476..7579 of consensus"  
 complement(21823..22281)

repeat\_region  
 4657..5169  
 /note="L2 repeat: matches 2580..2750 of consensus"  
 6304..6577  
 /note="AluX repeat: matches 9..282 of consensus"  
 6589..6721  
 /note="AluSq/x repeat: matches 1..133 of consensus"  
 6732..7036  
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 15732..15790  
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 19893..19948  
 /note="MADE1 repeat: matches 5..80 of consensus"  
 19949..20211  
 /note="L2 repeat: matches 1194..1452 of consensus"  
 20944..21113  
 /note="AluSq/x repeat: matches 129..299 of consensus"  
 21140..21264  
 /note="AluSc repeat: matches 1..125 of consensus"  
 21581..21650  
 /note="35 copies 2 mer tt 68% conserved"  
 21747..21896  
 /note="L1MD3 repeat: matches 7476..7579 of consensus"  
 complement(21823..22281)

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/misc_feature /note="match: GSS: Em:AQ714858"
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22608..22697
/repeat_region /note="L2 repeat: matches 2620..2710 of consensus"
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/repeat_region /note="20 copies 2 mer aa 80% conserved"
22998..23085
/repeat_region /note="L2 repeat: matches 413..509 of consensus"
23148..23417
/repeat_region /note="L2 repeat: matches 38..312 of consensus"
23454..23569
/repeat_region /note="L2 repeat: matches 2005..2146 of consensus"
23645..23819
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/repeat_region /note="L1MC3 repeat: matches 7250..7739 of consensus"
29898..30315
/repeat_region /note="MLT1B repeat: matches 6..390 of consensus"
30318..31382
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31290..31766
/misc_feature /note="match: GSS: Em:AQ735362"
31390..31669
/repeat_region /note="L2 repeat: matches 102..387 of consensus"
32151..32455
/repeat_region /note="AluB repeat: matches 1..304 of consensus"
33318..33468
/repeat_region /note="Charlie2 repeat: matches 327..504 of consensus"
34076..34305
/repeat_region /note="MIR repeat: matches 6..260 of consensus"
34434..34535
/repeat_region /note="L2 repeat: matches 2574..2687 of consensus"
34633..35136
/repeat_region /note="MER9 repeat: matches 1..511 of consensus"
36692..37186
/repeat_region /note="Cheshire repeat: matches 27..548 of consensus"
37183..38826
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Query Match 100.0%; Score 15; DB 9; Length 43347;
Best Local Similarity 100.0%; Pred. No. 8.e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCCTCCCTGTT 15
|||||
Db 27556 CCTTCCTCCCTGTT 27542

RESULT 15
AL583852
LOCUS Human DNA sequence from clone RP11-17G2 on chromosome 10, complete
DEFINITION sequence.
ACCESSION AL583852 AC011691
VERSION AL583852.6 GI:14702147
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 56701)
AUTHORS Chapman,J.
TITLE Direct Submission
JOURNAL Submitted (03-DEC-2001) Wellcome Trust Sanger Institute, Hinxton,

```

## COMMENT

Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk  
 On or before Jul 12, 2001 this sequence version replaced gi:7381811, gi:13396759.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at <http://www.sanger.ac.uk/Projects/Celegans/wormpep>

This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr10>

RP11-17G2 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBACE3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-17G2. It may be shorter because we sequence overlapping sections only once, except for a short overlap.

The true right end of clone RP11-17G2 is at 56701 in this sequence. The true right end of clone RP11-397115 is at 2000 in this sequence.

## FEATURES

## source

## Location/Qualifiers

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/db_xref="taxon:9606"
/chromosome="10"
/clone="RP11-17G2"
/clone_lib="RPCI-11.1"
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/repeat_region /note="MER20 repeat: matches 103..218 of consensus"
1266..1301
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1305..1352
/note="24 copies 2 mer ga 75% conserved"
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/misc_feature /note="match: GSS: Em:AQ358591"
2479..2823
/misc_feature /note="match: GSS: Em:AQ812738"
2586..2791
/repeat_region /note="MIR repeat: matches 45..258 of consensus"
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/note="MIR repeat: matches 61..212 of consensus"
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/misc_feature /note="match: GSS: Em:AQ475942"
4218..4317
/repeat_region /note="L2 repeat: matches 2645..2749 of consensus"
5477..5644
/note="MLT1I repeat: matches 68..240 of consensus"
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match: GSS: Em:AQ083388"
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/repeat_region /note="MER91A repeat: matches 5..95 of consensus"
6293..6521
/repeat_region /note="MIR repeat: matches 9..234 of consensus"
8688..8929

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8947. .9112
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misc_feature /note="MLT1A1 repeat: matches 337. .568 of consensus"
9753. .10220
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10458. .10642
repeat_region /note="L2 repeat: matches 2129. .2318 of consensus"
13448. .13763
repeat_region /note="MLT1A1 repeat: matches 1. .341 of consensus"
13847. .13898
repeat_region /note="2 copies 26 mer 94% conserved"
15428. .15572
repeat_region /note="MER5A repeat: matches 18. .178 of consensus"
16288. .16546
repeat_region /note="L2 repeat: matches 2242. .2521 of consensus"
16664. .16777
repeat_region /note="L2 repeat: matches 2596. .2708 of consensus"
16779. .16842
repeat_region /note="16 copies 4 mer gga 81% conserved"
16817. .16998
repeat_region /note="7 copies 26 mer 62% conserved"
16861. .16944
repeat_region /note="21 copies 4 mer gga 75% conserved"
16951. .16994
repeat_region /note="11 copies 4 mer gga 81% conserved"
17973. .18165
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18174. .18509
repeat_region /note="MER46C repeat: matches 7. .338 of consensus"
18670. .18785
repeat_region /note="MER5A repeat: matches 45. .163 of consensus"
18833. .19044
repeat_region /note="MIR repeat: matches 28. .260 of consensus"
21936. .22145
repeat_region /note="LIME repeat: matches 5599. .5820 of consensus"
22148. .22199
repeat_region /note="13 copies 4 mer caca 82% conserved"
22199. .22596
repeat_region /note="MSTA repeat: matches 1. .426 of consensus"
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22597. .22638
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22599. .22638
repeat_region /note="10 copies 4 mer caca 92% conserved"
22770. .22846
repeat_region /note="MIR repeat: matches 87. .165 of consensus"
22959. .23149
repeat_region /note="MER3 repeat: matches 1. .200 of consensus"
23508. .23698
repeat_region /note="L2 repeat: matches 2539. .2748 of consensus"
24378. .24458
repeat_region /note="L1 repeat: matches 2136. .2213 of consensus"
24486. .24581
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25073. .25451
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complement(25325. .25729)
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26471. .26619
repeat_region /note="MLTIF repeat: matches 105. .257 of consensus"
26933. .27097
repeat_region /note="MER5A repeat: matches 1. .188 of consensus"
27101. .27219
repeat_region /note="MIR repeat: matches 13. .134 of consensus"
27767. .27813
repeat_region /note="MIR repeat: matches 49. .103 of consensus"
28697. .28879
repeat_region /note="MIR repeat: matches 31. .225 of consensus"
29356. .29488
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```

```
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31974. .32354
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repeat_region /note="match: GSS: Em:AQ604754"
33407. .33823
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33833. .34015
repeat_region /note="MIR repeat: matches 50. .251 of consensus"
34122. .34214
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37028. .37195
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37274. .37413
repeat_region /note="L2 repeat: matches 2137. .2276 of consensus"
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38541. .39465
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39625. .39782
repeat_region /note="MIR repeat: matches 59. .220 of consensus"
41102. .41277
repeat_region /note="L2 repeat: matches 2517. .2691 of consensus"
41278. .41718
repeat_region /note="MLT1C repeat: matches 5. .462 of consensus"
41719. .41924
repeat_region /note="L2 repeat: matches 2308. .2517 of consensus"
42387. .42468
repeat_region /note="MIR repeat: matches 162. .246 of consensus"
42496. .42577
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43328. .43400
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43505. .43769
repeat_region /note="L2 repeat: matches 2161. .2419 of consensus"

Query Match 100.0%; Score 15; DB 9; Length 56701;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTCTGT 15
|||||
Db 2530 CCTTCTCCCTCTGT 2544
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Search completed: December 11, 2002, 14:35:48  
Job time : 1686 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 12:23:57 ; Search time 212.5 Seconds  
(without alignments)  
158.965 Million cell updates/sec

Title: US-09-750-609-10  
Perfect score: 15  
Sequence: 1 cttctcccccgtgtt 15

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues  
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_101002.\*  
1: /SIDS2/gcgdata/geneseq/geneseq-nbml/NA1980.DAT.\*  
2: /SIDS2/gcgdata/geneseq/geneseq-nbml/NA1981.DAT.\*  
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24: /SIDS2/gcgdata/geneseq/geneseq-nbml/NA2002.DAT.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	ID	Description
1	15	100.0	15	22	AAH28085	Probe for human no
2	15	100.0	352	21	AAC09241	Human secreted pro
3	15	100.0	445	23	ABV50337	Human prostate exp
4	15	100.0	549	23	AAS66052	DNA encoding novel
5	15	100.0	827	22	AAH04051	Human cDNA clone (
6	15	100.0	1689	22	AAH15437	Human cDNA sequenc
7	15	100.0	1854	22	AAH28083	DNA encoding human
8	15	100.0	1854	22	AAH28087	DNA encoding human
9	15	100.0	2159	23	ABK43728	DNA encoding novel

c	10	15	100.0	2451	23	AAS83288	DNA encoding novel
c	11	15	100.0	2520	23	ABL90474	Human polynucleoti
c	12	15	100.0	2522	24	ABK44004	DNA encoding novel
c	13	15	100.0	3580	21	AAH16697	Human secreted pro
c	14	15	100.0	3580	24	ABK35630	CDNA sequence #21
c	15	15	100.0	4215	23	ABV22746	Human prostate exp
c	16	15	100.0	4215	23	ABV28574	Human prostate exp
c	17	15	100.0	4366	22	AAH57556	Human brain cell s
c	18	15	100.0	15857	22	AAS26730	Human genomic DNA
c	19	15	100.0	31122	14	AAO40706	Bacillus subtilis
c	20	14	93.3	389	24	ABN96737	Gene #3235 used to
c	21	14	93.3	389	24	ABL66267	Lung cancer relate
c	22	14	93.3	482	24	ABT04065	Human ovary specif
c	23	14	93.3	594	22	ABA62115	Human foetal liver
c	24	14	93.3	594	22	AAK10435	Human brain expres
c	25	14	93.3	594	22	AAK36337	Human bone marrow
c	26	14	93.3	594	22	AAI42060	Probe #10746 used
c	27	14	93.3	599	23	AAS85439	DNA encoding novel
c	28	14	93.3	2349	21	AAAT6376	Human secreted pro
c	29	14	93.3	2415	18	AAT62067	Fission yeast prot
c	30	14	93.3	2775	22	AAH13954	Human cDNA sequenc
c	31	14	93.3	6959	23	AAS85443	DNA encoding novel
c	32	14	93.3	8894	22	AAL36698	Human musculoskele
c	33	14	93.3	8894	22	AAS26718	Human genomic DNA
c	34	14	93.3	16877	22	ABA20494	Human nervous syst
c	35	14	93.3	16877	22	AAL36984	Human musculoskele
c	36	14	93.3	61710	22	AAK83782	Human immune/haema
c	37	13.4	89.3	15	22	AAH28084	Probe for human no
c	38	13.4	89.3	108	19	AAH10384	Human biallelic po
c	39	13.4	89.3	134	21	AAC04726	Human secreted pro
c	40	13.4	89.3	198	24	ABK76772	Bacillus lichenifo
c	41	13.4	89.3	303	20	ABK76818	EST clone BG388.
c	42	13.4	89.3	315	22	AAH52042	Mycobacterium tube
c	43	13.4	89.3	332	22	AAD08846	Human G-protein co
c	44	13.4	89.3	337	21	AAC11522	Human secreted pro
c	45	13.4	89.3	342	22	AAS38882	Novel human diagno

ALIGNMENTS

RESULT 1  
AAH28085  
ID AAH28085 standard; DNA; 15 BP.  
XX AAH28085;  
AC AAH28085;  
XX  
DT 05-SEP-2001 (first entry)  
DE Probe for human norepinephrine transporter gene A457P variant allele.  
DE  
DE Norepinephrine transporter; orthostatic intolerance; gene therapy;  
KW mental illness; hypertension; heart disease; stimulant abuse; cocaine;  
KW amphetamine abuse; probe; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO200148246-A1.  
PN  
XX  
PD 05-JUL-2001.  
XX  
PF 28-DEC-2000; 2000WO-US35491.  
XX  
PR 29-DEC-1999; 99US-0173682.  
PR 11-JAN-2000; 2000US-0175456.  
XX (UYVA-) UNIV VANDERBILT.  
PI Robertson D, Blakely RD;  
XX  
XX WPI; 2001-425681/45.  
XX  
XX Screening for susceptibility to sub-optimal norepinephrine transport.

PT particularly orthostatic intolerance in a subject by detecting a  
 XX polymorphism of norepinephrine transporter gene -  
 PS Claim 15; Page 69; 133pp; English.  
 XX  
 CC The present sequence represents a probe for the A457P variant allele of  
 CC a human norepinephrine transporter gene. The specification a method  
 CC for screening for susceptibility to sub-optimal norepinephrine transport  
 CC in a subject. The method comprises obtaining a biological sample from  
 CC the subject and detecting a polymorphism of a norepinephrine transporter  
 CC gene in the sample from the subject, the presence of the polymorphism  
 CC indicating the susceptibility of the subject to sub-optimal  
 CC norepinephrine transport. The method is useful for screening for  
 CC susceptibility of a subject to orthostatic intolerance. Norepinephrine  
 CC transporter genes are useful for gene therapy for modulating  
 CC norepinephrine transport in a target cell and treating susceptibility  
 CC to impaired norepinephrine transporter function, orthostatic intolerance  
 CC or other relevant diseases in humans and animals such as mental illness,  
 CC hypertension, heart disease, psycho stimulant abuse e.g. cocaine or  
 CC amphetamine abuse.  
 XX  
 SQ Sequence 15 BP; 0 A; 8 C; 1 G; 6 T; 0 other;

Query Match 100.0%; Score 15; DB 22; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CCTTCTCCCGCTGTT 15  
 Db 1 CCTTCTCCCGCTGTT 15

RESULT 2  
 AAC09241/c  
 ID AAC09241 standard; cDNA; 352 BP.  
 AC AAC09241;  
 XX  
 XX 06-OCT-2000 (first entry)  
 XX  
 XX Human secreted protein 5' EST, SEQ ID NO: 13316.  
 XX  
 XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
 KW gene therapy; chromosome mapping; ss.  
 KW  
 OS Homo sapiens.  
 OS  
 PN EP1033401-A2.  
 XX  
 XX 06-SEP-2000.  
 PD  
 XX  
 XX 21-FEB-2000; 2000EP-0200610.  
 PF  
 XX  
 XX 26-FEB-1999; 99US-0122487.  
 PR  
 XX (GEST ) GENSET.  
 PA  
 XX Dumas Milne Edwards J, Duclert A, Giordano J;  
 PI  
 XX WPI; 2000-500381/45.  
 DR  
 XX  
 XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for  
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -  
 PT  
 XX  
 PS Claim 1; SEQ ID 13316; 71pp + CD-ROM; English.

CC The present sequence is one of a large number of 5' ESTs derived from  
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively  
 CC identified within the present sequence. The 5' ESTs were prepared from  
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST  
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)  
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA

CC libraries. Such ESTs are not well suited for isolating cDNA sequences  
 CC derived from the 5' ends of mRNAs and even in those cases where longer  
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included.  
 CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be  
 CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used  
 CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.  
 CC They are used to obtain upstream regulatory sequences and to design  
 CC expression and secretion vectors.

XX  
 SQ Sequence 352 BP; 111 A; 73 C; 97 G; 69 T; 2 other;

Query Match 100.0%; Score 15; DB 21; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCGCTGTT 15  
 Db 149 CCTTCTCCCGCTGTT 135

RESULT 3  
 ABV50337  
 ID ABV50337 standard; cDNA; 445 BP.  
 XX  
 AC ABV50337;  
 XX  
 XX 17-SEP-2002 (first entry)  
 DT  
 XX  
 XX Human prostate expression marker cDNA 50328.  
 DE  
 XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
 KW pharmacogenomic marker; gene; ss.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO200160860-A2.  
 PN  
 XX 23-AUG-2001.  
 PD  
 XX  
 XX 20-FEB-2001; 2001WO-US05171.  
 PF  
 XX  
 XX 17-FEB-2000; 2000US-183319P.  
 PR 16-MAR-2000; 2000US-189862P.  
 PR 25-MAY-2000; 2000US-207454P.  
 PR 09-JUN-2000; 2000US-211314P.  
 PR 18-JUL-2000; 2000US-219007P.  
 PR 13-DEC-2000; 2000US-255281P.  
 PR  
 XX

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Schlegel R, Endege WO, Monahan JE;

WPI; 2001-662795/76.

XX Novel isolated nucleic acid molecule associated with cancerous state of  
 PT prostate cells and correlating with presence of prostate cancer, useful  
 PT for detecting presence of prostate cancer, stage of prostate cancer -  
 PT  
 XX  
 PS Claim 1; Page 9798; 11750pp; English.

CC The invention relates to an isolated nucleic acid molecule (I) comprising  
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
 CC specification or its complement. (I) is useful for:  
 CC (a) assessing whether a patient is afflicted with prostate cancer;  
 CC (b) monitoring the progression of prostate cancer in a patient;  
 CC (c) assessing the efficacy of a test compound to inhibit prostate  
 CC cancer in a patient;  
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer  
 CC in a patient;  
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
 CC (f) assessing the prostate cell carcinogenic potential of a compound;  
 CC (g) determining whether prostate cancer has metastasized in a patient;  
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a

CC patient;  
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.  
XX  
SQ Sequence 445 BP; 109 A; 118 C; 109 G; 107 T; 2 other;  
  
Query Match 100.0%; Score 15; DB 23; Length 445;  
Best Local Similarity 100.0%; Pred. NO. 4.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CCTTCTCCCTGTT 15  
|||||  
Db 370 CCTTCTCCCTGTT 384  
  
RESULT 4  
AAS66052  
ID AAS66052 standard; cDNA; 549 BP.  
XX  
AC AAS66052;  
XX  
DT 13-FEB-2002 (first entry)  
XX  
DE DNA encoding novel human diagnostic protein #1856.  
XX  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US08631.  
XX  
PR 31-MAR-2000; 2000US-0540217.  
XX  
PR 23-AUG-2000; 2000US-0649167.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Drmanac RT, Liu C, Tang YT;  
XX  
DR P-PSDB; ABG01865.  
XX  
PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity -  
XX  
PS Claim 1; SEQ ID NO 1856; 103pp; English.  
XX  
CC The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC and responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AAS64197-AAS94564 represent novel human  
CC diagnostic coding sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX  
SQ Sequence 549 BP; 114 A; 178 C; 140 G; 117 T; 0 other;  
  
Query Match 100.0%; Score 15; DB 23; Length 549;  
Best Local Similarity 100.0%; Pred. NO. 4.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CCTTCTCCCTGTT 15  
|||||  
Db 423 CCTTCTCCCTGTT 437  
  
RESULT 5  
AAH04051/c  
ID AAH04051 standard; cDNA; 827 BP.  
XX  
AC AAH04051;  
XX  
DT 26-JUN-2001 (first entry)  
XX  
DE Human cDNA clone (5'-primer) SEQ ID NO:886.  
XX  
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP1074617-A2.  
XX  
PD 07-FEB-2001.  
XX  
PF 28-JUL-2000; 2000EP-0116126.  
XX  
PR 29-JUL-1999; 99JP-0248036.  
XX  
PR 27-AUG-1999; 99JP-0300253.  
XX  
PR 11-JAN-2000; 2000JP-0118776.  
XX  
PR 02-MAY-2000; 2000JP-0183767.  
XX  
PR 09-JUN-2000; 2000JP-0241899.  
XX  
PA (HELI-) HELIX RES INST.  
XX  
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
XX  
DR WPI; 2001-318749/34.  
XX  
PT Primer sets for synthesizing polynucleotides, particularly the 5602  
PT full-length cDNAs defined in the specification, and for the detection  
PT and/or diagnosis of the abnormality of the proteins encoded by the  
PT full-length cDNAs -  
XX  
PS Claim 1; SEQ ID 886; 2537pp + CD ROM; English.  
XX  
CC The present invention describes primer sets for synthesizing 5602  
CC full-length cDNAs defined in the specification. Where a primer set  
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary  
CC to the complementary strand of a polynucleotide which comprises one of  
CC the 5602 nucleotide sequences defined in the specification, where the  
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
CC of an oligonucleotide comprising a sequence complementary to the  
CC complementary strand of a polynucleotide which comprises a 5'-end  
CC sequence and an oligonucleotide comprising a sequence complementary to a  
CC polynucleotide which comprises a 3'-end sequence, where the  
CC oligonucleotide comprises at least 15 nucleotides and the combination of  
CC the 5'-end sequence/3'-end sequence is selected from those defined in  
CC the specification. The primer sets can be used in antisense therapy and  
CC in gene therapy. The primers are useful for synthesizing polynucleotides,  
CC particularly full-length cDNAs. The primers are also useful for the  
CC detection and/or diagnosis of the abnormality of the proteins encoded by  
CC the full-length cDNAs. The primers allow obtaining of the full-length  
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to  
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632  
CC represent oligonucleotides, all of which are used in the exemplification

```
CC of the present invention.
XX Sequence 827 BP; 264 A; 138 C; 199 G; 223 T; 3 other;
SQ

Query Match      100.0%; Score 15; DB 22; Length 827;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCTTCTCCCGCTGT 15
    |||||
Db 123 CCTTCTCCCGCTGT 109

RESULT 6
AAH15437/c
ID AAH15437 standard; cDNA; 1689 BP.
XX
AC AAH15437;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA sequence SEQ ID NO:13660.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
XX
PR 27-AUG-1999; 99JP-0300253.
XX
PR 11-JAN-2000; 2000JP-0118776.
XX
PR 02-MAY-2000; 2000JP-0183767.
XX
PR 09-JUN-2000; 2000JP-0241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
PS Claim 8; SEQ ID 13660; 2537pp + CD ROM; English.
XX
CC The present invention describes primer sets for synthesising 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC

CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.
XX
SQ Sequence 1689 BP; 555 A; 309 C; 366 G; 459 T; 0 other;
Query Match      100.0%; Score 15; DB 22; Length 1689;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCTTCTCCCGCTGT 15
    |||||
Db 123 CCTTCTCCCGCTGT 109

RESULT 7
AAH28083
ID AAH28083 standard; cDNA; 1854 BP.
XX
AC AAH28083;
XX
DT 05-SEP-2001 (first entry)
XX
DE DNA encoding human norepinephrine transporter variant A457P.
XX
KW Norepinephrine transporter; orthostatic intolerance; gene therapy;
KW mental illness; hypertension; heart disease; stimulant abuse; cocaine;
KW amphetamine abuse; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1854
FT /tag= a
FT /product= "norepinephrine transporter"
XX
PN WO200148246-A1.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US35491.
XX
PR 29-DEC-1999; 99US-0173682.
XX
PR 11-JAN-2000; 2000US-0175456.
XX
PA (UYVA-) UNIV VANDERBILT.
XX
PI Robertson D, Blakely RD;
XX
DR WPI; 2001-425681/45.
DR P-PSDB; AAB84533.
XX
PT Screening for susceptibility to sub-optimal norepinephrine transport,
PT particularly orthostatic intolerance in a subject by detecting a
PT polymorphism of norepinephrine transporter gene -
XX
PS Claim 43; Page 104-108; 133pp; English.
XX
CC The present sequence encodes a variant norepinephrine transporter. The
CC specification a method for screening for susceptibility to sub-optimal
CC norepinephrine (NE) transport in a subject. The method comprises
CC obtaining a biological sample from the subject and detecting a
CC polymorphism of a norepinephrine transporter gene in the sample from
CC the subject, the presence of the polymorphism indicating the
CC susceptibility of the subject to sub-optimal norepinephrine transport.
CC The method is useful for screening for susceptibility of a subject to
CC orthostatic intolerance. Norepinephrine transporter genes are useful
CC for gene therapy for modulating norepinephrine transport in a target
CC cell and treating susceptibility to impaired norepinephrine transporter
CC function, orthostatic intolerance or other relevant diseases in humans
CC and animals such as mental illness, hypertension, heart disease, psycho
CC stimulant abuse e.g. cocaine or amphetamine abuse.
XX
SQ Sequence 1854 BP; 356 A; 555 C; 493 G; 450 T; 0 other;
```



Query Match 100.0%; Score 15; DB 22; Length 1854;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15  
|||||  
Db 1362 CCTTCTCCCCCTGTT 1376

RESULT 8  
AAH28087  
ID AAH28087 standard; cDNA; 1854 BP.

XX  
AC AAH28087;

XX  
DT 05-SEP-2001 (first entry)

XX  
DE DNA encoding human norepinephrine transporter variant.

XX  
KW Norepinephrine transporter; orthostatic intolerance; gene therapy;  
KW mental illness; hypertension; heart disease; stimulant abuse; cocaine;  
KW amphetamine abuse; ss.

XX  
OS Homo sapiens.

XX  
FH Key Location/Qualifiers

FT CDS 1..1854

FT /tag= a

FT /product= "norepinephrine transporter"

XX  
PN WO200148246-A1.

XX  
PD 05-JUL-2001.

XX  
PF 28-DEC-2000; 2000WO-US35491.

XX  
PR 29-DEC-1999; 99US-0173682.

PR 11-JAN-2000; 2000US-0175456.

XX  
PA (UYVA-) UNIV VANDERBILT.

XX  
PI Robertson D, Blakely RD;

DR WPI: 2001-425681/45.

DR P-PSDB; AAB84535.

XX  
PT Screening for susceptibility to sub-optimal norepinephrine transport,  
PT particularly orthostatic intolerance in a subject by detecting a  
PT polymorphism of norepinephrine transporter gene

PS Claim 43; Page 119-121; 133pp; English.

XX  
CC The present sequence encodes a variant norepinephrine transporter. The  
CC specification a method for screening for susceptibility to sub-optimal  
CC norepinephrine (NE) transport in a subject. The method comprises  
CC obtaining a biological sample from the subject and detecting a  
CC polymorphism of a norepinephrine transporter gene in the sample from  
CC the subject, the presence of the polymorphism indicating the  
CC susceptibility of the subject to sub-optimal norepinephrine transport.  
CC The method is useful for screening for susceptibility of a subject to  
CC orthostatic intolerance. Norepinephrine transporter genes are useful  
CC for gene therapy for modulating norepinephrine transport in a target  
CC cell and treating susceptibility to impaired norepinephrine transporter  
CC function, orthostatic intolerance or other relevant diseases in humans  
CC and animals such as mental illness, hypertension, heart disease, psycho  
CC stimulant abuse e.g. cocaine or amphetamine abuse.

SQ Sequence 1854 BP; 357 A; 554 C; 493 G; 450 T; 0 other;

Query Match 100.0%; Score 15; DB 22; Length 1854;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15  
|||||  
Db 1362 CCTTCTCCCCCTGTT 1376

RESULT 9

ABK43728

ID ABK43728 standard; cDNA; 2159 BP.

XX  
AC ABK43728;

XX  
DT 05-JUN-2002 (first entry)

XX  
DE DNA encoding novel central nervous system protein #308.

XX  
KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;  
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;  
KW cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;  
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;  
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;  
KW adenocarcinoma; reproductive system disorder; testicular feminisation;  
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;  
KW respiratory disorder; renal disorder; kidney failure; blood disorder;  
KW myocardial infarction; wound healing; cell proliferation; skin aging;  
KW food additive; food preservative; gene therapy; gene; ss.

XX  
OS Homo sapiens.

XX  
PN WO200155318-A2.

XX  
PD 02-AUG-2001.

XX  
PF 17-JAN-2001; 2001WO-US01332.

XX  
PR 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209467.

PR 28-JUN-2000; 2000US-0214886.

PR 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.

PR 07-JUL-2000; 2000US-0216880.

PR 11-JUL-2000; 2000US-0217487.

PR 11-JUL-2000; 2000US-0217496.

PR 14-JUL-2000; 2000US-0218290.

PR 26-JUL-2000; 2000US-0220963.

PR 26-JUL-2000; 2000US-0220964.

PR 14-AUG-2000; 2000US-0224518.

PR 14-AUG-2000; 2000US-0224519.

PR 14-AUG-2000; 2000US-0225213.

PR 14-AUG-2000; 2000US-0225214.

PR 14-AUG-2000; 2000US-0225266.

PR 14-AUG-2000; 2000US-0225267.

PR 14-AUG-2000; 2000US-0225268.

PR 14-AUG-2000; 2000US-0225270.

PR 14-AUG-2000; 2000US-0225447.

PR 14-AUG-2000; 2000US-0225757.

PR 14-AUG-2000; 2000US-0225758.

PR 14-AUG-2000; 2000US-0225759.

PR 18-AUG-2000; 2000US-0226279.

PR 22-AUG-2000; 2000US-0226681.

PR 22-AUG-2000; 2000US-0226868.

PR 22-AUG-2000; 2000US-0227182.

PR 23-AUG-2000; 2000US-0227009.

PR 30-AUG-2000; 2000US-0228924.

PR 01-SEP-2000; 2000US-0229287.

PR 01-SEP-2000; 2000US-0229343.

PR 01-SEP-2000; 2000US-0229344.  
 PR 01-SEP-2000; 2000US-0229345.  
 PR 05-SEP-2000; 2000US-0229509.  
 PR 05-SEP-2000; 2000US-0229513.  
 PR 06-SEP-2000; 2000US-0230437.  
 PR 06-SEP-2000; 2000US-0230438.  
 PR 08-SEP-2000; 2000US-0231242.  
 PR 08-SEP-2000; 2000US-0231243.  
 PR 08-SEP-2000; 2000US-0231244.  
 PR 08-SEP-2000; 2000US-0231413.  
 PR 08-SEP-2000; 2000US-0231414.  
 PR 08-SEP-2000; 2000US-0232080.  
 PR 08-SEP-2000; 2000US-0232081.  
 PR 12-SEP-2000; 2000US-0231968.  
 PR 14-SEP-2000; 2000US-0232397.  
 PR 14-SEP-2000; 2000US-0232398.  
 PR 14-SEP-2000; 2000US-0232399.  
 PR 14-SEP-2000; 2000US-0232400.  
 PR 14-SEP-2000; 2000US-0232401.  
 PR 14-SEP-2000; 2000US-0233063.  
 PR 14-SEP-2000; 2000US-0233064.  
 PR 14-SEP-2000; 2000US-0233065.  
 PR 21-SEP-2000; 2000US-0234223.  
 PR 21-SEP-2000; 2000US-0234274.  
 PR 25-SEP-2000; 2000US-0234997.  
 PR 25-SEP-2000; 2000US-0234998.  
 PR 26-SEP-2000; 2000US-0234984.  
 PR 27-SEP-2000; 2000US-0235834.  
 PR 27-SEP-2000; 2000US-0235836.  
 PR 29-SEP-2000; 2000US-0236327.  
 PR 29-SEP-2000; 2000US-0236367.  
 PR 29-SEP-2000; 2000US-0236368.  
 PR 29-SEP-2000; 2000US-0236369.  
 PR 29-SEP-2000; 2000US-0236370.  
 PR 02-OCT-2000; 2000US-0236802.  
 PR 02-OCT-2000; 2000US-0237037.  
 PR 02-OCT-2000; 2000US-0237038.  
 PR 02-OCT-2000; 2000US-0237039.  
 PR 02-OCT-2000; 2000US-0237040.  
 PR 13-OCT-2000; 2000US-0239935.  
 PR 13-OCT-2000; 2000US-0239937.  
 PR 20-OCT-2000; 2000US-0240960.  
 PR 20-OCT-2000; 2000US-0241221.  
 PR 20-OCT-2000; 2000US-0241785.  
 PR 20-OCT-2000; 2000US-0241786.  
 PR 20-OCT-2000; 2000US-0241787.  
 PR 20-OCT-2000; 2000US-0241808.  
 PR 20-OCT-2000; 2000US-0241809.  
 PR 20-OCT-2000; 2000US-0241826.  
 PR 01-NOV-2000; 2000US-0244617.  
 PR 08-NOV-2000; 2000US-0246474.  
 PR 08-NOV-2000; 2000US-0246475.  
 PR 08-NOV-2000; 2000US-0246476.  
 PR 08-NOV-2000; 2000US-0246477.  
 PR 08-NOV-2000; 2000US-0246478.  
 PR 08-NOV-2000; 2000US-0246523.  
 PR 08-NOV-2000; 2000US-0246524.  
 PR 08-NOV-2000; 2000US-0246525.  
 PR 08-NOV-2000; 2000US-0246526.  
 PR 08-NOV-2000; 2000US-0246527.  
 PR 08-NOV-2000; 2000US-0246528.  
 PR 08-NOV-2000; 2000US-0246532.  
 PR 08-NOV-2000; 2000US-0246609.  
 PR 08-NOV-2000; 2000US-0246610.  
 PR 08-NOV-2000; 2000US-0246611.  
 PR 08-NOV-2000; 2000US-0246613.  
 PR 17-NOV-2000; 2000US-0249207.  
 PR 17-NOV-2000; 2000US-0249208.  
 PR 17-NOV-2000; 2000US-0249209.  
 PR 17-NOV-2000; 2000US-0249210.  
 PR 17-NOV-2000; 2000US-0249211.  
 PR 17-NOV-2000; 2000US-0249212.  
 PR 17-NOV-2000; 2000US-0249213.

PR 17-NOV-2000; 2000US-0249214.  
 PR 17-NOV-2000; 2000US-0249215.  
 PR 17-NOV-2000; 2000US-0249216.  
 PR 17-NOV-2000; 2000US-0249217.  
 PR 17-NOV-2000; 2000US-0249218.  
 PR 17-NOV-2000; 2000US-0249244.  
 PR 17-NOV-2000; 2000US-0249245.  
 PR 17-NOV-2000; 2000US-0249264.  
 PR 17-NOV-2000; 2000US-0249265.  
 PR 17-NOV-2000; 2000US-0249297.  
 PR 17-NOV-2000; 2000US-0249299.  
 PR 17-NOV-2000; 2000US-0249300.  
 PR 01-DEC-2000; 2000US-0250160.  
 PR 01-DEC-2000; 2000US-0250391.  
 PR 05-DEC-2000; 2000US-0251030.  
 PR 05-DEC-2000; 2000US-0251988.  
 PR 05-DEC-2000; 2000US-0256719.  
 PR 06-DEC-2000; 2000US-0251479.  
 PR 08-DEC-2000; 2000US-0251856.  
 PR 08-DEC-2000; 2000US-0251868.  
 PR 08-DEC-2000; 2000US-0251869.  
 PR 08-DEC-2000; 2000US-0251989.  
 PR 08-DEC-2000; 2000US-0251990.  
 PR 11-DEC-2000; 2000US-0254097.  
 PR 05-JAN-2001; 2001US-0259678.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Rosen CA, Barash SC, Ruben SM;  
 WPI; 2001-581633/65.  
 P-PSDB; AAU87398.

New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -

Claim 1; SEQ ID No 318; 837pp; English.

The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease and amyotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. corneal infection, gastrointestinal disorders e.g. dysphagia, adenocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g. leukaemia, disorders involving neovascularisation e.g. malignancies, respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. acute kidney failure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,

Query Match 100.0%; Score 15; DB 23; Length 2159;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCTCTCCCTCTTT 15

Db 1070 CCTCTCTCCCTCTTT 1084

RESULT 10

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AAS83288/c
ID AAS83288 standard; cDNA; 2451 BP.
XX
AC AAS83288;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #19092.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
XX
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR P-PSDB; ABG19101.
XX
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity
XX
PS Claim 1; SEQ ID NO 19092; 103pp; English.
XX
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (I) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2451 BP; 670 A; 631 C; 671 G; 479 T; 0 other;
XX
XX
Query Match 100.0%; Score 15; DB 23; Length 2451;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 CCTTCTCCCCCTGTT 15
Db 164 CCTTCTCCCCCTGTT 150
XX
RESULT 11
ABL90474
ID ABL90474 standard; cDNA; 2520 BP.
XX
XX
AAS83288/c
ID AAS83288 standard; cDNA; 2451 BP.
XX
AC AAS83288;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #19092.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
XX
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR P-PSDB; ABG19101.
XX
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity
XX
PS Claim 1; SEQ ID NO 19092; 103pp; English.
XX
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (I) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2451 BP; 670 A; 631 C; 671 G; 479 T; 0 other;
XX
XX
Query Match 100.0%; Score 15; DB 23; Length 2451;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 CCTTCTCCCCCTGTT 15
Db 164 CCTTCTCCCCCTGTT 150
XX
RESULT 11
ABL90474
ID ABL90474 standard; cDNA; 2520 BP.
XX
XX
ABL90474;
XX
DT 24-MAY-2002 (first entry)
XX
DE Human polynucleotide SEQ ID NO 1036.
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
KW vulnarant; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiac; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200190304-A2.
XX
PD 29-NOV-2001.
XX
PF 18-MAY-2001; 2001WO-US16450.
XX
PR 19-MAY-2000; 2000US-205515P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Birse CE, Rosen CA;
XX
DR WPI: 2002-122018/16.
DR P-PSDB; ABB90065.
XX
XX
PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
PT prevention of neural, immune system, muscular, reproductive,
PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
PT disorders
XX
PS Claim 4; SEQ ID NO 1036; 2081pp + Sequence Listing; English.
XX
XX
CC The invention relates to novel genes (ABL89449-ABL90853) and proteins
CC (ABB89040-ABB90444) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2520 BP; 583 A; 687 C; 623 G; 626 T; 1 other;
XX
XX
Query Match 100.0%; Score 15; DB 24; Length 2520;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 CCTTCTCCCCCTGTT 15
Db 1062 CCTTCTCCCCCTGTT 1076
XX
RESULT 12
ABK44004/c
ID ABK44004 standard; cDNA; 2522 BP.
XX
AC ABK44004;
XX
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DT 05-JUN-2002 (first entry)  
XX DNA encoding novel central nervous system protein #584.  
DE  
XX  
KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;  
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;  
KW cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis;  
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;  
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;  
KW adenocarcinoma; reproductive system disorder; testicular feminisation;  
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;  
KW respiratory disorder; renal disorder; kidney failure; blood disorder;  
KW myocardial infarction; wound healing; cell proliferation; skin aging;  
KW food additive; food preservative; gene therapy; gene; ss.  
XX  
OS Homo sapiens.  
XX WO200155318-A2.  
PN  
XX  
XX  
PD 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US01332.  
XX  
XX 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
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PR 14-AUG-2000; 2000US-0225213.  
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PR 14-AUG-2000; 2000US-0225266.  
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PR 22-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228924.  
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PR 05-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
PR 08-SEP-2000; 2000US-0231242.  
PR 08-SEP-2000; 2000US-0231243.  
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PR 08-SEP-2000; 2000US-0232080.  
PR 08-SEP-2000; 2000US-0232081.  
PR 12-SEP-2000; 2000US-0231968.  
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PR 21-SEP-2000; 2000US-0234223.  
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PR 27-SEP-2000; 2000US-0235834.  
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PR 29-SEP-2000; 2000US-0236327.  
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PR 29-SEP-2000; 2000US-0236368.  
PR 29-SEP-2000; 2000US-0236369.  
PR 29-SEP-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037.  
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PR 02-OCT-2000; 2000US-0237039.  
PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239935.  
PR 13-OCT-2000; 2000US-0239937.  
PR 20-OCT-2000; 2000US-0240960.  
PR 20-OCT-2000; 2000US-0241221.  
PR 20-OCT-2000; 2000US-0241785.  
PR 20-OCT-2000; 2000US-0241786.  
PR 20-OCT-2000; 2000US-0241787.  
PR 20-OCT-2000; 2000US-0241808.  
PR 20-OCT-2000; 2000US-0241809.  
PR 20-OCT-2000; 2000US-0241826.  
PR 01-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0246474.  
PR 08-NOV-2000; 2000US-0246475.  
PR 08-NOV-2000; 2000US-0246476.  
PR 08-NOV-2000; 2000US-0246477.  
PR 08-NOV-2000; 2000US-0246478.  
PR 08-NOV-2000; 2000US-0246523.  
PR 08-NOV-2000; 2000US-0246524.  
PR 08-NOV-2000; 2000US-0246525.  
PR 08-NOV-2000; 2000US-0246526.  
PR 08-NOV-2000; 2000US-0246527.  
PR 08-NOV-2000; 2000US-0246528.  
PR 08-NOV-2000; 2000US-0246532.  
PR 08-NOV-2000; 2000US-0246609.  
PR 08-NOV-2000; 2000US-0246610.  
PR 08-NOV-2000; 2000US-0246611.  
PR 08-NOV-2000; 2000US-0246613.  
PR 17-NOV-2000; 2000US-0249207.  
PR 17-NOV-2000; 2000US-0249208.  
PR 17-NOV-2000; 2000US-0249209.  
PR 17-NOV-2000; 2000US-0249210.  
PR 17-NOV-2000; 2000US-0249211.  
PR 17-NOV-2000; 2000US-0249212.  
PR 17-NOV-2000; 2000US-0249213.  
PR 17-NOV-2000; 2000US-0249214.  
PR 17-NOV-2000; 2000US-0249215.  
PR 17-NOV-2000; 2000US-0249216.  
PR 17-NOV-2000; 2000US-0249217.  
PR 17-NOV-2000; 2000US-0249218.  
PR 17-NOV-2000; 2000US-0249219.  
PR 17-NOV-2000; 2000US-0249244.  
PR 17-NOV-2000; 2000US-0249245.  
PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249266.  
PR 17-NOV-2000; 2000US-0249297.  
PR 17-NOV-2000; 2000US-0249299.  
PR 17-NOV-2000; 2000US-0249300.

PR 01-DEC-2000; 2000US-0250160.  
PR 01-DEC-2000; 2000US-0250391.  
PR 05-DEC-2000; 2000US-0251030.  
PR 05-DEC-2000; 2000US-0251988.  
PR 05-DEC-2000; 2000US-0256719.  
PR 06-DEC-2000; 2000US-0251479.  
PR 08-DEC-2000; 2000US-0251856.  
PR 08-DEC-2000; 2000US-0251868.  
PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251989.  
PR 08-DEC-2000; 2000US-0251990.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Barash SC, Ruben SM;  
XX  
DR WPI; 2001-581633/65.  
DR P-PSDB; AAU87674.  
XX  
XX  
PT New isolated nucleic acid encoding a protein for diagnosing,  
PT preventing, treating or ameliorating medical conditions and used as  
PT food additives or preservatives -  
XX  
XX  
XX Claim 1; SEQ ID No 594; 837pp; English.  
PS  
XX  
CC The invention describes an isolated nucleic acid molecule (I) encoding a  
CC novel central nervous system protein. (I) and polypeptides (II) encoded  
CC by (I), are used to treat a medical conditions and in diagnosis of a  
CC pathological condition. Disorders which are diagnosed or treated include  
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative  
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders  
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia,  
CC anglogenesis, nervous system disorders e.g. Alzheimer's disease and  
CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses  
CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders  
CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,  
CC adenocarcinomas and irritable bowel syndrome, reproductive system  
CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes  
CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.  
CC leukaemia, disorders involving neovascularisation e.g. malignancies,  
CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.  
CC acute kidney failure and blood related disorders e.g. myocardial  
CC infarction. The polypeptides can also be used to aid wound healing and  
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to  
CC maintain organs before transplantation, for supporting cell culture of  
CC primary tissues, to regenerate tissues and in chemotaxis. The  
CC polypeptides can also be used as a food additive or preservative to  
CC increase or decrease storage capabilities, fat content, lipid, protein,  
Query Match 100.0%; Score 15; DB 23; Length 2522;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CCTCTCCCCCTGTT 15  
Db 1460 CCTTCTCCCCCTGTT 1446  
RESULT 13  
AAAL16697  
ID AAAL16697 standard; cDNA; 3580 BP.  
XX  
AC AAAL16697;  
XX  
XX 16-JUN-2000 (first entry)  
XX  
XX Human secreted protein clone as180\_1 nucleotide sequence SEQ ID NO:159.  
XX  
XX Human; secreted protein; immunestimulant; immunesuppressant; virucide;  
KW antibacterial; antifungal; cytostatic; antiinflammatory; dermatological;  
KW antidiabetic; antiasthmatic; antiarthritic; antirheumatic; protozoacide;

KW antithyroid; immune deficiency; severe combined immunodeficiency; SCID;  
KW infection; HIV; hepatitis; malaria; autoimmune disorder; systemic lupus;  
KW connective tissue disease; multiple sclerosis; erythematosis;  
KW rheumatoid arthritis; autoimmune pulmonary inflammation; asthma;  
KW Guillain-Barre syndrome; autoimmune thyroiditis; myasthenia gravis;  
KW insulin dependent diabetes mellitus; graft-versus-host-disease;  
KW autoimmune inflammatory eye disease; allergy; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO2000009552-A1.  
XX  
XX 24-FEB-2000.  
PD  
XX  
XX 13-AUG-1999; 99WO-US18298.  
PF  
XX  
PR 14-AUG-1998; 98US-0096622.  
PR 17-AUG-1998; 98US-0096815.  
PR 04-SEP-1998; 98US-0099229.  
PR 23-OCT-1998; 98US-0105368.  
PR 08-JAN-1999; 99US-0115234.  
PR 12-FEB-1999; 99US-0119931.  
PR 18-FEB-1999; 99US-0120575.  
PR 30-APR-1999; 99US-0132020.  
PR 11-AUG-1999; 99US-0096622.  
XX  
PA (GEMY ) GENETICS INST INC.  
XX  
XX Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;  
PI Merberg D, Treacy M, Agostino MJ, Steininger RJ, Spaulding V;  
PI Wong GG, Clark HF, Fechtel K;  
XX  
XX WPI; 2000-205979/18.  
DR P-PSDB; AAY94977.  
XX  
XX New polynucleotides encoding secreted proteins, which may have e.g.  
XX nutritional, chemokine, immune stimulating or suppressing,  
XX hematopoiesis regulating, tissue growth, activin/inhibin  
XX antiinflammatory or tumor inhibition activity -  
PS  
XX Claim 168; Page 613-614; 641pp; English.  
XX  
XX AAAL16618 to AAAL16697 encode the human secreted proteins given in  
CC AAY94898 to AAY94980, isolated from human adult brain, adult thyroid,  
CC adult retina, foetal carcinoma, adult blood, adult neural, foetal kidney,  
CC adult placenta, adult testis, whole embryo, adult cartilage, kidney,  
CC foetal brain, adult thymus, foetal placenta, adult uterus, adult tumour,  
CC and adult bladder, cDNA libraries. The polynucleotides and proteins are  
CC predicted to have biological activities which would make them suitable  
CC for treating, preventing or ameliorating medical conditions in humans  
CC and animals. The polynucleotides can be used as markers for tissues in  
CC which the protein is preferentially expressed, as molecular weight  
CC markers on Southern gels, and as chromosome markers or tags to identify  
CC chromosomes or to map gene positions. The proteins can be used in the  
CC treatment of immune deficiencies and disorders, such as severe combined  
CC immunodeficiency (SCID), as well as viral, bacterial, fungal and other  
CC infections. These infections include human immunodeficiency virus (HIV),  
CC hepatitis, herpesviruses, mycobacteria, Leishmania spp., malaria and  
CC candidiasis. The proteins can be used to treat autoimmune disorders such  
CC as connective tissue disease, multiple sclerosis, systemic lupus  
CC erythematosis, rheumatoid arthritis, autoimmune pulmonary inflammation,  
CC Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent  
CC diabetes mellitus, myasthenia gravis, graft-versus-host-disease and  
CC autoimmune inflammatory eye disease. The proteins can also be used to  
CC treat allergic conditions, such as asthma. AAAL16698 to AAAL16774 represent  
XX probes for the human secreted proteins from the present invention.  
SQ  
Sequence 3580 BP; 734 A; 942 C; 1024 G; 880 T; 0 Other;  
Query Match 100.0%; Score 15; DB 21; Length 3580;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCTTCTCCCCCTGTT 15  
DB 2528 CCTTCTCCCCCTGTT 2542

RESULT 14  
ABK35630/C  
ID ABK35630 standard: cDNA; 3580 BP.

XX AC  
XX ABK35630;

XX 08-MAY-2002 (first entry)

XX cDNA sequence #21 encoding novel human secreted protein.

XX Human secreted protein; hyperproliferative disorder; autoimmune disorder;  
KW immune deficiency disorder; blood disorder; inflammatory disorder;  
KW infectious disorder; allergic condition; neurodegenerative disorder;  
KW liver fibrosis; coagulation disorder; gene therapy; antimicrobial;  
KW tumour; cancer; hepatotropic; immunosuppressive; antirheumatic; gene; ss.

XX OS Homo sapiens.

XX WO200177289-A2.

XX PD 18-OCT-2001.

XX PF 29-MAR-2001; 2001WO-US10232.

XX PR 06-APR-2000; 2000US-195605P.

XX PA (GEMV) GENETICS INST INC.

XX Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;  
PI Merberg D, Treacy M, Agostino MJ, Bowman MR, Spaulding V, Wong GG;  
PI Clark HF, Fechtel K, Howes SH, Resnick RJ, Gulukota K, Graham JR;  
XX WPI: 2002-179322/23.

XX Six hundred and twenty three polynucleotides derived from a variety of  
PT human tissue sources which encode secreted proteins, useful for  
PT treating immune deficiencies and disorders such as autoimmune disorders

XX Claim 1; Page 85-86; 393pp; English.

XX The present invention relates to the isolation of novel cDNA sequences  
CC which encode human secreted proteins. The cDNA sequences have been  
CC derived from a variety of human tissues. The invention also provides  
CC a method for producing proteins from these polynucleotide sequences.  
CC The proteins are useful for identifying compounds that modulate their  
CC activity and production. The sequences of the invention are  
CC useful for treating diseases such as hyperproliferative disorders  
CC (e.g. cancer), immune deficiency disorders (e.g. severe combined  
CC immunodeficiency (SCID)), autoimmune disorders (e.g. multiple  
CC sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory  
CC disorders (e.g. arthritis), infectious disorders (e.g. hepatitis),  
CC allergic conditions (e.g. asthma), neurodegenerative disorders (e.g.  
CC Alzheimer's disease), liver fibrosis, coagulation disorders (e.g.  
CC haemophilia), and tumours. The polynucleotide sequences of the  
CC invention are also useful in gene therapy. ABK35610-ABK36232 represent  
CC the cDNA sequences of the invention that encode for novel human  
CC secreted proteins.

XX Sequence 3580 BP; 880 A; 1024 C; 942 G; 734 T; 0 other;

Query Match 100.0%; Score 15; DB 24; Length 3580;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCTTCTCCCCCTGTT 15  
DB 1053 CCTTCTCCCCCTGTT 1039

RESULT 15

ABV22746/C  
ID ABV22746 standard; cDNA; 4215 BP.

XX AC  
XX ABV22746;

XX 13-SEP-2002 (first entry)

XX Human prostate expression marker cDNA 22737.

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
KW pharmacogenomic marker; gene; ss.

XX OS Homo sapiens.

XX WO200160860-A2.

XX PD 23-AUG-2001.

XX PF 20-FEB-2001; 2001WO-US05171.

XX PR 17-FEB-2000; 2000US-183319P.

XX PR 16-MAR-2000; 2000US-189862P.

XX PR 25-MAY-2000; 2000US-207454P.

XX PR 09-JUN-2000; 2000US-211314P.

XX PR 18-JUL-2000; 2000US-219007P.

XX PR 13-DEC-2000; 2000US-255281P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Schlegel R, Endege WO, Monahan JE;

XX WPI: 2001-662795/76.

XX Novel isolated nucleic acid molecule associated with cancerous state of  
PT prostate cells and correlating with presence of prostate cancer, useful  
PT for detecting presence of prostate cancer, stage of prostate cancer -

XX Claim 1; Page 4005-4006; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising  
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
CC specification or its complement. (I) is useful for:  
CC (a) assessing whether a patient is afflicted with prostate cancer;  
CC (b) monitoring the progression of prostate cancer in a patient;  
CC (c) assessing the efficacy of a test compound to inhibit prostate  
CC cancer in a patient;  
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer  
CC in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound;  
CC (g) determining whether prostate cancer has metastasized in a patient;  
CC (h) assessing the aggressiveness or indolence of prostate cancer in a  
CC patient;  
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX Sequence 4215 BP; 1325 A; 808 C; 818 G; 1251 T; 13 other;

Query Match 100.0%; Score 15; DB 23; Length 4215;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCTTCTCCCCCTGTT 15  
DB 166 CCTTCTCCCCCTGTT 152

Search completed: December 11, 2002, 13:38:16  
Job time : 213.5 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 13:29:32 ; Search time 47 seconds  
(without alignments)  
97.876 Million cell updates/sec

Title: US-09-750-609-10  
Perfect score: 15  
Sequence: 1 ccttctccccctgtt 15

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/2/ina/5A.COMB.seq.\*  
2: /cgn2\_6/ptodata/2/ina/5B.COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS.COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
		%			
C 1	13.4	89.3	735	4	US-09-502-653-11
C 2	13.4	89.3	738	4	US-09-605-785-747
C 3	13.4	89.3	1074	2	US-08-975-316-54
C 4	13.4	89.3	1074	4	US-09-615-192A-54
C 5	13.4	89.3	1075	2	US-08-975-316-55
C 6	13.4	89.3	1075	4	US-09-615-192A-55
C 7	13.4	89.3	1374	4	US-08-482-746-9
C 8	13.4	89.3	1514	1	US-08-381-433A-1
C 9	13.4	89.3	1626	1	US-08-381-433A-3
C 10	13.4	89.3	1875	3	US-09-258-373-21
C 11	13.4	89.3	2169	1	US-08-379-496-1
C 12	13.4	89.3	3182	1	US-08-484-044-11
C 13	13.4	89.3	3224	4	US-08-965-729A-2
C 14	13.4	89.3	3279	5	PCT-US93-03077-2
C 15	13.4	89.3	3481	4	US-08-965-729A-1
C 16	13.4	89.3	4287	1	US-08-244-189-1
C 17	13.4	89.3	4287	1	US-08-306-691B-53
C 18	13.4	89.3	4396	4	US-09-821-736-1
C 19	13.4	89.3	4503	2	US-08-770-301A-2
C 20	13.4	89.3	4503	3	US-09-175-581-2
C 21	13.4	89.3	6405	4	US-09-281-481A-18
C 22	13.4	89.3	10322	4	US-09-330-330-3
C 23	13.4	89.3	11613	1	US-08-484-044-10
C 24	13.4	89.3	18073	4	US-09-078-294-12
C 25	13.4	89.3	43795	3	US-08-742-185-101
C 26	13.4	89.3	56516	2	US-08-996-306-1
C 27	13.4	89.3	56516	4	US-09-338-907-1

Sequence 1, Appli  
Sequence 179, App  
Sequence 179, App  
Sequence 3, Appli  
Sequence 1, Appli  
Sequence 82, Appl  
Sequence 29, Appl  
Sequence 1, Appli  
Sequence 351, App  
Sequence 8, Appli  
Sequence 1, Appli  
Sequence 12, Appl  
Sequence 3, Appli  
Sequence 37, Appl  
Sequence 48, Appl  
Sequence 20, Appl

28 13.4 89.3 56516 4 US-09-218-207-1  
29 13.4 89.3 56520 4 US-09-338-907-179  
30 13.4 89.3 56520 4 US-09-218-207-179  
31 13.4 89.3 65042 4 US-09-784-316-3  
32 13.4 89.3 4411529 4 US-09-103-840A-1  
33 13 86.7 776 4 US-09-484-970B-82  
34 13 86.7 1419 2 US-08-619-542B-29  
35 13 86.7 1905 4 US-09-295-744A-1  
36 13 86.7 2431 4 US-09-221-017B-351  
37 13 86.7 2687 1 US-08-149-695-8  
38 13 86.7 2687 1 US-08-377-228-8  
39 13 86.7 2873 1 US-08-149-695-1  
40 13 86.7 2873 1 US-08-377-228-1  
41 13 86.7 6032 4 US-09-295-744A-12  
42 13 86.7 55827 4 US-09-813-133A-3  
43 12.4 82.7 23 4 US-09-177-650-37  
44 12.4 82.7 110 4 US-09-037-990B-48  
45 12.4 82.7 130 4 US-09-037-990B-20

ALIGNMENTS

RESULT 1  
US-09-502-653-11/c  
; Sequence 11, Application US/09502653  
; Patent No. 6331426  
; GENERAL INFORMATION:  
; APPLICANT: Bj invad, Mads Eskelund  
; APPLICANT: Clausen, Ib Groth  
; APPLICANT: Schleim, Martin  
; APPLICANT: Bech, Lisbeth  
; APPLICANT: stergaard, Peter rahbek  
; APPLICANT: Sj holm, Carsten  
; TITLE OF INVENTION: NOVEL GALACTANASES  
; FILE REFERENCE: 5481.200-US  
; CURRENT APPLICATION NUMBER: US/09/502,653  
; CURRENT FILING DATE: 2000-02-11  
; EARLIER APPLICATION NUMBER: PA 1999 00184  
; EARLIER FILING DATE: 1999-02-11  
; EARLIER APPLICATION NUMBER: PA 1999 00799  
; EARLIER FILING DATE: 1999-06-07  
; EARLIER APPLICATION NUMBER: 60/125,885  
; EARLIER FILING DATE: 1999-03-24  
; EARLIER APPLICATION NUMBER: 60/138,445  
; EARLIER FILING DATE: 1999-06-10  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 11  
; LENGTH: 735  
; TYPE: DNA  
; ORGANISM: Bacillus agaradhaerens AC13 (DSM 8721)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(735)  
; OTHER INFORMATION: DNA encoding the Galactanase shown in SEQ ID  
; OTHER INFORMATION: NO.12.  
US-09-502-653-11

Query Match 89.3%; Score 13.4; DB 4; Length 735;  
Best Local Similarity 93.3%; Pred. No. 2.7e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15  
|||||  
Db 305 CTTCTCCCCATGTT 291

RESULT 2  
US-09-605-785-747/c  
; Sequence 747, Application US/09605785  
; Patent No. 6321716  
; GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yuqui  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedwick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Li, Samuel  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Hepler, William  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
FILE REFERENCE: 210121.427C16  
CURRENT APPLICATION NUMBER: US/09/605,785  
CURRENT FILING DATE: 2000-06-27  
NUMBER OF SEQ ID NOS: 835  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 747  
LENGTH: 738  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(738)  
OTHER INFORMATION: n-A,T,C or G  
US-09-605-785-747

Query Match 89.3%; Score 13.4; DB 4; Length 738;  
Best Local Similarity 93.3%; Pred. No. 2.7e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGTT 15  
Db 469 CCTTCTCCCCCTGTT 455

RESULT 3  
US-08-975-316-54/c  
Sequence 54, Application US/08975316  
Patent No. 5952486  
GENERAL INFORMATION:  
APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka  
APPLICANT: and GRIERSON, Alastair W.  
TITLE OF INVENTION: MATERIALS AND METHODS FOR  
TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Ann W. Speckman  
STREET: 2601 Elliott Avenue, Suite 4185  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/975,316  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/713,000  
FILING DATE: September 11, 1996  
ATTORNEY/AGENT INFORMATION:

NAME: SLEATH, Janet  
REGISTRATION NUMBER: 37,007  
REFERENCE/DOCKET NUMBER: 11000/1003C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-269-0565  
TELEFAX: 206-269-0563  
TELEX:

INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1074 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-975-316-54

Query Match 89.3%; Score 13.4; DB 2; Length 1074;  
Best Local Similarity 93.3%; Pred. No. 2.8e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGTT 15  
Db 581 CCTTCTCCCCCTTTT 567

RESULT 4  
US-09-615-192A-54/c  
Sequence 54, Application US/09615192A  
Patent No. 6410718  
GENERAL INFORMATION:  
APPLICANT: BLOKSBERG, Leonard N.  
APPLICANT: Havukkala, Ilkka  
TITLE OF INVENTION: Materials and Methods for the  
TITLE OF INVENTION: Modification of Plant Lignin Content  
FILE REFERENCE: 11000.1003C4U  
CURRENT APPLICATION NUMBER: US/09/615,192A  
CURRENT FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 08/975,316  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: US 08/713,000  
PRIOR FILING DATE: 1996-09-11  
PRIOR APPLICATION NUMBER: US 09/169,789  
PRIOR FILING DATE: 1998-10-09  
NUMBER OF SEQ ID NOS: 405  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 54  
LENGTH: 1074  
TYPE: DNA  
ORGANISM: Pinus radiata  
US-09-615-192A-54

Query Match 89.3%; Score 13.4; DB 4; Length 1074;  
Best Local Similarity 93.3%; Pred. No. 2.8e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGTT 15  
Db 581 CCTTCTCCCCCTTTT 567

RESULT 5  
US-08-975-316-55/c  
Sequence 55, Application US/08975316  
Patent No. 5952486  
GENERAL INFORMATION:  
APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka  
APPLICANT: and GRIERSON, Alastair W.  
TITLE OF INVENTION: MATERIALS AND METHODS FOR  
TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Ann W. Speckman  
STREET: 2601 Elliott Avenue, Suite 4185  
CITY: Seattle



STATE: WA  
COUNTRY: USA  
ZIP: 98121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/975,316  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/713,000  
FILING DATE: September 11, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: SLEATH, Janet  
REGISTRATION NUMBER: 37,007  
REFERENCE/DOCKET NUMBER: 11000/1003C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-269-0565  
TELEFAX: 206-269-0563  
TELEX:  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1075 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-975-316-55

Query Match 89.3%; Score 13.4; DB 2; Length 1075;  
Best Local Similarity 93.3%; Pred. No. 2.8e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15  
|||||  
DB 582 CCTTCTCCCCCTTT 568

RESULT 6  
US-09-615-192A-55/c  
Sequence 55, Application US/09615192A  
Patent No. 6410718  
GENERAL INFORMATION:  
APPLICANT: Biokberg, Leonard N.  
APPLICANT: Havukkala, Ilkka  
TITLE OF INVENTION: Materials and Methods for the  
TITLE OF INVENTION: Modification of Plant Lignin Content  
FILE REFERENCE: 11000.1003c4U  
CURRENT APPLICATION NUMBER: US/09/615,192A  
CURRENT FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 08/975,316  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: US 08/713,000  
PRIOR FILING DATE: 1996-09-11  
PRIOR APPLICATION NUMBER: US 09/169,789  
PRIOR FILING DATE: 1998-10-09  
NUMBER OF SEQ ID NOS: 405  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 55  
LENGTH: 1075  
TYPE: DNA  
ORGANISM: Pinus radiata  
US-09-615-192A-55

Query Match 89.3%; Score 13.4; DB 4; Length 1075;  
Best Local Similarity 93.3%; Pred. No. 2.8e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15  
|||||  
DB 582 CCTTCTCCCCCTTT 568

RESULT 7  
US-08-482-746-9  
Sequence 9, Application US/08482746B  
Patent No. 6399315  
GENERAL INFORMATION:  
APPLICANT: Perrin, Marilyn H.  
APPLICANT: Chen, Ruoping A.  
APPLICANT: Lewis, Kathy A.  
APPLICANT: Vale Jr., Wylie W.  
APPLICANT: Donaldson, Cynthia J.  
APPLICANT: Sawchenko, Paul  
TITLE OF INVENTION: Cloning and Recombinant Production of  
TITLE OF INVENTION: CRF Receptor(s)  
FILE REFERENCE: P41-90002  
CURRENT APPLICATION NUMBER: US/08/482,746B  
CURRENT FILING DATE: 1995-06-07  
EARLIER APPLICATION NUMBER: US 08/374,009  
EARLIER FILING DATE: 1995-01-17  
EARLIER APPLICATION NUMBER: US 08/353,537  
EARLIER FILING DATE: 1994-12-09  
EARLIER APPLICATION NUMBER: PCT/US94/05908  
EARLIER FILING DATE: 1994-05-25  
EARLIER APPLICATION NUMBER: US 08/110,286  
EARLIER FILING DATE: 1993-08-23  
EARLIER APPLICATION NUMBER: US 08/079,320  
EARLIER FILING DATE: 1993-06-18  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 9  
LENGTH: 1374  
TYPE: DNA  
ORGANISM: Mus musculus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (79)...(1371)  
US-08-482-746-9

Query Match 89.3%; Score 13.4; DB 4; Length 1374;  
Best Local Similarity 93.3%; Pred. No. 2.8e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15  
|||||  
DB 1080 CCTTCTCCCCCTGTT 1094

RESULT 8  
US-08-381-433A-1  
Sequence 1, Application US/08381433A  
Patent No. 5786203  
GENERAL INFORMATION:  
APPLICANT: Lovenberg, Timothy W.  
APPLICANT: Oltersdorf, Tilman  
APPLICANT: Liaw, Chen  
APPLICANT: Grigoriadis, Dimitri E.  
APPLICANT: Desouza, Errol B.  
TITLE OF INVENTION: CORTICOTROPIN RELEASING FACTOR 2  
TITLE OF INVENTION: RECEPTORS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/381,433A  
;; FILING DATE: 31-JAN-1995  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: McMasters, David D.  
;; REGISTRATION NUMBER: 33,963  
;; REFERENCE/DOCKET NUMBER: 690068.401C1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (206) 622-4900  
;; TELEFAX: (206) 682-6031  
;; TELEX: 3723836 SEEDANDBERRY  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1514 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: cDNA  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: 44..1336  
US-08-381-433A-1

Query Match 89.3%; Score 13.4; DB 1; Length 1514;  
Best Local Similarity 93.3%; Pred. No. 2.8e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTCTCCCCCTGTT 15  
||| |||||

Db 1045 CCTCTCCCCCTGTT 1059

## RESULT 9

US-08-381-433A-3  
; Sequence 3, Application US/08381433A  
; Patent No. 5786203

## GENERAL INFORMATION:

; APPLICANT: Lovenberg, Timothy W.  
; APPLICANT: Oltersdorf, Tilman  
; APPLICANT: Liaw, Chen  
; APPLICANT: Grigoriadis, Dimitri E.  
; APPLICANT: DeSouza, Errol B.  
; TITLE OF INVENTION: CORTICOTROPIN RELEASING FACTOR 2  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/381,433A  
; FILING DATE: 31-JAN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 690068.401C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; TELEX: 3723836 SEEDANDBERRY  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1626 base pairs

; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 216..1449  
US-08-381-433A-3

Query Match 89.3%; Score 13.4; DB 1; Length 1626;  
Best Local Similarity 93.3%; Pred. No. 2.8e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTCTCCCCCTGTT 15  
||| |||||

Db 1157 CCTCTCCCCCTGTT 1171

## RESULT 10

US-09-258-373-21  
; Sequence 21, Application US/09258373  
; Patent No. 6150110

## GENERAL INFORMATION:

; APPLICANT: Fletcher, Jonathan A.  
; APPLICANT: Xiao, Sheng  
; TITLE OF INVENTION: HMGI(Y)-LAMA4\* FUSION ONCOGENE,  
; FILE REFERENCE: B0801/7135/ERP  
; CURRENT APPLICATION NUMBER: US/09/258,373  
; CURRENT FILING DATE: 1998-02-26  
; EARLIER APPLICATION NUMBER: 60/076,401  
; EARLIER FILING DATE: 1998-02-28  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 21  
; LENGTH: 1875

## TYPE: DNA

## ORGANISM: Homo Sapiens

## US-09-258-373-21

Query Match 89.3%; Score 13.4; DB 3; Length 1875;  
Best Local Similarity 93.3%; Pred. No. 2.9e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTCTCCCCCTGTT 15  
||| |||||

Db 1755 CCTCTCCCCCTGTT 1769

## RESULT 11

US-08-379-496-1/c  
; Sequence 1, Application US/08379496  
; Patent No. 5593833

## GENERAL INFORMATION:

; APPLICANT: MORRISON, Nigel A  
; APPLICANT: EISMAN, John A  
; APPLICANT: KELLY, Paul J  
; TITLE OF INVENTION: Assessment of Trans-Acting Factors Allelic  
; TITLE OF INVENTION: Variation  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz  
; STREET: Suite 701-E, 555 13th Street.N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/379,496

; FILING DATE: 02-MAR-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ERNST, Barbara G  
; REGISTRATION NUMBER: 30,377  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202 783-6040  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2169 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-379-496-1

Query Match 89.3%; Score 13.4; DB 1; Length 2169;  
Best Local Similarity 93.3%; Pred. No. 2.9e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15  
Db 164 CCTTCTCCCCCTGTT 150

RESULT 12  
US-08-484-044-11  
; Sequence 11, Application US/08484044  
; Patent No. 552282  
; GENERAL INFORMATION:  
; APPLICANT: Caskey, C. T.  
; APPLICANT: Fu, Ying-Hui  
; APPLICANT: Friedman, David L.  
; APPLICANT: Pizzuti, Antonio  
; APPLICANT: Fenwick, Raymond G.  
; TITLE OF INVENTION: Diagnosis of Myotonic Muscular Dystrophy  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fulbright & Jaworski, L.L.P.  
; STREET: 1301 McKinney, Suite 5100  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: U.S.A.  
; ZIP: 77010-3095  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,044  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/019,940  
; FILING DATE: 19-FEB-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Paul, Thomas D.  
; REGISTRATION NUMBER: 32,714  
; REFERENCE/DOCKET NUMBER: D-5443  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 713/651-5325  
; TELEFAX: 713/651-5246  
; TELEX: 762829  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3182 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-484-044-11

Query Match 89.3%; Score 13.4; DB 1; Length 3182;  
Best Local Similarity 93.3%; Pred. No. 3e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15  
Db 414 CCTTCTCCCCCTGTT 428

RESULT 13  
US-08-965-729A-2  
; Sequence 2, Application US/08965729A  
; Patent No. 6200751  
; GENERAL INFORMATION:  
; APPLICANT: Jian-Ming Gu and Charles T. Esmon  
; TITLE OF INVENTION: ENDOTHELIAL SPECIFIC EXPRESSION  
; TITLE OF INVENTION: REGULATED BY EPCR CONTROL ELEMENTS  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 2800 One Atlantic Center, 1201 West Peachtree Street  
; CITY: Atlanta  
; STATE: GA  
; COUNTRY: USA  
; ZIP: 30309-4530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/965,729A  
; FILING DATE: 07-NOV-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/030,718  
; FILING DATE: 08-NOV-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: OMRP 164 PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 404-873-8794  
; TELEFAX: 404-873-8795  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3224 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: /note= "Nucleotides 2272 through 2729 are a  
; OTHER INFORMATION: thrombin responsive element"; Human  
US-08-965-729A-2

Query Match 89.3%; Score 13.4; DB 4; Length 3224;  
Best Local Similarity 93.3%; Pred. No. 3e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15  
Db 2759 CCTTCTCCCCCTTT 2773

RESULT 14  
PCT-US93-03077-2  
; Sequence 2, Application PC/TUS9303077  
; GENERAL INFORMATION:

APPLICANT: Board of Regents, The University of Texas System  
APPLICANT: Gaynor, Richard B.  
APPLICANT: Wu, Foon Kin  
TITLE OF INVENTION: PROTEIN CELLULAR FACTOR USEFUL FOR  
TITLE OF INVENTION: REGULATING GENE EXPRESSION  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/03077  
FILING DATE: 19930331  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/862,025  
FILING DATE: April 2, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Kammerer, Patricia A.  
REGISTRATION NUMBER: 29,775  
REFERENCE/DOCKET NUMBER: UTFD270PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713-787-1540  
TELEFAX: 713-749-2679  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3279 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: CDNA  
PCT-US93-03077-2

Query Match 89.3%; Score 13.4; DB 5; Length 3279;  
Best Local Similarity 93.3%; Pred. No. 3e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CCTTCTCCCCCTGTT 15  
|||||  
Db 724 CCTTCTCTCTCTGTT 738

RESULT 15  
US-08-965-729A-1  
Sequence 1, Application US/08965729A  
Patent No. 6200751  
GENERAL INFORMATION:  
APPLICANT: Jian-Ming Gu and Charles T. Esmon  
TITLE OF INVENTION: ENDOTHELIAL SPECIFIC EXPRESSION  
TITLE OF INVENTION: REGULATED BY EPCR CONTROL ELEMENTS  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabst  
STREET: 2800 One Atlantic Center, 1201 West Peachtree Street  
CITY: Atlanta  
STATE: GA  
COUNTRY: USA  
ZIP: 30309-4530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/965,729A  
FILING DATE: 07-NOV-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/030,718  
FILING DATE: 08-NOV-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: OMRF 164 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404-873-8794  
TELEFAX: 404-873-8795  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3481 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: misc.feature  
OTHER INFORMATION: /note= "Nucleotides 2270 through 2840 are a  
OTHER INFORMATION: large endothelial specific element"; murine  
FEATURE:  
NAME/KEY: misc.feature  
OTHER INFORMATION: /note= "Nucleotides 2990 through 3061 are a  
OTHER INFORMATION: serum response element"; murine  
FEATURE:  
NAME/KEY: misc.feature  
OTHER INFORMATION: /note= "Nucleotides 3007 through 3014 are a  
OTHER INFORMATION: thrombin responsive element"; murine  
FEATURE:  
NAME/KEY: misc.feature  
OTHER INFORMATION: /note= "Nucleotides 3130 through 3350 are an  
OTHER INFORMATION: endothelial specific element"; murine  
US-08-965-729A-1  
Query Match 89.3%; Score 13.4; DB 4; Length 3481;  
Best Local Similarity 93.3%; Pred. No. 3e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CCTTCTCCCCCTGTT 15  
|||||  
Db 3053 CCTTCTCCCCCTTTT 3067  
Search completed: December 11, 2002, 15:30:47  
Job time : 51 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 14:35:52 ; Search time 52.5 Seconds  
(without alignments)  
111.409 Million cell updates/sec

Title: US-09-750-609-10  
Perfect score: 15  
Sequence: 1 ccttctccccctgtt 15

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	15	100.0	15857	10	US-09-764-864-1704
2	14	93.3	389	10	US-09-764-864-1704
3	14	93.3	389	10	US-09-954-456-1577
4	14	93.3	389	10	US-09-880-107-3234
5	14	93.3	482	9	US-10-001-835-84
6	14	93.3	493	10	US-09-833-381-1570
7	14	93.3	594	10	US-09-864-761-13104
8	14	93.3	8894	10	US-09-764-864-1692
9	14	93.3	8894	10	US-09-764-877-3063
10	14	93.3	16877	10	US-09-764-877-3349
11	13.4	89.3	198	10	US-09-974-300-4063
12	13.4	89.3	264	10	US-09-783-590-10753
13	13.4	89.3	363	10	US-09-712-363-96
14	13.4	89.3	401	9	US-09-946-807-1267
15	13.4	89.3	401	9	US-09-946-807-1268
16	13.4	89.3	401	9	US-09-946-807-1269
17	13.4	89.3	401	9	US-09-795-668-1267
18	13.4	89.3	401	10	US-09-795-668-1268
19	13.4	89.3	401	10	US-09-795-668-1269

20	13.4	89.3	401	10	US-09-795-686-1267	Sequence 1267, Ap
21	13.4	89.3	401	10	US-09-795-686-1268	Sequence 1268, Ap
22	13.4	89.3	401	10	US-09-795-686-1269	Sequence 1269, Ap
23	13.4	89.3	419	9	US-09-954-531-332	Sequence 332, App
24	13.4	89.3	419	9	US-09-954-531-355	Sequence 555, App
25	13.4	89.3	419	10	US-09-962-832-210	Sequence 210, App
26	13.4	89.3	419	10	US-09-954-456-1100	Sequence 1100, Ap
27	13.4	89.3	419	10	US-09-954-456-1784	Sequence 1784, Ap
28	13.4	89.3	419	10	US-09-880-107-2007	Sequence 2007, Ap
29	13.4	89.3	419	10	US-09-967-768A-134	Sequence 134, App
30	13.4	89.3	469	10	US-09-864-761-551	Sequence 551, App
31	13.4	89.3	477	10	US-09-917-800A-701	Sequence 701, App
32	13.4	89.3	738	10	US-09-759-143-747	Sequence 747, App
33	13.4	89.3	738	10	US-09-780-669-747	Sequence 747, App
34	13.4	89.3	738	10	US-09-822-827-747	Sequence 747, App
35	13.4	89.3	928	10	US-09-770-445-393	Sequence 393, App
36	13.4	89.3	1016	10	US-09-925-301-438	Sequence 438, App
37	13.4	89.3	1374	10	US-09-191-724-9	Sequence 9, Appli
38	13.4	89.3	1514	10	US-09-881-401-1	Sequence 1, Appli
39	13.4	89.3	1557	10	US-09-900-700-1	Sequence 1, Appli
40	13.4	89.3	1626	10	US-09-881-401-3	Sequence 3, Appli
41	13.4	89.3	1802	10	US-09-822-830A-401	Sequence 401, App
42	13.4	89.3	1945	9	US-09-974-298-189	Sequence 189, App
43	13.4	89.3	2617	10	US-09-853-386-123	Sequence 123, App
44	13.4	89.3	2766	9	US-09-938-842A-703	Sequence 703, App
45	13.4	89.3	3282	10	US-09-864-864-298	Sequence 298, App

ALIGNMENTS

RESULT 1  
US-09-764-864-1704  
; Sequence 1704, Application US/09764864  
; Patent No. US20020132753A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT223  
; CURRENT APPLICATION NUMBER: US/09/764,864  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1792  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1704  
; LENGTH: 15857  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-764-864-1704

Query Match 100.0%; Score 15; DB 10; Length 15857;  
Best Local Similarity 100.0%; Pred. No. 94;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCTTCTCCCCCTGT 15  
|||||  
Db 13094 CCTTCTCCCCCTGT 13108

RESULT 2  
US-09-954-456-1577/c  
; Sequence 1577, Application US/09954456  
; Patent No. US20020115057A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, Paul  
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using  
; FILE OF INVENTION: Sets  
; FILE REFERENCE: 68290-76  
; CURRENT APPLICATION NUMBER: US/09/954,456  
; CURRENT FILING DATE: 2001-09-18  
; PRIOR APPLICATION NUMBER: US/60/233,617  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: US/60/234,052

PRIOR FILING DATE: 2000-09-20  
PRIOR APPLICATION NUMBER: US/60/234,923  
PRIOR FILING DATE: 2000-09-25  
PRIOR APPLICATION NUMBER: US/60/235,134  
PRIOR FILING DATE: 2000-09-25  
PRIOR APPLICATION NUMBER: US/60/235,637  
PRIOR FILING DATE: 2000-09-26  
PRIOR APPLICATION NUMBER: US/60/235,638  
PRIOR FILING DATE: 2000-09-26  
PRIOR APPLICATION NUMBER: US/60/235,711  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: US/60/235,720  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: US/60/235,840  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: US/60/235,863  
PRIOR FILING DATE: 2000-09-27  
NUMBER OF SEQ ID NOS: 2276  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1577  
LENGTH: 389  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: n=a,t,g or c  
US-09-954-456-1577

Query Match 93.3%; Score 14; DB 10; Length 389;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14  
| | | | | | | | | | | | | | | |  
DB 296 CCTTCTCCCCCTGT 283

RESULT 3  
US-09-880-107-3234/c  
Sequence 3234, Application US/09880107  
Patent No. US20020142981A1  
GENERAL INFORMATION:  
APPLICANT: Horne, Darci T.  
APPLICANT: Vockley, Joseph G.  
APPLICANT: Scherf, Uwe  
APPLICANT: Gene Logic, Inc.  
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer  
FILE REFERENCE: 44921-5028-WO  
CURRENT APPLICATION NUMBER: US/09/880,107  
CURRENT FILING DATE: 2001-06-14  
PRIOR APPLICATION NUMBER: US 60/211,379  
PRIOR FILING DATE: 2000-06-14  
PRIOR APPLICATION NUMBER: US 60/237,054  
PRIOR FILING DATE: 2000-10-02  
NUMBER OF SEQ ID NOS: 3950  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3234  
LENGTH: 389  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Genbank Accession No. US20020142981A1 T84491  
NAME/KEY: unsure  
LOCATION: (1)..(389)  
OTHER INFORMATION: n = a or c or g or t  
US-09-880-107-3234

Query Match 93.3%; Score 14; DB 10; Length 389;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14  
| | | | | | | | | | | | | | | |

Db 296 CCTTCTCCCCCTGT 283

RESULT 4  
US-10-001-835-84/c  
Sequence 84, Application US/10001835  
Patent No. US20020160387A1  
GENERAL INFORMATION:  
APPLICANT: Salceda, Susana  
APPLICANT: Macina, Roberto  
APPLICANT: Recipon, Herve  
APPLICANT: Caferkey, Robert  
APPLICANT: Sun, Yongming  
APPLICANT: Liu, Chenghua  
TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and  
FILE REFERENCE: DEX-0277  
CURRENT APPLICATION NUMBER: US/10/001,835  
CURRENT FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/249,997  
PRIOR FILING DATE: 2000-11-20  
NUMBER OF SEQ ID NOS: 228  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 84  
LENGTH: 482  
TYPE: DNA  
ORGANISM: Homo sapien  
US-10-001-835-84

Query Match 93.3%; Score 14; DB 9; Length 482;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTCTCCCCCTGTT 15  
| | | | | | | | | | | | | | | |  
DB 188 CTTCTCCCCCTGTT 175

RESULT 5  
US-09-833-381-1570/c  
Sequence 1570, Application US/09833381  
Patent No. US20020132090A1  
GENERAL INFORMATION:  
APPLICANT: Robison, Keith E.  
TITLE OF INVENTION: No. US20020132090A1el Nucleic Acid and Protein Homologs  
FILE REFERENCE: 5800-119  
CURRENT APPLICATION NUMBER: US/09/833,381  
CURRENT FILING DATE: 2001-04-11  
PRIOR APPLICATION NUMBER: 09/516,448  
PRIOR FILING DATE: 2000-02-29  
NUMBER OF SEQ ID NOS: 2050  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1570  
LENGTH: 493  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc.feature  
LOCATION: (1)..(493)  
OTHER INFORMATION: n = A,T,C or G  
US-09-833-381-1570

Query Match 93.3%; Score 14; DB 10; Length 493;  
Best Local Similarity 93.3%; Pred. No. 2.2e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15  
| | | | | | | | | | | | | | | |  
DB 120 CCTTCTNCCCCTGTT 106

RESULT 6  
US-09-864-761-13104  
Sequence 13104, Application US/09864761

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; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmics-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 13104
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL136968.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.76
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.68
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.82
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.7
US-09-864-761-13104
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Query Match 93.3%; Score 14; DB 10; Length 594;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 CCTTCTCCCTGT 14
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Db 192 CCTTCTCCCTGT 205
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```
RESULT 7
US-09-764-864-1692/c
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```
; Sequence 1692, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1692
; LENGTH: 8894
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-864-1692
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```
Query Match 93.3%; Score 14; DB 10; Length 8894;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 CCTTCTCCCTGT 14
|||||
Db 4843 CCTTCTCCCTGT 4830
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## RESULT 8

```
US-09-764-877-3063
; Sequence 3063, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3063
; LENGTH: 8894
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3063
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Query Match 93.3%; Score 14; DB 10; Length 8894;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 CCTTCTCCCTGT 14
|||||
Db 4052 CCTTCTCCCTGT 4065
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## RESULT 9

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US-09-764-877-3349/c
; Sequence 3349, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3349
; LENGTH: 16877
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3349
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Query Match 93.3%; Score 14; DB 10; Length 16877;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14  
|||||  
Db 1269 CCTTCTCCCCCTGT 1256

RESULT 10  
US-09-974-300-4063  
; Sequence 4063, Application US/09974300  
; Patent No. US20020146721A1  
; GENERAL INFORMATION:  
; APPLICANT: Berka, Randy M.  
; APPLICANT: Clausen, Ib Groth  
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene  
; FILE REFERENCE: 10085.500-US  
; CURRENT APPLICATION NUMBER: US/09/974,300  
; CURRENT FILING DATE: 2001-10-05  
; PRIOR APPLICATION NUMBER: 09/680,598  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/279,526  
; PRIOR FILING DATE: 2001-03-27  
; NUMBER OF SEQ ID NOS: 8481  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4063  
; LENGTH: 198  
; TYPE: DNA  
; ORGANISM: Bacillus licheniformis  
US-09-974-300-4063

Query Match 89.3%; Score 13.4; DB 10; Length 198;  
Best Local Similarity 93.3%; Pred. No. 3.9e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 15  
|||  
Db 69 CCCTCTCCCCCTGT 83

RESULT 11  
US-09-783-590-10753  
; Sequence 10753, Application US/09783590  
; Patent No. US20020110850A1  
; GENERAL INFORMATION:  
; APPLICANT: Dillon, Patrick J.  
; APPLICANT: Li, Haodong  
; APPLICANT: Rosen, Craig A.  
; APPLICANT: Ruben, Steven M.  
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2  
; FILE REFERENCE: PO-16.2C1  
; CURRENT APPLICATION NUMBER: US/09/783,590  
; CURRENT FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 08/420,856  
; PRIOR FILING DATE: 1995-04-12  
; PRIOR APPLICATION NUMBER: 08/346,731  
; PRIOR FILING DATE: 1994-11-21  
; NUMBER OF SEQ ID NOS: 12485  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10753  
; LENGTH: 264  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (5)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (32)  
; OTHER INFORMATION: n equals a,t,g, or c

US-09-783-590-10753  
Query Match 89.3%; Score 13.4; DB 10; Length 264;  
Best Local Similarity 93.3%; Pred. No. 4e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 15  
|||||  
Db 124 CCTTGTCCCCCTGT 138

RESULT 12  
US-09-712-363-96/c  
; Sequence 96, Application US/09712363  
; Patent No. US20020164588A1  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, David  
; APPLICANT: Rotstein, Sergio H.  
; APPLICANT: Marcotte, Edward M.  
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND  
; FILE REFERENCE: 07419-032001  
; CURRENT APPLICATION NUMBER: US/09/712,363  
; CURRENT FILING DATE: 2000-11-13  
; PRIOR APPLICATION NUMBER: PCT/US00/02246  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/179,531  
; PRIOR FILING DATE: 2000-02-01  
; PRIOR APPLICATION NUMBER: 60/117,844  
; PRIOR FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: 60/118,206,  
; PRIOR FILING DATE: 1999-02-01  
; PRIOR APPLICATION NUMBER: 60/126,593  
; PRIOR FILING DATE: 1999-03-26  
; PRIOR APPLICATION NUMBER: 60/134,093  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: 60/134,092  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: 60/165,124  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/165,086  
; PRIOR FILING DATE: 1999-11-12  
; NUMBER OF SEQ ID NOS: 292  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 96  
; LENGTH: 315  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
US-09-712-363-96

Query Match 89.3%; Score 13.4; DB 9; Length 315;  
Best Local Similarity 93.3%; Pred. No. 4.1e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 15  
|||||  
Db 106 CCTTCTCCCCCTGT 92

RESULT 13  
US-09-783-590-10470/c  
; Sequence 10470, Application US/09783590  
; Patent No. US20020110850A1  
; GENERAL INFORMATION:  
; APPLICANT: Dillon, Patrick J.  
; APPLICANT: Haseltine, William A.  
; APPLICANT: Li, Haodong  
; APPLICANT: Rosen, Craig A.  
; APPLICANT: Ruben, Steven M.  
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2  
; FILE REFERENCE: PO-16.2C1  
; CURRENT APPLICATION NUMBER: US/09/783,590  
; CURRENT FILING DATE: 2000-02-15



```
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10470
; LENGTH: 363
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (47)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (102)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (105)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (112)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (123)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (145)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (193)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (213)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (226)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (288)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (311)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (325)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (336)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (343)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (352)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (356)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-10470
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Query Match      89.3%; Score 13.4; DB 10; Length 363;
Best Local Similarity 93.3%; Pred. No. 4.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 CCTTCTCCCTGTT 15
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Db 41 CCTTCTCCACCTGTT 27
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RESULT 14
US-09-946-807-1267
; Sequence 1267, Application US/09946807
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; Patent No. US20020165144A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinthorsdottir, Valgerdur
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345.2004-001
; CURRENT APPLICATION NUMBER: US/09/946,807
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US/09/795,668
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,716
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1267
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-946-807-1267
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Query Match      89.3%; Score 13.4; DB 9; Length 401;
Best Local Similarity 93.3%; Pred. No. 4.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 CCTTCTCCCTGTT 15
      ||||| |||||
Db 345 CCTTCTCCTCTGTT 359
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```
RESULT 15
US-09-946-807-1268
; Sequence 1268, Application US/09946807
; Patent No. US20020165144A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinthorsdottir, Valgerdur
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345.2004-001
; CURRENT APPLICATION NUMBER: US/09/946,807
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US/09/795,668
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,716
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1268
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-946-807-1268
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Query Match      89.3%; Score 13.4; DB 9; Length 401;
Best Local Similarity 93.3%; Pred. No. 4.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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      ||||| |||||
Db 302 CCTTCTCCTCTGTT 316
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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)  
146.257 Million cell updates/sec

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Perfect score: 15  
Sequence: 1 ccttctccccctgtt 15

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 3: em\_estin:\*
- 4: em\_estnu:\*
- 5: em\_estov:\*
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- 7: em\_estro:\*
- 8: em\_hic:\*
- 9: gb\_est1:\*
- 10: gb\_est2:\*
- 11: gb\_hic:\*
- 12: gb\_est3:\*
- 13: gb\_est4:\*
- 14: gb\_est5:\*
- 15: em\_estfun:\*
- 16: em\_estom:\*
- 17: gb\_gss:\*
- 18: em\_gss\_hum:\*
- 19: em\_gss\_inv:\*
- 20: em\_gss\_pln:\*
- 21: em\_gss\_vrt:\*
- 22: em\_gss\_fun:\*
- 23: em\_gss\_mam:\*
- 24: em\_gss\_mus:\*
- 25: em\_gss\_other:\*
- 26: em\_gss\_pro:\*
- 27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	181	17	AZ284882
2	15	100.0	226	10	AV335397
c 3	15	100.0	246	9	AL708655
c 4	15	100.0	297	9	AV067076
5	15	100.0	378	14	F07213
6	15	100.0	393	14	T08889

c 7	15	100.0	399	9	AJ449549
8	15	100.0	401	17	TA8E07P
c 9	15	100.0	403	13	BI706542
c 10	15	100.0	410	10	AW139708
c 11	15	100.0	420	10	AW504644
c 12	15	100.0	421	12	BF514910
c 13	15	100.0	430	13	BG961625
14	15	100.0	430	13	BI136273
15	15	100.0	431	14	BQ339760
16	15	100.0	433	17	AQ640984
c 17	15	100.0	434	10	AW699666
c 18	15	100.0	445	14	BQ778842
c 19	15	100.0	452	12	BF926997
c 20	15	100.0	458	9	AI629376
c 21	15	100.0	469	17	BH635764
c 22	15	100.0	471	17	TA299E02P
23	15	100.0	473	14	R24819
24	15	100.0	475	17	BH620101
25	15	100.0	476	14	R87939
26	15	100.0	478	17	BH622683
27	15	100.0	510	17	TA359B06Q
28	15	100.0	520	9	AA206559
c 29	15	100.0	534	9	AJ446382
30	15	100.0	555	17	TA311G03P
c 31	15	100.0	557	9	AL700490
c 32	15	100.0	575	9	AJ397416
33	15	100.0	580	10	BE265171
c 34	15	100.0	590	12	BF674237
c 35	15	100.0	593	9	AJ447956
c 36	15	100.0	599	9	AJ398497
c 37	15	100.0	602	17	AQ656394
c 38	15	100.0	608	12	BF962681
c 39	15	100.0	611	17	AQ661274
40	15	100.0	643	10	BE875768
c 41	15	100.0	649	10	AW956920
c 42	15	100.0	650	9	AJ450711
c 43	15	100.0	659	9	AJ454058
c 44	15	100.0	667	13	BI859096
c 45	15	100.0	676	9	AJ450146

ALIGNMENTS

RESULT 1	AZ284882	181 bp	DNA	linear	GSS 27-JUL-2000							
LOCUS	RPCI-23-442E20.TV	RPCI-23	Mus musculus	genomic clone	RPCI-23-442E20							
DEFINITION	, DNA sequence.											
ACCESSION	AZ284882											
VERSION	AZ284882.1	GI:95266668										
KEYWORDS	GSS.											
SOURCE	house mouse.											
ORGANISM	Mus musculus											
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.											
AUTHORS	Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret ,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. and Fraser,C.M.											
TITLE	Mouse BAC End Sequences from Library RPCI-23											
JOURNAL	Unpublished (1999)											
COMMENT	Other GSSs: RPCI-23-442E20.TJ											

BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics ([inforesgen.com](http://inforesgen.com)). BAC end page: [http://www.tigr.org/tdb/bac\\_ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html)  
 Plate: 442 row: E column: 20  
 Seq primer: T7  
 Class: BAC ends.

#### FEATURES

Location/Qualifiers  
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 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="RPCI-23-442E20"  
 /clone\_lib="RPCI-23"  
 /sex="Female"  
 /lab\_host="DH10B"  
 /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site:1: EcoRI; Site:2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

#### BASE COUNT

54 a 54 c 26 g 47 t

#### ORIGIN

Query Match 100.0%; Score 15; DB 17; Length 181;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGTT 15

|||||

Db 165 CCTTCTCCCCCTGTT 179

#### RESULT 2

AV335397

LOCUS

DEFINITION AV335397 RIKEN full-length enriched, adult male medulla oblongata Mus musculus cDNA clone 6330571M18 3' similar to AF006196 Mus musculus metalloprotease-disintegrin MDC15 mRNA, mRNA sequence.

AV335397

AV335397.1 GI:6375449

EST.

KEYWORDS

SOURCE

ORGANISM

house mouse.

Mus musculus

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 226)

Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Takahashi,F., Tateno,M., Tominaga,N., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A., Yokota,T., Yoshihiki,A., Yoshino,M., Yamamura,T., Yasunishi,A., Yokota,T., RIKEN Mouse ESTs (Konno,H., et al. 1999)

Unpublished (1999)

contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: [genome-res@sc.riken.go.jp](mailto:genome-res@sc.riken.go.jp), [genome-gsc.riken.go.jp/](mailto:genome-gsc.riken.go.jp/)

URL: <http://genome-gsc.riken.go.jp/>

Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y., Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

Transcriptional sequencing: A method for DNA sequencing using RNA

polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)  
 Itoh,M., Kitsuai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.  
 Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)  
 Carninci,P. and Hayashizaki,Y.  
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)  
 Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

#### FEATURES

##### source

1. .226  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="6330571M18"  
 /clone\_lib="RIKEN full-length enriched, adult male medulla oblongata"  
 /sex="male"  
 /tissue\_type="medulla oblongata"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /note="Site:1: SalI; Site:2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGATCCAGAGCTCTTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCGAGTTAAATTAATCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI"

BASE COUNT 55 a 51 c 63 g 56 t 1 others  
 ORIGIN

Query Match 100.0%; Score 15; DB 10; Length 226;  
 Best Local Similarity 100.0%; Pred. No. 5.7e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGTT 15

|||||

Db 77 CCTTCTCCCCCTGTT 91

#### RESULT 3

LOCUS

AL708655/c

DEFINITION DKF2p686J0853.r1 686 (synonym: hlcc3) Homo sapiens cDNA clone

AL708655

VERSION

AL708655.1 GI:19692010

KEYWORDS

EST.

SOURCE

ORGANISM

human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 246)

Wambutt,R., Heubner,D., Mewes,W., Weil,B. and Wiemann,S.

EST (Wambutt,R., Heubner,D., Mewes,H.W., Weil,B. and Wiemann,S.)

Unpublished (1999)

CONTACT: Wambutt R

MIPS

Am Klopferspitz 18a D-82152 Martinsried, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKF2); Email s.wiemann@dkfz-heidelberg.de; sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.

No sl sequence available.  
This clone (DKF2p86J0853) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

## FEATURES

Source

```
1..246
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="DKF2p86J0853"
/clone_lib="686 (synonym: hlcc3)"
/tissue_type="human skeletal muscle"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
cDNA collection"
```

BASE COUNT 71 a 47 c 88 g 40 t

Query Match 100.0%; Score 15; DB 9; Length 246;

Best Local Similarity 100.0%; Pred. No. 5.8e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGTT 15

|||||

Db 176 CCTTCTCCCCCTGTT 162

## RESULT 4

AV067076/c

LOCUS

AV067076 297 bp mRNA linear EST 24-JUN-1999  
cDNA clone 2010200P09, mRNA sequence.

ACCESSION

AV067076

VERSION

AV067076.1 GI:5186904

KEYWORDS

EST.

SOURCE

house mouse.

ORGANISM

Mus musculus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 297)

AUTHORS

Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,

Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara

, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J.,

Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H., Owa, C.,

Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara

, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N.,

Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M.,

Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

RIKEN Mouse ESTs

Unpublished (1999)

Contact: Chie Owa

Genome Science Laboratory

RIKEN

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

Tel: 81-298-36-9145

Fax: 81-298-36-9098

Email: genome-res@rtc.riken.go.jp

Thermostabilization and thermoactivation of thermolabile enzymes by

trehalose and its application for the synthesis of full length cDNA

(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))

Transcriptional sequencing: A method for DNA sequencing using RNA

polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))

Please visit our web site (<http://genome.rtc.riken.go.jp>) for

further details.

## FEATURES

Source

```
1..297
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
```

```
/clone="2010200P09"
/clone_lib="Mus musculus small intestine C57BL/6J adult"
/sex="male"
/tissue_type="small intestine"
/dev_stage="adult"
/note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5',
TGTTCACCAATCTGAAGTCGGAGCGCGGATGGTTTTTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."
```

BASE COUNT 95 a 62 c 79 g 61 t

## ORIGIN

Query Match 100.0%; Score 15; DB 9; Length 297;

Best Local Similarity 100.0%; Pred. No. 6.1e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCCCCCTGTT 15

|||||

Db 45 CTTCTCCCCCTGTT 31

## RESULT 5

F07213

LOCUS

F07213 378 bp mRNA linear EST 20-FEB-1995  
HSC1ZB021 normalized infant brain cDNA Homo sapiens cDNA clone

DEFINITION

c-1zb02, mRNA sequence.

ACCESSION

F07213

VERSION

F07213.1 GI:672862

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 378)

AUTHORS

AufRAY, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Devignes

, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B., Lorenzo, F.,

Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y.,

Sebastiani-Kabakchis, C. and Tessier, A.

IMAGE: molecular integration of the analysis of the human genome

and its expression

C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)

95277534

Contact: Genethon

Genethon

Genethon

Genethon Centre de recherche sur le Genome Humain

1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE

Tel: 33169472800

Fax: 33160778698

Email: [genexpress@genethon.fr](mailto:genexpress@genethon.fr)

Single read.

Genexpress\_library\_idt: C; Genexpress\_sequence\_idt: yic-1zb02

Seq primer: (-21)M13 universal.

Location/Qualifiers

1..378

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="c-1zb02"

/clone\_lib="normalized infant brain cDNA"

/sex="Female"

/tissue\_type="total brain"

/dev\_stage="3 months old"

/note="Organ: brain; Vector: lafmid BA; Site\_1: HindIII;

Site\_2: NotI; sex:Female; dev\_stage=3 months old;

isolate=muscular atrophy patient; tissue\_type=total brain

; total mRNA was oligo-(dT) primed and directionally

cloned 5' -&gt; 3' into the HindIII -&gt; NotI sites of the

```

lafmid BA vector. Clone library from B.Soaress, Psychiatry
Dept. Columbia University, USA.
Bento Soares, P.N.A.S in press"
68 a 111 c 98 t 2 others
BASE COUNT
ORIGIN

Query Match 100.0%; Score 15; DB 14; Length 378;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGTT 15
Db 193 CCTTCTCCCCCTGTT 207

RESULT 6
T08889
LOCUS
DEFINITION T08889 393 bp mRNA linear EST 03-AUG-1993
5' end similar to p87 transporter-like protein, mRNA sequence.
ACCESSION T08889
VERSION T08889.1 GI:389917
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 393)
Adams,M.D., Soares,M.B., Kerlavage,A.R., Fields,C. and Venter,J.C.
Rapid cDNA sequencing (expressed sequence tags) from a
directionally cloned human infant brain cDNA library
Nat. Genet. 4, 373-380 (1993)
94004965
Contact: Adams, MD
The Institute for Genomic Research
932 Clopper Road, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: mdadams@tigr.org
Seq primer: W13 Reverse
Location/Qualifiers
1..399
/organism="Homo sapiens"
/db_xref="ATCC (inhost):85383"
/db_xref="taxon:9606"
/clone="HIBBL71"
/clone_lib="Infant Brain, Bento Soares"
/note="Vector: Lafmid; The IB library was constructed by
directional cloning and oligo(dT)-priming in the lafmid
vector, utilizing a three month old infant human brain
(total brain)."
```

```

78 a 114 c 101 g 99 t 1 others
BASE COUNT
ORIGIN

Query Match 100.0%; Score 15; DB 14; Length 393;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGTT 15
Db 130 CCTTCTCCCCCTGTT 144
```

```

RESULT 7
AJ449549/c
LOCUS
DEFINITION AJ449549 riken1 Gallus gallus cDNA clone 22gilrl, mRNA sequence.
ACCESSION AJ449549
VERSION AJ449549.1 GI:20216770
KEYWORDS EST.
SOURCE chicken.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 399)
Buerstedde,J.M.
Gallus gallus bursal lymphocyte EST
Unpublished (2002)
Contact: Buerstedde JM
Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
1..399
/organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="22gilrl"
/clone_lib="riken1"
/cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
/note="CB inbred strain"
BASE COUNT 120 a 78 c 103 g 97 t 1 others
ORIGIN

Query Match 100.0%; Score 15; DB 9; Length 399;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGTT 15
Db 107 CCTTCTCCCCCTGTT 93

RESULT 8
TA8E07P
LOCUS
DEFINITION TA8E07P 401 bp DNA linear GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 8e07, forward sequence, genomic
survey sequence.
ACCESSION AL452614
VERSION AL452614.1 GI:11861158
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 401)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/t_brucei/.
Location/Qualifiers
1..401
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="8e07"
BASE COUNT 81 a 91 c 118 g 111 t
ORIGIN
```

Query Match 100.0%; Score 15; DB 17; Length 401;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCGCTGTT 15  
 |||||  
 DB 67 CCTTCTCCCGCTGTT 81

RESULT 9  
 BI706542/c  
 LOCUS  
 DEFINITION 403 bp mRNA linear EST 13-FEB-2002  
 f07c03.y1 zebrafish adult retina cDNA Danio rerio cDNA clone  
 4790765.5, similar to TR:Q9UH03 Q9UH03 BK250D10.3 ;, mRNA sequence.  
 ACCESSION BI706542  
 VERSION BI706542.1 GI:15682237  
 KEYWORDS EST.  
 SOURCE zebrafish.  
 ORGANISM Danio rerio

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes  
 ; Cyprinidae; Danio.  
 1 (bases 1 to 403)  
 AUTHORS Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy  
 ,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood  
 ,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,  
 Swaller,T., Gibbons,M., Fape,D., Harvey,N., Schurk,R., Ritter,E.,  
 Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.  
 and Wilson,R.  
 TITLE WashU Zebrafish EST Project 1998  
 JOURNAL Unpublished (1998)  
 COMMENT Contact: Stephen L. Johnson  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: zbrfish@wustl.edu

Library constructed by: Chandra Tucker and Gregory Niemi DNA  
 Sequencing by: Washington University Genome Sequencing Center Clone  
 distribution: RessourcenZentrumPrimaDatenbank, Berlin, Germany  
 (web address: www.rzpd.de)  
 Seq primer: T3 ET from Amersham  
 High quality sequence stop: 396.  
 FEATURES Location/Qualifiers  
 1..403  
 /organism="Danio rerio"  
 /strain="wild-type"  
 /db\_xref="taxon:7955"  
 /clone="4790765"  
 /clone\_lib="zebrafish adult retina cDNA"  
 /sex="mixed"  
 /dev\_stage="1-2 years"  
 /lab\_host="E.Coli XL1-Blue MRF"  
 /note="Vector: Lambda ZAP II (pBluescript SK-); Site\_1:  
 EcoRI; Site\_2: SalI; This Zebrafish library was  
 constructed by Dr. Susan E. Brockerhoff (email:  
 sbrocker@u.washington.edu) RZPD library number: 760"  
 BASE COUNT 105 a 89 c 116 g 93 t

ORIGIN  
 Query Match 100.0%; Score 15; DB 13; Length 403;  
 Best Local Similarity 100.0%; Pred. No. 6.5e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CCTTCTCCCGCTGTT 15  
 |||||  
 DB 114 CCTTCTCCCGCTGTT 100

RESULT 10  
 AW139708/c  
 LOCUS  
 DEFINITION 410 bp mRNA linear EST 30-OCT-1999  
 AW139708  
 Query Match 100.0%; Score 15; DB 10; Length 410;  
 Best Local Similarity 100.0%; Pred. No. 6.5e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DEFINITION UI-H-B11-aeb-a-03-0-UI.s1 NCI\_CGAP\_Sub3 Homo sapiens cDNA clone  
 IMAGE:2718605 3', mRNA sequence.  
 ACCESSION AW139708  
 VERSION AW139708.1 GI:6144426  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 410)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs@mail.nih.gov  
 Oligo-dt track not found, Not I site shown in beginning of sequence  
 is likely internal to the message. cDNA Library Preparation: M.B.  
 Soares Lab Clone distribution: NCI-CGAP clone distribution  
 information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html The following repetitive  
 elements were found in this cDNA sequence: 151-216, >(GGGA  
 )n\$Simple\_repeat  
 Seq primer: M13 Forward  
 POLYA=NO.

FEATURES Location/Qualifiers  
 1..410  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2718605"  
 /clone\_lib="NCI\_CGAP\_Sub3"  
 /lab\_host="DH10B (Life Technologies)"  
 /note="Vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker; Site\_1: Not I; Site\_2: Eco RI; The  
 NCI-CGAP\_Sub3 library is a subtracted library derived from  
 the NCI-CGAP\_Sub1 library, which is a subtracted library  
 derived from BI. BI constitutes a mixture of 21  
 normalized or subtracted NCI-CGAP libraries: NCI\_CGAP\_Co4  
 , NCI\_CGAP\_Pr22, NCI\_CGAP\_Pr28, NCI\_CGAP\_Co10,  
 NCI\_CGAP\_Co16, NCI\_CGAP\_Kid5, NCI\_CGAP\_Kid12,  
 NCI\_CGAP\_Kid3, NCI\_CGAP\_Kid11, NCI\_CGAP\_Lym2,  
 NCI\_CGAP\_Br2, NCI\_CGAP\_Co8, NCI\_CGAP\_GLI1, NCI\_CGAP\_Le12,  
 NCI\_CGAP\_Brn23, NCI\_CGAP\_Lu5, NCI\_CGAP\_Lu24,  
 NCI\_CGAP\_Lu19, NCI\_CGAP\_GC4, NCI\_CGAP\_GC6,  
 NCI\_CGAP\_Brn25. These 21 libraries were pooled and a  
 single-stranded DNA preparation of the resulting mixture  
 was used as a tracer in a subtractive hybridization with  
 a driver whose composition is detailed below:  
 NCI\_CGAP\_Kid3 pool 1 LLAM 3334-3337, 3682-3683,  
 3798-3803 (IMAGE Clones 132376-132391, 1456008-1456775  
 , 1500552-1502855); NCI\_CGAP\_Kid5 pool 1, LLAM 3338-3342  
 , 3722-3725, 3776-3778 (IMAGE Clones 1323912-1325831,  
 1471368-1472903, 1492104-1493255); NCI\_CGAP\_Lu5 pool 1  
 LLAM 3575-3582, 3851-3854 (IMAGE Clones 1414920-1417991,  
 1520904-1522439); NCI\_CGAP\_GC4 pool 1 LLAM 3164-3167,  
 3716-3720, 3733-3735 (IMAGE Clones 1257096-1258631,  
 1469064-1470983, 1475592-1476743); NCI\_CGAP\_Pr22 pool 1  
 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clones  
 985608-986759, 1101192-1101959, 1217928-1220615);  
 NCI\_CGAP\_Co10 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE  
 Clones 1057416-1061255, 1144584-1145351). Subtraction  
 was performed as previously described [Bonaldi, Lennon &  
 Soares (1996): Normalization and Subtraction: Two  
 Approaches To Facilitate Gene Discovery. Genome Research  
 6, 791-806.  
 TAG\_LIB=NCI\_CGAP\_Kid3  
 TAG\_TISSUE=Kidney  
 TAG\_SEQ=AATGC"

BASE COUNT 110 a 124 c 91 g 85 t  
 ORIGIN  
 Query Match 100.0%; Score 15; DB 10; Length 410;  
 Best Local Similarity 100.0%; Pred. No. 6.5e+03;

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGTT 15
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Db 396 CCTTCTCCCCCTGTT 382

RESULT 11
AW504644/c
LOCUS
DEFINITION
  UI-HF-BN0-alk-h-12-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone
IMAGE:3079943 5', mRNA sequence.
ACCESSION
  AW504644
VERSION
  AW504644.1 GI:7142311
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 420)
AUTHORS
  NIH-MGC http://mgc.nci.nih.gov/.
TITLE
  National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
  Unpublished (1999)
COMMENT
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-remail.nih.gov
  Eco RI site shown at the beginning of the sequence.
  Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
  cDNA Library Preparation: M.B. Soares Lab
  cDNA Library Arrayed by: M.B. Soares Lab
  DNA Sequencing by: M.B. Soares Lab
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  www-bio.llnl.gov/bbrp/image/image.html
  Seq primer: M13 Forward.
  Location/Qualifiers
    1..420
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="IMAGE:3079943"
    /clone_lib="NIH_MGC_50"
    /tissue_type="lymph"
    /cell_type="germinal center B cells"
    /cell_line="MGC85"
    /lab_host="DH10B (LTI)"
    /note="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
    Constructed from size fractionated cytoplasmic mRNA
    (3.5-4.4kb). Directionally cloned. Cells provided by
    Louis M. Staudt, Ph.D. Library preparation by Maria de
    Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D. "
BASE COUNT 124 a 72 c 126 g 98 t
ORIGIN
  Query Match 100.0%; Score 15; DB 10; Length 420;
  Best Local Similarity 100.0%; Pred. No. 6.5e+03;
  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGTT 15
    |||||||
Db 159 CCTTCTCCCCCTGTT 145

RESULT 12
BF514910/c
LOCUS
DEFINITION
  UI-H-BW1-anp-a-11-0-UI.sl NCI_CGAP_Sub7 Homo sapiens cDNA clone
IMAGE:3083036 3', mRNA sequence.
ACCESSION
  BF514910
VERSION
  BF514910.1 GI:11600078
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 421)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
The sequence contained an oligo-dT track that was present in the  
oligonucleotide that was used to prime the synthesis of first A  
strand cDNA and therefore this may represent a bonafide poly A  
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:  
NCI-CGAP clone distribution information can be found through the  
I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Seq primer: M13 Forward  
POLYA=Yes

FEATURES  
source

Location/Qualifiers  
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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3083036"  
/clone\_lib="NCI\_CGAP\_Sub7"  
/lab\_host="DH10B (Life Technologies)"  
/note="Vector: pT73B-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; NCI\_CGAP\_Sub7  
is a subtracted library derived from NCI\_CGAP\_Sub6. The  
NCI\_CGAP\_Sub7 library had 12 million recombinants. A  
single-stranded DNA preparation of NCI\_CGAP\_Sub6 was used  
as a tracer in a subtractive hybridization with a driver  
comprising: the IMAGE pool (NCI\_CGAP\_Kid3 pool 1 LLAM  
3334-3337, 3682-3683, 3798-3803 (IMAGE Cloned)  
1323376-1323911, 1456008-1456775, 1500552-1502855);  
NCI\_CGAP\_Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778  
(IMAGE Cloned) 1323912-1325831, 1471368-1472903,  
1492104-1493255); NCI\_CGAP\_Lu5 pool 1 LLAM 3575-3582,  
3851-3854 (IMAGE Cloned) 1414920-1417991, 1520904-1522439  
); NCI\_CGAP\_GC4 pool 1 LLAM 3164-3167, 3716-3720  
3733-3735 (IMAGE Cloned) 1257096-1258631, 1469064-1470983  
, 1475592-1476743); NCI\_CGAP\_Pr22 pool 1 LLAM 2457-2459,  
2758-2759, 3062-3068 (IMAGE Cloned) 985608-986759,  
1101192-1101959, 1217928-1220615); NCI\_CGAP\_Co10 pool 1  
LLAM 2644-2653, 2871-2872 (IMAGE Cloned) 1057416-1061255  
, 114584-1145351). (6% of the driver population), plus a  
pool of 3,840 arrayed clones from NCI\_CGAP\_Sub1 (IMAGE  
Cloned) 2708616-2710535) and NCI\_CGAP\_Sub2 (IMAGE  
Cloned) 2710536-2712455) (4% of the driver population  
, plus a pool of 11,136 clones from NCI\_CGAP\_Sub3 (IMAGE  
Cloned) 2712456-2723591) (10% of the driver population),  
plus a pool of 5,472 clones from NCI\_CGAP\_Sub4 (IMAGE  
Cloned) 2723592-2729326) (40% of the driver population),  
plus a pool of 4032 clones from NCI\_CGAP\_Sub6 (IMAGE  
Cloned) 2728969-2733190) (40% of the driver population).  
Subtraction was performed as previously described (Bonaldo  
, Lennon & Soares (1996): Normalization and Subtraction:  
Two Approaches To Facilitate Gene Discovery. Genome  
Research 6, 791-806.  
TAG\_LIB=NCI\_CGAP\_Brn50  
TAG\_TISSUE=brain  
TAG\_SEQ=TTTCG"

BASE COUNT 114 a 95 c 111 g 101 t  
ORIGIN

Query Match 100.0%; Score 15; DB 12; Length 421;  
Best Local Similarity 100.0%; Pred. No. 6.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGTT 15  
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Db 130 CCTTCTCCCCCTGTT 116

RESULT 13  
BG961625/c



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LOCUS      BG961625          430 bp      mRNA      linear      EST 12-JUN-2001
DEFINITION PM0-CT0642-240401-007-C09 CT0642 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BG961625
VERSION     BG961625.1  GI:14379796
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 430)
AUTHORS     Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
TITLE       Gene expression in Populus
JOURNAL     Unpublished (2001)
COMMENT     Contact: Erlandsson R
            Department of Biotechnology
            Royal Institute of Technology
            Teknikringen 30, Stockholm S-10044, Sweden
            Tel: 46 8 790 8287
            Fax: 46 8 245452
            Email: rikerl@biochem.kth.se.
FEATURES   Location/Qualifiers
            1..430
            /organism="Populus balsamifera subsp. trichocarpa"
            /db_xref="taxon:3694"
            /clone_lib="Populus flower cDNA library"
            /note="Organ: flower"
BASE COUNT 126 a 113 c 78 g 113 t
ORIGIN
Query Match      100.0%; Score 15; DB 13; Length 430;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCTCTCCCTGTT 15
    |||||
Db 220 CCTCTCTCCCTGTT 234

RESULT 15
BQ339760          431 bp      mRNA      linear      EST 20-MAY-2002
LOCUS           QV2-NN0045-211100-494-c07 NN0045 Homo sapiens cDNA, mRNA sequence.
DEFINITION     BQ339760
ACCESSION      BQ339760
VERSION         BQ339760.1  GI:209999826
KEYWORDS        EST.
SOURCE          human.
ORGANISM        Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1 (bases 1 to 431)
AUTHORS         Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
TITLE           Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
JOURNAL         Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE         20202663
COMMENT         Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM0&t2=PM0&t4=1)
            240401-007-C09&t3=2001-04-24&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 16
            High quality sequence stop: 376.
FEATURES       Location/Qualifiers
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            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_lib="CT0642"
            /dev_stage="Adult"
            /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
            SmaI; A mini-library was made by cloning products derived
            from ORESTES PCR (U.S. Letters Patent application No. 196
            ,716 - Ludwig Institute for Cancer Research) profiles
            into the puc 18 vector. Reverse transcription of tissue
            mRNA and cDNA amplification were performed under low
            stringency conditions."
BASE COUNT 141 a 83 c 118 g 88 t
ORIGIN
Query Match      100.0%; Score 15; DB 13; Length 430;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCTCTCCCTGTT 15
    |||||
Db 132 CCTCTCTCCCTGTT 118

RESULT 14
B1136273
LOCUS           F065P87Y Populus flower cDNA library Populus balsamifera subsp.
DEFINITION     trichocarpa cDNA, mRNA sequence.
ACCESSION      B1136273
VERSION         B1136273.1  GI:18017201
KEYWORDS        EST.
SOURCE          Populus balsamifera subsp. trichocarpa.
ORGANISM        Populus balsamifera subsp. trichocarpa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.

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/clone_lib="NN0045"  
/dev_stage="Adult"  
note="Organ: nervous_normal; Vector: puc18; Site_1: SmaI;  
Site_2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."  
BASE COUNT 75 a 138 c 108 g 110 t  
ORIGIN
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Query Match 100.0%; Score 15; DB 14; Length 431;  
Best Local Similarity 100.0%; Pred. No. 6.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CCTTCTCCCCCTGTT 15  
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Db 399 CCTTCTCCCCCTGTT 413
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Search completed: December 11, 2002, 15:28:57  
Job time : 1665 secs
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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 15:30:52 : Search time 1652 Seconds  
(without alignments)  
264.251 Million cell updates/sec

Title: US-09-750-609-9

Perfect score: 15  
Sequence: 1 cctctcgcctgtt 15

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl:\*

1: gb.ba:\*

2: gb.htg:\*

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6: gb.ph:\*

7: gb.pl:\*

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19: em.mu:\*

20: em.om:\*

21: em.or:\*

22: em.ov:\*

23: em.pat:\*

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26: em.ro:\*

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30: em.htg\_hum:\*

31: em.htg\_inv:\*

32: em.htg\_other:\*

33: em.htg\_mus:\*

34: em.htg\_pln:\*

35: em.htg\_rod:\*

36: em.htg\_mam:\*

37: em.htg\_vrt:\*

38: em.sy:\*

39: em.htgo\_hum:\*

40: em.htgo\_mus:\*

41: em.htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	15	100.0	920	6	AX194629 Sequence
2	15	100.0	920	6	AX194634 Sequence
3	15	100.0	980	9	HSNETEX9
4	15	100.0	1411	9	BC000563 Homo sapi
5	15	100.0	1983	9	HUMNORTR
6	15	100.0	2127	9	HUMCOLA1XV
7	15	100.0	5161	9	HUMCOLXVAL
8	15	100.0	14621	2	AC020425
9	15	100.0	61956	2	AC101376
10	15	100.0	65851	2	AC124280 Homo sapi
11	15	100.0	80669	2	AC130797
12	15	100.0	90280	2	AC009031
13	15	100.0	110000	2	LMFLCHR12_1
14	15	100.0	150765	2	AC094766
15	15	100.0	160755	6	AX195074
16	15	100.0	167094	9	AC007602
17	15	100.0	169763	2	AC120748 Rattus no
18	15	100.0	178965	2	AC096167
19	15	100.0	181066	2	AC099635
20	15	100.0	181650	2	AC097825
21	15	100.0	183105	3	AC104606
22	15	100.0	187359	8	OSJN00259
23	15	100.0	188913	9	AC026802
24	15	100.0	224592	2	AC074209
25	15	100.0	285272	3	AE003441
26	14	93.3	708	6	AX120618
27	14	93.3	1773	9	AB057774
28	14	93.3	1987	10	AF158025
29	14	93.3	1989	10	MUSCAT2A
30	14	93.3	1989	10	MUSCRAT2X
31	14	93.3	2072	3	AF145606
32	14	93.3	2306	9	AK054811
33	14	93.3	2324	8	SCYGR002C
34	14	93.3	2393	8	AF435646
35	14	93.3	2397	6	AR054116
36	14	93.3	2397	6	IL13751
37	14	93.3	2723	10	MUSTAB
38	14	93.3	3507	10	AF301152
39	14	93.3	3698	10	MUSMEMPROT
40	14	93.3	4420	1	CGL300822
41	14	93.3	5245	1	AF130462
42	14	93.3	12563	1	AE000769
43	14	93.3	13782	1	AE009777
44	14	93.3	16387	5	AP002935
45	14	93.3	18518	1	AE001068
46	14	93.3	20539	9	HS349E10
47	14	93.3	20603	9	AL359534
48	14	93.3	28235	2	AC014089
49	14	93.3	58335	2	AC113007
50	14	93.3	66789	2	AC103807
51	14	93.3	70665	9	HS696H22
52	14	93.3	71605	2	AC119332
53	14	93.3	80820	2	AC126581
54	14	93.3	89651	2	AC099422
55	14	93.3	90547	9	HS265J14
56	14	93.3	101898	2	AC111973
57	14	93.3	104268	9	AC068120
58	14	93.3	104492	2	AC124910
59	14	93.3	110977	2	AC103120
60	14	93.3	113375	9	AC073878
61	14	93.3	114715	2	AC103165
62	14	93.3	120937	10	AL591911
63	14	93.3	123520	9	HSJ447E21
64	14	93.3	130926	9	HS453A3
65	14	93.3	135171	2	AC120056

c 66	14	93.3	138335	8	AC119148	Genomic s	139	13	86.7	1090	8	AY042856	Arabidops
c 67	14	93.3	139884	10	AC110379	Mus muscu	c 140	13	86.7	1117	1	AB016861	Burkholde
c 68	14	93.3	140043	2	AC109444	Homo sapi	c 141	13	86.7	1122	1	STMDRG	M51029 S.typhimuri
c 69	14	93.3	144949	2	AC040935	Homo sapi	c 142	13	86.7	1122	1	STYLF2MDH	M95049 Salmonella
c 70	14	93.3	145679	2	AC027249	Homo sapi	c 143	13	86.7	1359	3	AY061092	AY061092 Drosophil
c 71	14	93.3	147910	2	AC105988	Mus muscu	c 144	13	86.7	1369	1	RRU317975	AJ317975 Rhodospir
c 72	14	93.3	153533	2	AC095199	Rattus no	c 145	13	86.7	1385	10	BC025516	BC025516 Mus muscu
c 73	14	93.3	155001	2	AL356474	Homo sapi	c 146	13	86.7	1385	10	HSTSHR	AF035361 Homo sapi
c 74	14	93.3	155001	2	AL356474	Homo sapi	c 147	13	86.7	1681	1	SC6GL0A	AF035361 Homo sapi
c 75	14	93.3	155670	3	AC012097	Drosophil	c 148	13	86.7	1721	8	ABU86007	AL45343 Streptomy
c 76	14	93.3	156413	9	HSAL19E20	Human DNA	c 149	13	86.7	1811	9	ABU18602	U18602 Alouatta be
c 77	14	93.3	160376	2	AC036118	Homo sapi	c 150	13	86.7	1886	5	AB067770	AB067770 Oncohyne
c 78	14	93.3	160379	2	AC118296	Rattus no	c 151	13	86.7	2001	6	AR163597	AR163597 Sequence
c 79	14	93.3	161519	9	AC097459	Homo sapi	c 152	13	86.7	2003	1	ECNDAG	V00274 E. coli dna
c 80	14	93.3	163395	2	AC103726	Homo sapi	c 153	13	86.7	2161	9	AK094594	AK094594 Homo sapi
c 81	14	93.3	166447	2	AC121202	Rattus no	c 154	13	86.7	2232	6	AX280771	AX280771 Sequence
c 82	14	93.3	168706	2	AC092199	Typanoso	c 155	13	86.7	2292	6	AX280775	AX280775 Sequence
c 83	14	93.3	169457	2	AC009216	Drosophil	c 156	13	86.7	2292	6	AX280779	AX280779 Sequence
c 84	14	93.3	169633	2	AC111280	Rattus no	c 157	13	86.7	2292	6	AX280783	AX280783 Sequence
c 85	14	93.3	172032	2	AC112620	Rattus no	c 158	13	86.7	2292	6	AX280787	AX280787 Sequence
c 86	14	93.3	175675	2	AC119762	Rattus no	c 159	13	86.7	2292	6	AX280791	AX280791 Sequence
c 87	14	93.3	177126	2	AC123188	Rattus no	c 160	13	86.7	2292	6	AX280795	AX280795 Sequence
c 88	14	93.3	179502	9	AL591543	Human DNA	c 161	13	86.7	2380	1	AF274869	AF274869 Pasteurel
c 89	14	93.3	181596	2	AC069467	Homo sapi	c 162	13	86.7	2413	9	HUMTSNR	M73747 Homo sapien
c 90	14	93.3	182301	9	AC012498	Rattus no	c 163	13	86.7	2415	6	A34990	A34990 H.sapiens T
c 91	14	93.3	182749	2	AC094882	Rattus no	c 164	13	86.7	2415	6	A34990	A34990 H.sapiens T
c 92	14	93.3	182755	2	AC127835	Rattus no	c 165	13	86.7	2415	6	A34990	A34990 H.sapiens T
c 93	14	93.3	183269	9	AP001024	Homo sapi	c 166	13	86.7	2470	9	HUMTSNR	M32215 Human thyro
c 94	14	93.3	184338	2	AC124901	Rattus no	c 167	13	86.7	2470	9	HUMTSNR	M32215 Human thyro
c 95	14	93.3	185174	2	AC118184	Rattus no	c 168	13	86.7	2512	10	MMU02601	U02601 Mus musculu
c 96	14	93.3	186748	3	AC101263	Drosophil	c 169	13	86.7	2512	10	MMU02601	U02601 Mus musculu
c 97	14	93.3	190735	2	AC109750	Rattus no	c 170	13	86.7	2545	3	AY118724	AY118724 Drosophil
c 98	14	93.3	193024	2	AC108538	Rattus no	c 171	13	86.7	2934	1	AF012632	AF012632 Raistonia
c 99	14	93.3	193159	9	AC006946	Homo sapi	c 172	13	86.7	2934	1	AF007804	AF007804 Brucella
c 100	14	93.3	194355	2	AC116511	Mus muscu	c 173	13	86.7	3209	3	DROSERCA	BC032200 Mus muscu
c 101	14	93.3	197183	2	AC102636	Mus muscu	c 174	13	86.7	3209	3	DROSERCA	BC032200 Mus muscu
c 102	14	93.3	197743	10	AL591711	Mouse DNA	c 175	13	86.7	3235	10	MMU02601	U02601 Mus musculu
c 103	14	93.3	199386	8	NCB14D6	Neurospor	c 176	13	86.7	3240	8	AF056976	AF056976 Acromoni
c 104	14	93.3	202605	9	AP002353	Homo sapi	c 177	13	86.7	3249	3	AY095510	AY095510 Drosophil
c 105	14	93.3	213386	2	AC115746	Mus muscu	c 178	13	86.7	3349	6	AX280963	AX280963 Sequence
c 106	14	93.3	214004	2	AC109620	Mus muscu	c 179	13	86.7	3349	6	AX280963	AX280963 Sequence
c 107	14	93.3	219414	2	AC101931	Mus muscu	c 180	13	86.7	3366	9	HSAL3125	HSAL3125 Homo sapi
c 108	14	93.3	219564	2	AC103021	Mus muscu	c 181	13	86.7	3366	9	HSAL3125	HSAL3125 Homo sapi
c 109	14	93.3	220898	2	AC098941	Rattus no	c 182	13	86.7	3448	6	E03374	E03374 DNA sequenc
c 110	14	93.3	221951	10	AC122857	Mus muscu	c 183	13	86.7	3448	6	E03374	E03374 DNA sequenc
c 111	14	93.3	225016	2	AC063967	Mus muscu	c 184	13	86.7	3482	1	D84222	D84222 Thermus 76
c 112	14	93.3	226402	2	AC105706	Rattus no	c 185	13	86.7	3482	1	D84222	D84222 Thermus 76
c 113	14	93.3	229422	2	AC097544	Rattus no	c 186	13	86.7	3482	1	D84222	D84222 Thermus 76
c 114	14	93.3	235302	2	AC073784	Rattus no	c 187	13	86.7	3482	1	D84222	D84222 Thermus 76
c 115	14	93.3	242048	2	AC110537	Mus muscu	c 188	13	86.7	3482	1	D84222	D84222 Thermus 76
c 116	14	93.3	256073	9	AE006464	Homo sapi	c 189	13	86.7	3482	1	D84222	D84222 Thermus 76
c 117	14	93.3	297308	3	AE003507	Drosophil	c 190	13	86.7	3482	1	D84222	D84222 Thermus 76
c 118	14	93.3	349980	6	AX127144	Sequence	c 191	13	86.7	3482	1	D84222	D84222 Thermus 76
c 119	13	86.7	107	19	DOGSF1RB	L7224 Canis fami	c 192	13	86.7	3482	1	D84222	D84222 Thermus 76
c 120	13	86.7	107	19	RSPUPFA03	M02899 R.rubrum pu	c 193	13	86.7	3482	1	D84222	D84222 Thermus 76
c 121	13	86.7	392	11	AU047565	AU047565 Rattus no	c 194	13	86.7	3482	1	D84222	D84222 Thermus 76
c 122	13	86.7	416	5	AF012928	AF012928 Gallus ga	c 195	13	86.7	3482	1	D84222	D84222 Thermus 76
c 123	13	86.7	485	6	AF163602	AF163602 Sequence	c 196	13	86.7	3482	1	D84222	D84222 Thermus 76
c 124	13	86.7	491	6	AF163603	AF163603 Sequence	c 197	13	86.7	3482	1	D84222	D84222 Thermus 76
c 125	13	86.7	497	6	AF163604	AF163604 Sequence	c 198	13	86.7	3482	1	D84222	D84222 Thermus 76
c 126	13	86.7	625	1	AB051733	AB051733 Sequence	c 199	13	86.7	3482	1	D84222	D84222 Thermus 76
c 127	13	86.7	809	8	AF072470	AF072470 Arabidops	c 200	13	86.7	3482	1	D84222	D84222 Thermus 76
c 128	13	86.7	827	2	AF230658	AF230658 Escherich	c 201	13	86.7	3482	1	D84222	D84222 Thermus 76
c 129	13	86.7	849	1	SEU04765	U04765 Salmonella	c 202	13	86.7	3482	1	D84222	D84222 Thermus 76
c 130	13	86.7	849	1	SEU04765	U04765 Salmonella	c 203	13	86.7	3482	1	D84222	D84222 Thermus 76
c 131	13	86.7	927	9	HSCOLXV16	HSCOLXV16 Sequence	c 204	13	86.7	3482	1	D84222	D84222 Thermus 76
c 132	13	86.7	934	1	AF217261	AF217261 Homo sapi	c 205	13	86.7	3482	1	D84222	D84222 Thermus 76
c 133	13	86.7	964	5	L231072	L231072 Lampetra	c 206	13	86.7	3482	1	D84222	D84222 Thermus 76
c 134	13	86.7	979	14	AF118618	AF118618 Hepatitis	c 207	13	86.7	3482	1	D84222	D84222 Thermus 76
c 135	13	86.7	979	14	AF118619	AF118619 Hepatitis	c 208	13	86.7	3482	1	D84222	D84222 Thermus 76
c 136	13	86.7	979	14	AF118621	AF118621 Hepatitis	c 209	13	86.7	3482	1	D84222	D84222 Thermus 76
c 137	13	86.7	1027	3	AY118855	AY118855 Drosophil	c 210	13	86.7	3482	1	D84222	D84222 Thermus 76
c 138	13	86.7	1049	8	AY084467	AY084467 Arabidops	c 211	13	86.7	3482	1	D84222	D84222 Thermus 76

c 212	13	86.7	9000	1	AB032368	AB032368 Thermus t	285	13	86.7	65446	2	AC105034	AC105034 Homo sapi
c 213	13	86.7	9241	2	AC017570	AC017570 Drosophila	286	13	86.7	65875	2	AC101523	AC101523 Mus muscu
c 214	13	86.7	9785	6	I24403	I24403 Sequence 1	287	13	86.7	65902	2	AC100235	AC100235 Mus muscu
c 215	13	86.7	10029	1	AE009572	AE009572 Brucella	288	13	86.7	67129	2	AC095673	AC095673 Rattus no
c 216	13	86.7	10029	1	AE011656	AE011656 Xanthomon	c 289	13	86.7	67129	2	AC127128	AC127128 Rattus no
c 217	13	86.7	10124	1	TP036839	TP036839 Treponema p	c 290	13	86.7	67349	8	AF003752	AF003752 Rattus no
c 218	13	86.7	10140	1	AE009086	AE009086 Agrobacte	c 291	13	86.7	68631	2	AC102051	AC102051 Drosophila
c 219	13	86.7	10334	1	AE000388	AE000388 Escherich	c 292	13	86.7	69169	2	AC102380	AC102380 Mus muscu
c 220	13	86.7	10365	1	AE005536	AE005536 Escherich	c 293	13	86.7	69201	9	AC004109	AC004109 Homo sapi
c 221	13	86.7	10576	1	AE000957	AE000957 Archaeogl	c 294	13	86.7	69314	2	AC090447	AC090447 Homo sapi
c 222	13	86.7	10576	1	AE011689	AE011689 Xanthomon	c 295	13	86.7	71538	2	AC118243	AC118243 Mus muscu
c 223	13	86.7	10683	1	AE008052	AE008052 Agrobacte	c 296	13	86.7	72893	2	AC113515	AC113515 Mus muscu
c 224	13	86.7	10750	1	AE012010	AE012010 Xanthomon	c 297	13	86.7	76334	2	AC128007	AC128007 Rattus no
c 225	13	86.7	10986	1	AE005188	AE005188 Escherich	c 298	13	86.7	77630	7	AF222060	AF222060 Halovirus
c 226	13	86.7	11069	1	AE004124	AE004124 Vibrio ch	c 299	13	86.7	77678	8	AC007260	AC007260 Arabidops
c 227	13	86.7	11411	1	AE007649	AE007649 Clostridi	c 300	13	86.7	78500	8	SCD9461	SCD9461 Saccharomyc
c 228	13	86.7	11584	1	AE006049	AE006049 Pasteurel	c 301	13	86.7	80460	10	AL513014	AL513014 Mouse DNA
c 229	13	86.7	11622	1	AE004519	AE004519 Pseudomon	c 302	13	86.7	80609	1	AF116907	AF116907 Rhodococc
c 230	13	86.7	12248	1	AE001929	AE001929 Deinococc	c 303	13	86.7	80610	1	AF001204	AF001204 Rhodococc
c 231	13	86.7	12541	9	AL162736	AL162736 Human DNA	c 304	13	86.7	81344	9	AC079770	AC079770 Homo sapi
c 232	13	86.7	12600	1	AE006102	AE006102 Pasteurel	c 305	13	86.7	85219	9	AC073520	AC073520 Homo sapi
c 233	13	86.7	13041	1	AE005983	AE005983 Caenobact	c 306	13	86.7	85829	9	AC011382	AC011382 Homo sapi
c 234	13	86.7	13205	1	AE001225	AE001225 Treponema	c 307	13	86.7	87166	2	AC014242	AC014242 Drosophila
c 235	13	86.7	13605	1	AE009309	AE009309 Agrobacte	c 308	13	86.7	87217	2	AC012260	AC012260 Homo sapi
c 236	13	86.7	13899	1	AE013637	AE013637 Yersinia	c 309	13	86.7	87526	2	AC018485	AC018485 Drosophila
c 237	13	86.7	14309	1	AE004759	AE004759 Pseudomon	c 310	13	86.7	88028	9	AC004938	AC004938 Homo sapi
c 238	13	86.7	14939	1	AE008304	AE008304 Agrobacte	c 311	13	86.7	88080	2	AC097591	AC097591 Rattus no
c 239	13	86.7	15304	1	AE000692	AE000692 Aquifex a	c 312	13	86.7	89286	2	AC095922	AC095922 Rattus no
c 240	13	86.7	15861	3	AF036685	AF036685 Caenorhab	c 313	13	86.7	91268	8	AF004895	AF004895 Lotus jap
c 241	13	86.7	16876	1	AE000002	AE000002 Mycoplasma	c 314	13	86.7	91331	9	AL450386	AL450386 Human DNA
c 242	13	86.7	20285	3	AC024852	AC024852 Caenorhab	c 315	13	86.7	92491	8	ATF17114	ATF17114 Arabidops
c 243	13	86.7	20674	1	AE008854	AE008854 Salmonell	c 316	13	86.7	94984	9	AC114804	AC114804 Homo sapi
c 244	13	86.7	23838	2	AC019968	AC019968 Drosophila	c 317	13	86.7	95922	1	AL358934	AL358934 Human DNA
c 245	13	86.7	24089	2	AC013138	AC013138 Drosophila	c 318	13	86.7	96208	1	AL596174	AL596174 Listeria
c 246	13	86.7	25464	2	AC104234	AC104234 Homo sapi	c 319	13	86.7	96975	9	AC004975	AC004975 Homo sapi
c 247	13	86.7	25638	1	EC028379	EC028379 Escherichia	c 320	13	86.7	97846	9	AC015980	AC015980 Homo sapi
c 248	13	86.7	26536	1	AE001244	AE001244 Treponema	c 321	13	86.7	98597	9	AC008416	AC008416 Homo sapi
c 249	13	86.7	27653	2	AC094247	AC094247 Rattus no	c 322	13	86.7	98645	3	AC005267	AC005267 Drosophila
c 250	13	86.7	29774	1	AF193754	AF193754 Zymomonas	c 323	13	86.7	98770	9	HS36411	HS36411 Human DNA
c 251	13	86.7	31427	2	AC013843	AC013843 Drosophila	c 324	13	86.7	99329	2	AC099247	AC099247 Rattus no
c 252	13	86.7	32727	3	AF047660	AF047660 Caenorhab	c 325	13	86.7	100002	2	AC020372	AC020372 Drosophila
c 253	13	86.7	33001	1	SCC123	SCC123 Streptomy	c 326	13	86.7	101607	8	AF004334	AF004334 Oryza sat
c 254	13	86.7	33148	2	AC015180	AC015180 Streptomy	c 327	13	86.7	103242	2	AC097649	AC097649 Homo sapi
c 255	13	86.7	33810	1	SCB6	SCB6 Streptomy	c 328	13	86.7	103531	2	AC106260	AC106260 Rattus no
c 256	13	86.7	34074	1	SCF81	SCF81 Streptomy	c 329	13	86.7	106553	2	AC094270	AC094270 Rattus no
c 257	13	86.7	35100	6	I96182	I96182 Sequence 19	c 330	13	86.7	107262	2	AC105668	AC105668 Rattus no
c 258	13	86.7	36413	2	AC097272	AC097272 Hylobates	c 331	13	86.7	107372	2	AC098415	AC098415 Rattus no
c 259	13	86.7	36615	2	AC014144	AC014144 Drosophila	c 332	13	86.7	110000	2	AC091528_1	AC091528_1 Continuation (2 of
c 260	13	86.7	39250	1	SV1011500	SV1011500 Streptomy	c 333	13	86.7	110000	2	AC125124_0	AC125124_0 Mus muscu
c 261	13	86.7	40835	2	AC101263	AC101263 Mus muscu	c 334	13	86.7	110000	2	AC125124_3	AC125124_3 Continuation (4 of
c 262	13	86.7	42006	2	AC118022	AC118022 Drosophila	c 335	13	86.7	111701	2	AC130906	AC130906 Rattus no
c 263	13	86.7	42706	2	AC115087	AC115087 Homo sapi	c 336	13	86.7	113794	2	AC129353	AC129353 Rattus no
c 264	13	86.7	42947	8	SPAC343	SPAC343 Human CSF-1	c 337	13	86.7	113916	9	HUAC003007	HUAC003007 Rattus no
c 265	13	86.7	44151	9	AL831769	AL831769 S.pombe c	c 338	13	86.7	114259	2	AC117057	AC117057 Rattus no
c 266	13	86.7	44334	3	AF077534	AF077534 Caenorhab	c 339	13	86.7	114963	2	AC100180	AC100180 Mus muscu
c 267	13	86.7	44334	3	AF077534	AF077534 Caenorhab	c 340	13	86.7	116481	9	AC092287	AC092287 Homo sapi
c 268	13	86.7	44496	10	AL645975	AL645975 Mouse DNA	c 341	13	86.7	116679	9	AC123416	AC123416 Rattus no
c 269	13	86.7	44588	2	AC020529	AC020529 Drosophila	c 342	13	86.7	118068	9	AL356798	AL356798 Human DNA
c 270	13	86.7	45848	2	AC013885	AC013885 Drosophila	c 343	13	86.7	118294	2	AC121447	AC121447 Rattus no
c 271	13	86.7	51288	9	AL627210	AL627210 Human DNA	c 344	13	86.7	119087	2	CNS08C86	CNS08C86 Oryza sat
c 272	13	86.7	51411	2	AC101008	AC101008 Mus muscu	c 345	13	86.7	119141	2	AC096826	AC096826 Rattus no
c 273	13	86.7	52286	2	AC115957	AC115957 Mus muscu	c 346	13	86.7	119593	2	AC015799	AC015799 Homo sapi
c 274	13	86.7	54233	2	AC100456	AC100456 Mus muscu	c 347	13	86.7	119806	9	AL137795	AL137795 Human DNA
c 275	13	86.7	56376	2	AC084338	AC084338 Homo sapi	c 348	13	86.7	120510	9	AL356457	AL356457 Human DNA
c 276	13	86.7	59096	2	AC101634	AC101634 Mus muscu	c 349	13	86.7	120841	9	AC008162	AC008162 Homo sapi
c 277	13	86.7	59389	2	AC095557	AC095557 Rattus no	c 350	13	86.7	120849	2	AC087148	AC087148 Mus muscu
c 278	13	86.7	59805	2	AC101151	AC101151 Mus muscu	c 351	13	86.7	121492	8	OSJN00104	OSJN00104 Oryza sat
c 279	13	86.7	60009	39	AC015507	AC015507 Homo sapi	c 352	13	86.7	121679	2	AC120952	AC120952 Rattus no
c 280	13	86.7	60740	8	AB016557	AB016557 Homo sapi	c 353	13	86.7	122557	2	AC069013	AC069013 Mus muscu
c 281	13	86.7	61290	8	AB017065	AB017065 Arabidops	c 354	13	86.7	123907	9	AC083851	AC083851 Homo sapi
c 282	13	86.7	62355	3	AC084472	AC084472 Caenorhab	c 355	13	86.7	125099	9	AC006251	AC006251 Homo sapi
c 283	13	86.7	63229	2	AC111184	AC111184 Homo sapi	c 356	13	86.7	126128	2	AC111941	AC111941 Rattus no
c 284	13	86.7	63493	2	AC102474	AC102474 Mus muscu	c 357	13	86.7	126220	2	AC103157	AC103157 Rattus no

C 358	13	86.7	127452	2	AC110099	Rattus no	C 431	13	86.7	157546	9	AC108360	Homo sapi
C 359	13	86.7	127824	9	AL592205	Human DNA	C 432	13	86.7	157968	2	AC118890	Rattus no
C 360	13	86.7	128137	2	AP003798	Oryza sat	C 433	13	86.7	158043	2	AC105270	Homo sapi
C 361	13	86.7	129413	9	AC020992	Homo sapi	C 434	13	86.7	158382	2	AC016507	Homo sapi
C 362	13	86.7	129923	2	AC126617	Rattus no	C 435	13	86.7	158395	9	AC010614	Homo sapi
C 363	13	86.7	130569	9	CNS08CBB	Human chr	C 436	13	86.7	158897	2	AC116207	Rattus no
C 364	13	86.7	130628	2	AC010992	D90907 synechocyst	C 437	13	86.7	158919	2	AC108624	Rattus no
C 365	13	86.7	132419	1	D90907	AC109059 Rattus no	C 438	13	86.7	159158	9	AL359915	Human DNA
C 366	13	86.7	133213	2	AC109059	AC087147 Mus muscu	C 439	13	86.7	159688	2	AC087311	Homo sapi
C 367	13	86.7	133276	2	AC087147	AC125305 Rattus no	C 440	13	86.7	160083	2	AC129367	Rattus no
C 368	13	86.7	134353	2	AC125305	AL354923 Human DNA	C 441	13	86.7	160141	8	AP003142	Oryza sat
C 369	13	86.7	134965	9	AL354923	AC118514 Rattus no	C 442	13	86.7	160147	8	OSJN00232	Oryza sat
C 370	13	86.7	136062	2	AC118514	AP005443 Oryza sat	C 443	13	86.7	160678	2	AC097200	Rattus no
C 371	13	86.7	136767	8	AP005443	AC010918 Drosophil	C 444	13	86.7	161150	2	AC126240	Felis cat
C 372	13	86.7	137956	2	AC010918	AP005128 Oryza sat	C 445	13	86.7	161970	2	AC027706	Homo sapi
C 373	13	86.7	138340	2	AP005128	AC022778 Homo sapi	C 446	13	86.7	162000	2	AC122666	Rattus no
C 374	13	86.7	138953	9	AC022778	AP002525 Oryza sat	C 447	13	86.7	162609	2	AC097083	Rattus no
C 375	13	86.7	139152	8	AP002525	AF325155 Spodopter	C 448	13	86.7	162693	3	AC097083	Rattus no
C 376	13	86.7	139342	14	AF325155	AC007285 Oryza sat	C 449	13	86.7	162923	2	AL391359	Drosophil
C 377	13	86.7	140619	9	AC007285	AP005558 Oryza sat	C 450	13	86.7	162996	2	AC044808	Mus muscu
C 378	13	86.7	141428	2	AP005558	AC120739 Rattus no	C 451	13	86.7	163849	2	AC044808	Mus muscu
C 379	13	86.7	142127	2	AC120739	AP002899 Oryza sat	C 452	13	86.7	163888	2	AC024432	Homo sapi
C 380	13	86.7	143710	8	AP002899	AC120290 Rattus no	C 453	13	86.7	163908	9	AC007050	Homo sapi
C 381	13	86.7	144097	2	AC120290	AC097178 Rattus no	C 454	13	86.7	164018	2	AC097104	Homo sapi
C 382	13	86.7	144348	2	AC097178	AC123948 Mus muscu	C 455	13	86.7	164304	2	AC095537	Rattus no
C 383	13	86.7	144734	2	AC123948	AC096856 Oryza sat	C 456	13	86.7	164468	2	AC112594	Rattus no
C 384	13	86.7	145472	2	AC096856	AC027473 Homo sapi	C 457	13	86.7	165098	3	AC018490	Rattus no
C 385	13	86.7	146017	2	AC027473	AC123262 Rattus no	C 458	13	86.7	165399	2	AL840627	Danio rer
C 386	13	86.7	146308	2	AC123262	AC128902 Rattus no	C 459	13	86.7	166299	2	AC127244	Mus muscu
C 387	13	86.7	146587	2	AC128902	AC127100 Rattus no	C 460	13	86.7	166667	9	AC108513	Homo sapi
C 388	13	86.7	146853	2	AC127100	AP004675 Oryza sat	C 461	13	86.7	166697	2	AC115290	Mus muscu
C 389	13	86.7	146884	2	AP004675	AC120235 Rattus no	C 462	13	86.7	166697	2	AC115290	Mus muscu
C 390	13	86.7	147327	9	AC097455	AC094684 Rattus no	C 463	13	86.7	166847	9	AC008393	Homo sapi
C 391	13	86.7	147522	2	AC120235	AC012610 Rattus no	C 464	13	86.7	167022	9	AC010238	Homo sapi
C 392	13	86.7	147554	2	AC094684	AC012615 Homo sapi	C 465	13	86.7	167164	2	AC098167	Rattus no
C 393	13	86.7	147688	2	AC012610	AC012615 Homo sapi	C 466	13	86.7	167667	2	AL449084	Homo sapi
C 394	13	86.7	148252	9	AC012615	AC123735 Rattus no	C 467	13	86.7	167735	2	AC009794	Homo sapi
C 395	13	86.7	149599	2	AC112375	AP000556 Homo sapi	C 468	13	86.7	167830	2	AC027768	Homo sapi
C 396	13	86.7	149618	9	AP000556	AL772263 Danio rer	C 469	13	86.7	167926	3	AC023685	Drosophil
C 397	13	86.7	150036	9	AP000557	AC119667 Rattus no	C 470	13	86.7	168008	9	AC008544	Homo sapi
C 398	13	86.7	150259	2	AL772263	AC119667 Rattus no	C 471	13	86.7	168263	9	AC009124	Homo sapi
C 399	13	86.7	151021	9	AC119667	AL592285 Human DNA	C 472	13	86.7	168316	2	AC101775	Mus muscu
C 400	13	86.7	151465	2	AC119667	AC016747 Homo sapi	C 473	13	86.7	168544	9	AL513307	Human DNA
C 401	13	86.7	152113	9	AL592285	AC016506 Homo sapi	C 474	13	86.7	168601	3	AC007471	Drosophil
C 402	13	86.7	152345	9	AC016747	AC128193 Rattus no	C 475	13	86.7	168820	2	AC131149	Homo sapi
C 403	13	86.7	152533	2	AC016506	AC006020 Homo sapi	C 476	13	86.7	169335	2	AP005566	Oryza sat
C 404	13	86.7	152668	2	AC128193	AC093981 Rattus no	C 477	13	86.7	169464	2	AC098176	Rattus no
C 405	13	86.7	152811	9	AC006020	AC093981 Rattus no	C 478	13	86.7	170094	2	AC120811	Rattus no
C 406	13	86.7	153166	2	AC093981	AC008332 Drosophil	C 479	13	86.7	170163	3	AC009457	Drosophil
C 407	13	86.7	153250	3	AC008332	AC022953 Homo sapi	C 480	13	86.7	170596	2	AC099185	Rattus no
C 408	13	86.7	153315	2	AC022953	AC090484 Genomic s	C 481	13	86.7	170924	2	AC128333	Rattus no
C 409	13	86.7	153322	8	AC090484	AC018933 Homo sapi	C 482	13	86.7	171004	2	AC034202	Homo sapi
C 410	13	86.7	153348	2	AC018933	AC098544 Rattus no	C 483	13	86.7	172400	9	AC090883	Homo sapi
C 411	13	86.7	153358	2	AC098544	AC108343 Rattus no	C 484	13	86.7	172462	2	AL833789	Danio rer
C 412	13	86.7	153798	2	AC108343	AC097886 Rattus no	C 485	13	86.7	172854	3	AC023706	Drosophil
C 413	13	86.7	153904	2	AC097886	AC006197 Homo sapi	C 486	13	86.7	172902	2	AL358816	Homo sapi
C 414	13	86.7	154354	9	AC006197	AC073620 Homo sapi	C 487	13	86.7	173249	2	AC123468	Rattus no
C 415	13	86.7	154608	2	AC073620	AC099472 Mus muscu	C 488	13	86.7	173302	2	AC008137	Drosophil
C 416	13	86.7	154673	3	AC099472	AC099018 Drosophil	C 489	13	86.7	173441	2	AC080112	Homo sapi
C 417	13	86.7	154840	3	AC099018	AP004222 Oryza sat	C 490	13	86.7	173713	2	AC095840	Rattus no
C 418	13	86.7	155263	8	AP004222	AL354997 Human DNA	C 491	13	86.7	173765	9	AC090457	Homo sapi
C 419	13	86.7	156077	2	AL354997	AC109563 Rattus no	C 492	13	86.7	173836	9	AC027125	Homo sapi
C 420	13	86.7	156088	2	AC109563	AC006472 Drosophil	C 493	13	86.7	173836	9	AC118421	Rattus no
C 421	13	86.7	156346	3	AC006472	AL357774 Human DNA	C 494	13	86.7	173909	2	AC128406	Rattus no
C 422	13	86.7	156498	9	AL357774	AC013363 Homo sapi	C 495	13	86.7	174151	2	AC120483	Rattus no
C 423	13	86.7	156619	2	AC013363	AL049594 Human DNA	C 496	13	86.7	174157	3	AC023711	Drosophil
C 424	13	86.7	156791	9	AL049594	AC127950 Rattus no	C 497	13	86.7	174265	2	AL772355	Homo sapi
C 425	13	86.7	156874	2	AC127950	AC020006 Drosophil	C 498	13	86.7	174406	3	AC104516	Drosophil
C 426	13	86.7	156908	2	AC020006	AL606591 Oryza sat	C 499	13	86.7	174569	9	AC022533	Homo sapi
C 427	13	86.7	156939	2	OSJN00030	AC011095 Homo sapi	C 500	13	86.7	174661	2	AC098609	Rattus no
C 428	13	86.7	157051	9	AC011095	AL358856 Homo sapi	C 501	13	86.7	174688	2	AC124395	Mus muscu
C 429	13	86.7	157080	2	AL358856	AC036212 Homo sapi	C 502	13	86.7	174719	2	AL840636	Danio rer
C 430	13	86.7	157393	2	AC036212		C 503	13	86.7	175507	2	AL807799	Danio rer

504	13	86.7	175511	2	AC023924	AC023924 Homo sapi	13	86.7	193690	2	AC121603	AC121603 Mus muscu
c 505	13	86.7	175669	3	AC008235	AC008235 Drosophil	13	86.7	193924	2	AC098275	AC098275 Rattus no
c 506	13	86.7	175945	2	AC022147	AC022147 Homo sapi	13	86.7	194056	9	AL590708	AL590708 Human DNA
c 507	13	86.7	176051	9	AC023490	AC023490 Homo sapi	13	86.7	194078	9	AL590708	AL590708 Human DNA
c 508	13	86.7	176099	2	AC167779	AC167779 Mus muscu	13	86.7	194178	9	AL590708	AL590708 Human DNA
c 509	13	86.7	176310	2	AC109004	AC109004 Rattus no	13	86.7	194914	2	AC114359	AC114359 Rattus no
c 510	13	86.7	176547	2	AC126433	AC126433 Mus muscu	13	86.7	195783	2	AC109104	AC109104 Rattus no
c 511	13	86.7	176933	3	AC009350	AC009350 Drosophil	13	86.7	196560	2	AC023640	AC023640 Homo sapi
c 512	13	86.7	176954	2	AC126680	AC126680 Mus muscu	13	86.7	196724	10	AL590963	AL590963 Mouse DNA
c 513	13	86.7	177028	3	AC008315	AC008315 Drosophil	13	86.7	197389	9	AL358791	AL358791 Human DNA
c 514	13	86.7	177407	9	AC073916	AC073916 Homo sapi	13	86.7	197561	2	AC093407	AC093407 Mus muscu
c 515	13	86.7	177514	2	AC126919	AC126919 Bos tauru	13	86.7	197841	2	AC105322	AC105322 Mus muscu
c 516	13	86.7	177739	2	AC127423	AC127423 Mus muscu	13	86.7	198412	2	AC098236	AC098236 Rattus no
c 517	13	86.7	178254	9	AL731541	AL731541 Human DNA	13	86.7	198413	2	AC130022	AC130022 Rattus no
c 518	13	86.7	178627	3	AC010068	AC010068 Drosophil	13	86.7	198489	2	AC067809	AC067809 Homo sapi
c 519	13	86.7	178676	2	AC087868	AC087868 Mus muscu	13	86.7	199016	3	AC068204	AC068204 Drosophil
c 520	13	86.7	178892	2	AC130794	AC130794 Fells cat	13	86.7	199050	1	AJ414159	AJ414159 Yersinia
c 521	13	86.7	180154	2	AC123464	AC123464 Rattus no	13	86.7	199268	2	AC099523	AC099523 Homo sapi
c 522	13	86.7	180179	2	AC018881	AC018881 Homo sapi	13	86.7	199420	9	CNS01DVV	AL136040 Human chr
c 523	13	86.7	180355	2	AC022167	AC022167 Homo sapi	13	86.7	199777	2	AC098064	AC098064 Rattus no
c 524	13	86.7	180425	3	AC008229	AC008229 Drosophil	13	86.7	199794	2	AC026633	AC026633 Homo sapi
c 525	13	86.7	180485	2	AC027145	AC027145 Homo sapi	13	86.7	200123	2	AC126764	AC126764 Homo sapi
c 526	13	86.7	180766	9	AC090691	AC090691 Homo sapi	13	86.7	200289	2	AC090681	AC090681 Homo sapi
c 527	13	86.7	180790	9	AC012173	AC012173 Homo sapi	13	86.7	200594	9	AC005632	AC005632 Homo sapi
c 528	13	86.7	181026	2	AC119640	AC119640 Rattus no	13	86.7	200883	2	AL590107	AL590107 Homo sapi
c 529	13	86.7	181261	2	AC010899	AC010899 Mus muscu	13	86.7	201001	2	AC118088	AC118088 Rattus no
c 530	13	86.7	181320	2	AC095303	AC095303 Rattus no	13	86.7	201105	9	AC025668	AC025668 Mus muscu
c 531	13	86.7	181827	2	AC055854	AC055854 Homo sapi	13	86.7	201155	9	AC020703	AC020703 Homo sapi
c 532	13	86.7	182280	9	AL136981	AL136981 Human DNA	13	86.7	201155	9	AC009086	AC009086 Homo sapi
c 533	13	86.7	182289	2	AC115341	AC115341 Rattus no	13	86.7	203216	2	AC097328	AC097328 Pan trogl
c 534	13	86.7	182427	2	AC061992	AC061992 Homo sapi	13	86.7	204379	2	AC131113	AC131113 Mus muscu
c 535	13	86.7	182601	3	AC009904	AC009904 Drosophil	13	86.7	204442	3	AE003747	AE003747 Drosophil
c 536	13	86.7	183089	10	AL663115	AL663115 Mouse DNA	13	86.7	206030	9	AC021439	AC021439 Homo sapi
c 537	13	86.7	183342	9	AC087490	AC087490 Homo sapi	13	86.7	207380	2	AC124566	AC124566 Mus muscu
c 538	13	86.7	183402	2	AC126231	AC126231 Bos tauru	13	86.7	207424	10	AC090489	AC090489 Genomic s
c 539	13	86.7	183591	9	AC008462	AC008462 Homo sapi	13	86.7	207739	2	AC113528	AC113528 Mus muscu
c 540	13	86.7	183656	9	AC009487	AC009487 Homo sapi	13	86.7	208064	9	AL392043	AL392043 Human DNA
c 541	13	86.7	183675	2	AL845320	AL845320 Danio rer	13	86.7	209320	2	AC060776	AC060776 Homo sapi
c 542	13	86.7	183714	2	AC103508	AC103508 Rattus no	13	86.7	209502	2	AC093930	AC093930 Rattus no
c 543	13	86.7	184026	2	AC098923	AC098923 Rattus no	13	86.7	209706	2	AC067885	AC067885 Homo sapi
c 544	13	86.7	184140	9	AC090630	AC090630 Homo sapi	13	86.7	210472	9	AC035139	AC035139 Homo sapi
c 545	13	86.7	184346	2	AC069138	AC069138 Homo sapi	13	86.7	210514	10	AC117199	AC117199 Mus muscu
c 546	13	86.7	185329	2	AC023587	AC023587 Homo sapi	13	86.7	210727	2	AC122864	AC122864 Mus muscu
c 547	13	86.7	185415	9	HS121M24	AL354046 Homo sapi	13	86.7	212208	2	AC079024	AC079024 Mus muscu
c 548	13	86.7	185589	2	AC098143	AC098143 Rattus no	13	86.7	213288	2	AL773558	AL773558 Danio rer
c 549	13	86.7	185600	8	AP003563	AP003563 Oryza sat	13	86.7	213732	1	AE001862	AE001862 Deinococc
c 550	13	86.7	185617	2	AC126920	AC126920 Bos tauru	13	86.7	214465	9	AC023027	AC023027 Mus muscu
c 551	13	86.7	186241	3	AC007086	AC007086 Drosophil	13	86.7	214702	9	AC020689	AC020689 Homo sapi
c 552	13	86.7	186341	2	AL844197	AL844197 Danio rer	13	86.7	215050	1	AL646057	AL646057 Ralstonia
c 553	13	86.7	186542	2	AC130961	AC130961 Rattus no	13	86.7	215366	10	AL603836	AL603836 Mouse DNA
c 554	13	86.7	186980	2	AC093667	AC093667 Homo sapi	13	86.7	215788	9	AC007308	AC007308 Homo sapi
c 555	13	86.7	187215	2	AL158822	AL158822 Human DNA	13	86.7	216105	10	AC091777	AC091777 Mus muscu
c 556	13	86.7	187336	9	AC025880	AC025880 Homo sapi	13	86.7	217422	9	AC108721	AC108721 Homo sapi
c 557	13	86.7	187347	2	AC025880	AC025880 Homo sapi	13	86.7	217622	3	AE003743	AE003743 Drosophil
c 558	13	86.7	188563	9	AL136965	AL136965 Homo sapi	13	86.7	217859	2	AC112891	AC112891 Rattus no
c 559	13	86.7	188696	2	AL512629	AL512629 Human DNA	13	86.7	218952	2	AL606984	AL606984 Mus muscu
c 560	13	86.7	188926	9	AC012182	AC012182 Homo sapi	13	86.7	219125	2	AL772165	AL772165 Mus muscu
c 561	13	86.7	189050	1	AL646069	AL646069 Ralstonia	13	86.7	219200	10	AL589701	AL589701 Mouse DNA
c 562	13	86.7	189333	1	RME603647	RME603647 Rhizobium	13	86.7	219218	2	AC020817	AC020817 Mus muscu
c 563	13	86.7	189534	2	AL354656	AL354656 Homo sapi	13	86.7	219809	2	AC125058	AC125058 Mus muscu
c 564	13	86.7	189805	2	AC109479	AC109479 Homo sapi	13	86.7	220940	10	AL671913	AL671913 Mouse DNA
c 565	13	86.7	190301	3	AC009352	AC009352 Drosophil	13	86.7	221049	2	AL691421	AL691421 Mus muscu
c 566	13	86.7	190757	10	AC087840	AC087840 Mus muscu	13	86.7	221792	2	AC124711	AC124711 Mus muscu
c 567	13	86.7	190856	2	AC009160	AC009160 Homo sapi	13	86.7	222235	2	AC074148	AC074148 Mus muscu
c 568	13	86.7	190944	2	AC122960	AC122960 Rattus no	13	86.7	222574	2	AL772227	AL772227 Mus muscu
c 569	13	86.7	191023	2	AC128255	AC128255 Rattus no	13	86.7	224067	2	AC092259	AC092259 Mus muscu
c 570	13	86.7	191108	9	AC097265	AC097265 Pan trogl	13	86.7	225448	2	AC122296	AC122296 Mus muscu
c 571	13	86.7	191358	9	AC012533	AC012533 Homo sapi	13	86.7	225514	2	AC024142	AC024142 Mus muscu
c 572	13	86.7	191549	9	AC010582	AC010582 Homo sapi	13	86.7	226903	2	AC079272	AC079272 Mus muscu
c 573	13	86.7	191590	3	AC023722	AC023722 Drosophil	13	86.7	229655	3	AE003707	AE003707 Drosophil
c 574	13	86.7	191630	2	AC114875	AC114875 Rattus no	13	86.7	236043	2	AC115234	AC115234 Rattus no
c 575	13	86.7	191672	2	AC020794	AC020794 Mus muscu	13	86.7	236679	2	AC118545	AC118545 Mus muscu
c 576	13	86.7	192802	9	AC011753	AC011753 Homo sapi	13	86.7	241753	2	AC019149	AC019149 Homo sapi



650	13	86.7	243076	3	AE003683	AE003683 Drosophill	c 723	12	80.0	414	5	AF401585	AF401585 Ictalarus
c 651	13	86.7	250688	2	AC098059	AC098059 Rattus no	c 724	12	80.0	414	6	AX329865	AX329865 Sequence
c 652	13	86.7	253648	3	AE003638	AE003638 Drosophill	c 725	12	80.0	414	6	AX331438	AX331438 Sequence
c 653	13	86.7	254438	3	AE003614	AE003614 Drosophill	c 726	12	80.0	438	8	ZMFBFERUM	X73300 Z.mays sequ
654	13	86.7	256972	2	AC116577	AC116577 Mus muscu	727	12	80.0	447	6	ARI53967	ARI53967 Sequence
655	13	86.7	260699	2	AC006893	AC006893 Caenorhab	728	12	80.0	455	9	HSSPGSC02	AF080512 Homo sapi
c 656	13	86.7	266574	2	AC087129	AC087129 Mus muscu	c 729	12	80.0	461	6	AX331371	AX331371 Sequence
c 657	13	86.7	267759	2	AC079418	AC079418 Mus muscu	c 730	12	80.0	462	9	HSEMX1	X68879 H.sapiens E
658	13	86.7	268200	1	AP000061	AP000061 Aeropyrum	c 731	12	80.0	480	9	AB041354S2	AB041355 Homo sapi
c 659	13	86.7	271743	3	AE003835	AE003835 Drosophill	c 732	12	80.0	490	11	G72657	G72657 MARC 5847-5
c 660	13	86.7	281530	1	AP002550	AP002550 Escherich	c 733	12	80.0	495	1	AY072237	AY072237 Unculture
c 661	13	86.7	294250	1	AP001517	AP001517 Bacillus	c 734	12	80.0	495	1	AY072238	AY072238 Unculture
c 662	13	86.7	296992	3	AE003833	AE003833 Drosophill	c 735	12	80.0	495	1	AF392405	AF392405 Homo sapi
c 663	13	86.7	298705	3	AE003510	AE003510 Drosophill	c 736	12	80.0	497	9	AY052945	AY052945 Homo sapi
c 664	13	86.7	298750	1	AP005375	AP005375 Thermosyn	c 737	12	80.0	504	9	HSLCC1F01	226256 H.sapiens i
c 665	13	86.7	299350	1	SME591786	AL591786 Sinorhizo	c 738	12	80.0	519	1	AY072232	AY072232 Unculture
c 666	13	86.7	303823	3	AE003462	AE003462 Drosophill	c 739	12	80.0	536	9	AF208488	AF208488 Homo sapi
c 667	13	86.7	307120	1	CNSPAX03	AJ248285 Pyrococcu	c 740	12	80.0	540	8	CNS01DPI	AL117101 Botrytis
668	13	86.7	307962	1	AP002564	AP002564 Escherich	741	12	80.0	543	1	AF246422	AF246422 Acidithio
669	13	86.7	311208	6	AX417049	AX417049 Sequence	742	12	80.0	550	6	AX154863	AX154863 Sequence
c 670	13	86.7	319012	3	AE003596	AE003596 Drosophill	c 743	12	80.0	552	1	AV123697	AV123697 Granulica
c 671	13	86.7	323461	3	AE003491	AE003491 Drosophill	c 744	12	80.0	552	8	AB075378	AB075378 Oryza sat
c 672	13	86.7	327927	3	AE003439	AE003439 Drosophill	c 745	12	80.0	576	6	ARI74766	ARI74766 Sequence
c 673	13	86.7	337133	2	AC110384	AC110384 Rattus no	746	12	80.0	588	6	AX381056	AX381056 Sequence
c 674	13	86.7	340857	1	AP003010	AP003010 Mesorhizo	747	12	80.0	605	8	AF284970	AF284970 Carex bas
c 675	13	86.7	341880	1	AP003589	AP003589 Nostoc sp	748	12	80.0	607	8	AF284972	AF284972 Carex ros
c 676	13	86.7	347800	1	AP000060	AP000060 Aeropyrum	749	12	80.0	608	8	AF027427	AF027427 Carex sup
c 677	13	86.7	349980	6	AX041919	AX041919 Sequence	750	12	80.0	608	8	AF285057	AF285057 Cymophyll
c 678	13	86.7	349980	6	AX417036	AX417036 Sequence	751	12	80.0	608	9	D86059	D86059 Homo sapien
c 679	12	80.0	19	6	AX129897	AX129897 Sequence	752	12	80.0	609	8	AF027425	AF027425 Carex wil
680	12	80.0	19	6	AX129898	AX129898 Sequence	753	12	80.0	610	8	AF284977	AF284977 Carex pen
681	12	80.0	19	6	AX129899	AX129899 Sequence	754	12	80.0	634	9	HS326873	HS326873 Homo sapi
c 682	12	80.0	49	6	AX194378	AX194378 Sequence	c 755	12	80.0	636	8	CNS01DGO	AL116776 Botrytis
c 683	12	80.0	76	10	MMCA2IV6	X02899 Mouse gene	c 756	12	80.0	644	9	HUMCOL22	U76585 Human 180 k
c 684	12	80.0	108	4	AB073620	AB073620 Oryctolag	c 757	12	80.0	647	4	OCU291432	AJ291432 Oryctolag
c 685	12	80.0	173	6	AX438778	AX438778 Sequence	c 758	12	80.0	651	9	HS342792	AJ342792 Homo sapi
c 686	12	80.0	198	8	AB019982	AB019982 Neolana sp	c 759	12	80.0	660	1	AF315434	AF315434 Unculture
c 687	12	80.0	198	10	NMEMX1	X68881 M.musculus	c 760	12	80.0	660	1	AF315444	AF315444 Unculture
c 688	12	80.0	221	8	AF027412	AF027412 Carex sax	c 761	12	80.0	660	1	AF315447	AF315447 Unculture
c 689	12	80.0	221	8	AF027413	AF027413 Carex sax	c 762	12	80.0	660	1	AF315448	AF315448 Unculture
c 690	12	80.0	221	8	AF027414	AF027414 Carex sax	c 763	12	80.0	660	1	AF315453	AF315453 Unculture
c 691	12	80.0	221	8	AF027417	AF027417 Carex jun	c 764	12	80.0	660	1	AF315456	AF315456 Unculture
c 692	12	80.0	221	8	AF027418	AF027418 Carex jun	c 765	12	80.0	660	1	AF315457	AF315457 Unculture
c 693	12	80.0	221	8	AF027419	AF027419 Carex jun	c 766	12	80.0	660	1	AF361791	AF361791 Azospiril
c 694	12	80.0	221	8	AF027420	AF027420 Carex jam	c 767	12	80.0	660	1	AF361795	AF361795 Alcaligen
c 695	12	80.0	221	8	AF027421	AF027421 Carex jam	c 768	12	80.0	660	1	AY074762	AY074762 Azospiril
c 696	12	80.0	221	8	AF027423	AF027423 Carex jam	c 769	12	80.0	661	6	AX381052	AX381052 Sequence
c 697	12	80.0	221	8	AF027430	AF027430 Carex bas	c 770	12	80.0	666	1	AF315441	AF315441 Unculture
c 698	12	80.0	222	8	AF027409	AF027409 Carex bac	c 771	12	80.0	667	6	AX401398	AX401398 Sequence
c 699	12	80.0	222	8	AF027411	AF027411 Carex bac	c 772	12	80.0	677	9	HSPFC2	AF005668 Homo sapi
c 700	12	80.0	222	8	AF027415	AF027415 Carex lat	c 773	12	80.0	681	1	AF048784	AF048784 Actinomyc
c 701	12	80.0	222	8	AF027416	AF027416 Carex lat	774	12	80.0	682	8	D64038	D64038 Oryza sativ
c 702	12	80.0	222	8	AF027424	AF027424 Carex wil	775	12	80.0	684	5	AF168081	AF168081 Guira gui
c 703	12	80.0	222	8	AF027426	AF027426 Carex wil	c 776	12	80.0	690	1	AY072227	AY072227 Achromoba
c 704	12	80.0	222	8	AF027431	AF027431 Carex bas	c 777	12	80.0	696	3	AF153423	AF153423 Drosophill
c 705	12	80.0	223	8	AF027410	AF027410 Carex bac	c 778	12	80.0	696	3	AF153424	AF153424 Drosophill
c 706	12	80.0	223	8	AF027428	AF027428 Carex sup	c 779	12	80.0	696	3	AF153425	AF153425 Drosophill
c 707	12	80.0	223	8	AF027429	AF027429 Carex sup	c 780	12	80.0	696	3	AF153426	AF153426 Drosophill
c 708	12	80.0	223	8	AF027432	AF027432 Carex bas	c 781	12	80.0	696	3	AF153427	AF153427 Drosophill
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c 710	12	80.0	281	9	HS164HL2F	257122 H.sapiens C	c 783	12	80.0	696	8	CNS01AXV	AF153429 Drosophill
c 711	12	80.0	318	1	AF246423	AF246423 Acidithio	c 784	12	80.0	696	9	HSTRUPFC6	AL113531 Botrytis
c 712	12	80.0	336	8	AY023844	AY023844 Oryza sat	c 785	12	80.0	700	2	AC105087	AC105087 Homo sapi
c 713	12	80.0	348	11	G36234	G36234 STS H14a225	786	12	80.0	711	6	AX046342	AX046342 Sequence
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c 800	12	80.0	815	8	AY074640	AY074640 Arabidops	c 873	12	80.0	1450	9	HSRARA1A1	AF088888 Homo sapi
c 801	12	80.0	819	10	AF033270	AF033270 Mus saxic	c 874	12	80.0	1471	10	MMU421520	AJ421520 Mus muscu
c 802	12	80.0	823	10	AF033273	AF033273 Mus minut	c 875	12	80.0	1473	6	A21795	A21795 F. oxysporum
c 803	12	80.0	824	3	AF001910	AF001910 Drosophill	c 876	12	80.0	1473	6	A23637	A23637 F. oxysporu
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c 808	12	80.0	846	6	AX081091	AX081091 Sequence	c 881	12	80.0	1473	6	AR072922	AR072922 Sequence
c 809	12	80.0	878	8	AF104107	AF104107 Triticum	c 882	12	80.0	1473	6	BD002249	BD002249 Cellulase
c 810	12	80.0	880	10	AF033271	AF033271 Mus cervi	c 883	12	80.0	1473	6	BD010853	BD010853 Cellulase
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c 824	12	80.0	963	1	AF322647	AF322647 Snorhizo	c 897	12	80.0	1543	6	AX409761	AX409761 Sequence
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c 837	12	80.0	1047	5	AF514365	AF514365 Hypseleot	c 910	12	80.0	1675	10	AF053328	AF053328 Cavia por
c 838	12	80.0	1047	5	AF514366	AF514366 Hypseleot	c 911	12	80.0	1684	9	HUMTTP	M63625 Human trist
c 839	12	80.0	1047	5	AF514369	AF514369 Hypseleot	c 912	12	80.0	1702	3	AF494043	AF494043 Physarum
c 840	12	80.0	1047	5	AF514370	AF514370 Hypseleot	c 913	12	80.0	1702	9	AK055976	AK055976 Homo sapi
c 841	12	80.0	1047	9	HUMBPAR	M63730 Human bullo	c 914	12	80.0	1715	9	AF246895	AF246895 Homo sapi
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c 847	12	80.0	1128	1	AF119937	AF119937 Unculture	c 920	12	80.0	1746	9	AF053327	AF053327 Cavia por
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c 850	12	80.0	1140	5	AF240745	AF240745 Morone ch	c 923	12	80.0	1823	8	AF099112	AF099112 Zea mays
c 851	12	80.0	1140	5	AF386579	AF386579 Percina a	c 924	12	80.0	1823	3	LMWCJNC	Z54138 L.major DNA
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c 861	12	80.0	1292	6	AR005009	AR005009 Sequence	c 934	12	80.0	1931	1	AF254578	AF254578 Mycobacte
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c 863	12	80.0	1292	6	AR076498	AR076498 Sequence	c 936	12	80.0	1948	10	AF053329	AF053329 Cavia por
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c 865	12	80.0	1351	3	AY071383	AY071383 Drosophill	c 938	12	80.0	1974	8	AK054866	AK054866 Homo sapi
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c 867	12	80.0	1380	3	AF116531	AF116531 Ceratitis	c 940	12	80.0	1999	8	TAFKBP77	Y07636 T.aestivum
c 868	12	80.0	1390	3	AF102237	AF102237 Drosophill	c 941	12	80.0	2000	8	ANGLAA5	X56442 A.niger gla

942	12	80.0	2010	9	AK057960 Homo sapi
943	12	80.0	2013	5	AB060971 Xenopus l
c 944	12	80.0	2013	6	AX429310 Sequence
945	12	80.0	2014	8	AF189369 Ajellomyc
946	12	80.0	2027	6	AX381046 Sequence
947	12	80.0	2042	9	AK057692 Homo sapi
948	12	80.0	2046	1	AJ404229 Rhodobact
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c 965	12	80.0	2179	1	MPHS970
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c 967	12	80.0	2192	1	STMAMV
968	12	80.0	2194	9	HSU10564
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c 970	12	80.0	2219	4	AF016649 Canis fam
c 971	12	80.0	2220	2	AC019634 Drosophil
972	12	80.0	2220	3	AE003068 Drosophil
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982	12	80.0	2295	4	AF338249 Sus scrof
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ACCESSION	AX194629	Sequence 99 from Patent WO0151659.			
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ORGANISM	Homo sapiens				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1	(bases 1 to 920)			
AUTHORS	Chu,T., Blumenfeld,M. and Cohen,D.				
TITLE	Biallelic markers derived from genomic regions carrying genes involved in central nervous system disorders				
JOURNAL	Patent: WO 0151659-A 99 19-JUL-2001;				
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Db	170 CCTTCTCGCCCTGTT 184				
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DEFINITION	Sequence 104 from Patent WO0151659.				
ACCESSION	AX194634				
VERSION	AX194634.1	GI:15385281			
KEYWORDS	human.				
SOURCE	human.				
ORGANISM	Homo sapiens				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1	(bases 1 to 920)			
AUTHORS	Chu,T., Blumenfeld,M. and Cohen,D.				
TITLE	Biallelic markers derived from genomic regions carrying genes involved in central nervous system disorders				
JOURNAL	Patent: WO 0151659-A 104 19-JUL-2001;				
GENSET (FR)					
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misc_feature	194..218				
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variation	206				
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ORIGIN					
Query Match	100.0%; Score 15; DB 6; Length 920;				

Best Local Similarity 100.0%; Pred. No. 47;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3  
HSETEX9  
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DEFINITION Homo sapiens partial SLC6A2 gene for norepinephrine transporter, exons 9-10.  
ACCESSION X91127  
VERSION X91127.1 GI:1143488  
KEYWORDS norepinephrine transporter; SLC6A2 gene.  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 980)  
AUTHORS Porzgen, P., Bonisch, H. and Bruss, M.  
TITLE Molecular cloning and organization of the coding region of the human norepinephrine transporter gene  
JOURNAL Biochem. Biophys. Res. Commun. 215 (3), 1145-1150 (1995)  
MEDLINE 96078050  
PUBMED 7488042  
REFERENCE 2 (bases 1 to 980)  
AUTHORS Porzgen, P., Bonisch, H., Hammermann, R. and Bruss, M.  
TITLE The human noradrenaline transporter gene contains multiple polyadenylation sites and two alternatively spliced C-terminal exons  
JOURNAL Biochim. Biophys. Acta 1398 (3), 365-370 (1998)  
MEDLINE 98322125  
PUBMED 9655936  
REFERENCE 3 (bases 1 to 980)  
AUTHORS Bonisch, H.  
TITLE Direct Submission  
JOURNAL Submitted (30-AUG-1995) H. Bonisch, Institut fuer Pharmakologie und Toxikologie, Universitaet Bonn, Reuterstr 2b, 53113 Bonn, FRG  
COMMENT Related sequences: M65105 and X57700.

## FEATURES

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218 a 275 c 246 g 238 t 3 others

BASE COUNT  
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 47;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCTCGCCCTGTT 15

Db 230 CCTTCTCGCCCTGTT 244

RESULT 4  
BC000563  
LOCUS BC000563 1411 bp mRNA linear PRI 12-JUL-2001  
DEFINITION Homo sapiens, clone IMAGE:3162672, mRNA, partial cds.  
ACCESSION BC000563  
VERSION BC000563.1 GI:12653576  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 1411)  
AUTHORS Strausberg, R.  
TITLE Direct Submission  
JOURNAL Submitted (15-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
COMMENT Contact: MGC help desk  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland.  
Web site: [http://www.nisc.nih.gov/nisc\\_mgc@nigr1.nih.gov](http://www.nisc.nih.gov/nisc_mgc@nigr1.nih.gov)  
Contact: [nisc\\_mgc@nigr1.nih.gov](mailto:nisc_mgc@nigr1.nih.gov)  
Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R., Lim, M., Maduro, O.L., Masiello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J., Tsong, L.-E., Touchman, J.W., Tsurgeon, C., Vogt, J.D., Walker, M.A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAL Plate: 5 Row: 1 Column: 7  
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

## FEATURES

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BASE COUNT  
ORIGIN

Query Match 100.0%; Score 15; DB 9; Length 1411;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CCTTCTCGCCCTGTT 15
Db 496 CCTTCTCGCCCTGTT 510

RESULT 5
LOCUS HUMNORTR 1983 bp mRNA linear PRI 07-JAN-1995
DEFINITION Human noradrenaline transporter mRNA, complete cds.
ACCESSION M65105
VERSION M65105.1 GI:189257
KEYWORDS noradrenaline transporter.
SOURCE Human, cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Pacholczyk,T., Blakely,R.D. and Amara,S.G.
TITLE Expression cloning of a cocaine- and antidepressant-sensitive human
noradrenaline transporter
JOURNAL Nature 350 (6316), 350-354 (1991)
MEDLINE 91179515
PUBMED 2008212
FEATURES
Location/Qualifiers
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61..1914
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BASE COUNT 383 a 602 c 530 g 468 t
ORIGIN
Query Match 100.0%; Score 15; DB 9; Length 1983;
Best Local Similarity 100.0%; pred. No. 46;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
Db 1422 CCTTCTCGCCCTGTT 1436

RESULT 6
LOCUS HUMCOLA1XV/c 2127 bp mRNA linear PRI 27-APR-1993
DEFINITION Homo sapiens alpha-1 type XV collagen mRNA sequence.
ACCESSION L01697
VERSION L01697.1 GI:180858
KEYWORDS alpha-1 type XV collagen.
SOURCE Homo sapiens (library: gt11 from Clonotech Laboratories) placenta
cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Myers,J.C., Kivirikko,S., Gordon,M.K., Dion,A.S. and
Pihlajaniemi,T.
TITLE Identification of a previously unknown human collagen chain, alpha
1(XV), characterized by extensive interruptions in the
triple-helical region
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (21), 10144-10148 (1992)
MEDLINE 93066196
PUBMED 1279671
REFERENCE
AUTHORS Kivirikko,S., Heinamaki,P., Rehn,M., Honkanen,N., Myers,J.C. and
Pihlajaniemi,T.
TITLE Primary structure of the alpha 1 chain of human type XV collagen
and exon-intron organization in the 3' region of the corresponding
gene
JOURNAL J. Biol. Chem. 269 (7), 4773-4779 (1994)
MEDLINE 94148920
PUBMED 8106446
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 44;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15
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Db 2673 CCTTCTCGCCCTGTT 2659

RESULT 8
AC020425
LOCUS      Drosophila melanogaster, 14621 bp DNA linear HTG 03-JAN-2000
DEFINITION Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
           pieces.
ACCESSION AC020425
VERSION AC020425.1 GI:6664472
KEYWORDS HTG; HTGS_PHASE2.
SOURCE Drosophila melanogaster.
ORGANISM Drosophila melanogaster
          Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
          Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
          Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 14621)
AUTHORS Adams,M. and Venter,J.C.
TITLE Direct Submission
JOURNAL Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
COMMENT This sequence was identified as CDM:10213135 by the submitter.
For more information on this record e-mail to flyecelera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
FEATURES
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Best Local Similarity 100.0%; Pred. No. 42;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15
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Db 4882 CCTTCTCGCCCTGTT 4896

RESULT 9
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LOCUS      Mus musculus clone RP23-117121, LOW-PASS SEQUENCE SAMPLING.
DEFINITION AC101376
ACCESSION AC101376
VERSION AC101376.1 GI:17060151
KEYWORDS HTG; HTGS_PHASE0.
SOURCE Mus musculus.
ORGANISM Mus musculus
          Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 61956)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Mus musculus, clone RP23-117121
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 61956)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
          Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B.,
          Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
          Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
          Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
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Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Hearford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kanat, A., Karatas, A., Kellis, C., LaRoque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, T., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RN/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

----- Project Information

Center project name: L16579

Center clone name: 117\_I\_21

-----

\* NOTE: This record contains 79 individual

\* sequencing reads that have not been assembled into

\* contigs. Runs of N are used to separate the reads

\* and the order in which they appear is completely

\* arbitrary. Low-pass sequence sampling is useful for

\* identifying clones that may be gene-rich and allows

\* overlap relationships among clones to be deduced.

\* However, it should not be assumed that this clone

\* will be sequenced to completion. In the event that

\* the record is updated, the accession number will

\* be preserved.

\* 1 630: contig of 630 bp in length

\* 631 730: gap of 100 bp

\* 731 1391: contig of 661 bp in length

\* 1392 1491: gap of 100 bp

\* 1492 2138: contig of 647 bp in length

\* 2139 2238: gap of 100 bp

\* 2239 3005: contig of 767 bp in length

\* 3006 3105: gap of 100 bp

\* 3106 3860: contig of 755 bp in length

\* 3861 3960: gap of 100 bp

\* 3961 4639: contig of 679 bp in length

\* 4640 4739: gap of 100 bp

\* 4740 5414: contig of 675 bp in length

\* 5415 5514: gap of 100 bp

\* 5515 6290: contig of 776 bp in length

\* 6291 6390: gap of 100 bp

\* 6391 7071: contig of 681 bp in length

\* 7072 7171: gap of 100 bp

\* 7172 7853: contig of 682 bp in length

\* 7854 7953: gap of 100 bp

\* 7954 8627: contig of 674 bp in length

\* 8628 8727: gap of 100 bp

\* 8728 9409: contig of 682 bp in length

\* 9410 9509: gap of 100 bp

\* 9510 10180: contig of 671 bp in length

\* 10181 10280: gap of 100 bp

\* 10281 10969: contig of 689 bp in length

\* 10970 11069: gap of 100 bp

\* 11070 11740: contig of 671 bp in length

\* 11741 11840: gap of 100 bp

\* 11841 12509: contig of 669 bp in length

\* 12510 12609: gap of 100 bp

\* 12610 13254: contig of 645 bp in length

\* 13255 13354: gap of 100 bp

\* 13355 14028: contig of 674 bp in length

\* 14029 14128: gap of 100 bp

\* 14129 14795: contig of 667 bp in length

\* 14796 14895: gap of 100 bp

\* 14896 15570: contig of 675 bp in length

\* 15571 15670: gap of 100 bp

\* 15671 16330: contig of 660 bp in length

\* 16331 16430: gap of 100 bp

\* 16431 17099: contig of 669 bp in length

\* 17100 17199: gap of 100 bp

\* 17200 17903: contig of 704 bp in length

\* 17904 18003: gap of 100 bp

\* 18004 18693: contig of 689 bp in length

\* 18693 18792: gap of 100 bp

\* 18793 19467: contig of 675 bp in length

\* 19468 19567: gap of 100 bp

\* 19568 20238: contig of 671 bp in length

\* 20239 20338: gap of 100 bp

\* 20339 21007: contig of 669 bp in length

\* 21008 21107: gap of 100 bp

\* 21109 21852: contig of 745 bp in length

\* 21853 21952: gap of 100 bp

\* 21953 22635: contig of 683 bp in length

\* 22636 22735: gap of 100 bp

\* 22736 23384: contig of 649 bp in length

\* 23385 23484: gap of 100 bp

\* 23485 24154: contig of 670 bp in length

\* 24155 24254: gap of 100 bp

\* 24255 24914: contig of 660 bp in length

\* 24915 25014: gap of 100 bp

\* 25015 25697: contig of 683 bp in length

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\* 25798 26470: contig of 673 bp in length

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\* 26571 27328: contig of 758 bp in length

\* 27329 27428: gap of 100 bp

\* 27429 28117: contig of 689 bp in length

\* 28118 28217: gap of 100 bp

\* 28218 28864: contig of 647 bp in length

\* 28865 28964: gap of 100 bp

\* 28965 29633: contig of 669 bp in length

\* 29634 29734: gap of 100 bp

\* 29734 30482: contig of 749 bp in length

\* 30483 30582: gap of 100 bp

\* 30583 31343: contig of 761 bp in length

\* 31344 31443: gap of 100 bp

\* 31444 32204: contig of 761 bp in length

\* 32205 32304: gap of 100 bp

\* 32305 32972: contig of 668 bp in length

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\* 33839 33938: gap of 100 bp

\* 33939 34620: contig of 682 bp in length

\* 34621 34720: gap of 100 bp

\* 34721 35467: contig of 747 bp in length

\* 35468 35567: gap of 100 bp

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\* 37871 38547: contig of 677 bp in length

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\* 39388 39487: gap of 100 bp

\* 39488 40243: contig of 756 bp in length

\* 40244 40343: gap of 100 bp

\* 40344 41003: contig of 660 bp in length

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* 41004 41103: gap of 100 bp
* 41104 41784: contig of 681 bp in length
* 41785 41884: gap of 100 bp
* 41885 42572: contig of 688 bp in length
* 42573 42672: gap of 100 bp
* 42673 43330: contig of 658 bp in length
* 43331 43430: gap of 100 bp
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* 44097 44196: gap of 100 bp
* 44197 44852: contig of 656 bp in length
* 44853 44952: gap of 100 bp
* 44953 45627: contig of 675 bp in length
* 45628 45727: gap of 100 bp
* 45728 46410: contig of 683 bp in length
* 46411 46510: gap of 100 bp
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* 47188 47287: gap of 100 bp
* 47288 48012: contig of 725 bp in length
* 48013 48112: gap of 100 bp
* 48113 48784: contig of 672 bp in length
* 48785 48884: gap of 100 bp
* 48885 49549: contig of 665 bp in length
* 49550 49649: gap of 100 bp
* 49650 50338: contig of 689 bp in length
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* 50439 51107: contig of 669 bp in length
* 51108 51207: gap of 100 bp
* 51208 51871: contig of 664 bp in length
* 51872 51971: gap of 100 bp
* 51972 52651: contig of 680 bp in length
* 52652 52751: gap of 100 bp
* 52752 53427: contig of 676 bp in length
* 53428 53527: gap of 100 bp
* 53528 54200: contig of 673 bp in length
* 54201 54300: gap of 100 bp

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Best Local Similarity 100.0%; Pred. No. 39;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CCTTCGCGCCCTGTT 15
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DB 57817 CCTTCGCGCCCTGTT 57831

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RESULT 10
AC124280
LOCUS Homo sapiens chromosome 17 clone RP13-519019 map 17, LOW-PASS
DEFINITION AC124280 65851 bp DNA linear HTG 30-JUL-2002
ACCESSION AC124280
VERSION AC124280.3 GI:22004380
KEYWORDS HTG; HTGS_PHASE0.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 65851)
Birren,B., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 17, clone RP13-519019
Unpublished
2 (bases 1 to 65851)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L.,
Boukhgalter,B., Brown,A., Camarata,J., Campolano,A., Chang,J.,
Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
Gardyna,J., Girdya,S., Ginde,S., Gordon,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I.,
Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K.,
Liu,G., Maclean,C., Macdonald,P., Major,J., Marquis,N.,

```

Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J.,  
Meneus,L., Mihova,T., Mlenda,V., Murphy,T., Naylor,J., Nguyen,C.,  
Nirol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P.,  
O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,  
Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C.,  
Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S.,  
Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N.,  
Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.,  
Theodore,J., Topham,K., Travers,M., Travis,N., Trioglio,J.,  
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,  
Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

## Direct Submission

Submitted (14-JUN-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE  
AUTHORS

3 (bases 1 to 65851)  
Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,  
Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhgalter,B.,  
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,  
Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,  
Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,  
Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,  
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,  
Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,  
Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,  
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenda,V.,  
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,  
O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,  
Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,  
Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P.,  
Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,  
Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,  
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,  
Zembek,L., Zimmer,A. and Zody,M.

TITLE  
JOURNAL

Submitted (30-JUL-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA

## COMMENT

On Jul 30, 2002 this sequence version replaced gi:21699374.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information  
Center project name: L27356  
Center clone name: 519\_O\_19  
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\* NOTE: This record contains 80 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1 707: contig of 707 bp in length  
\* 708 807: gap of 100 bp  
\* 808 1542: contig of 735 bp in length  
\* 1543 1642: gap of 100 bp  
\* 1643 2336: contig of 694 bp in length  
\* 2337 2436: gap of 100 bp  
\* 2437 3166: contig of 730 bp in length  
\* 3167 3266: gap of 100 bp  
\* 3267 3987: contig of 721 bp in length  
\* 3988 4087: gap of 100 bp  
\* 4088 4813: contig of 726 bp in length  
\* 4814 4913: gap of 100 bp  
\* 4914 5651: contig of 738 bp in length

\* 5652 5751: gap of 100 bp  
\* 5752 6473: contig of 722 bp in length  
\* 6474 6573: gap of 100 bp  
\* 6574 7300: contig of 727 bp in length  
\* 7301 7400: gap of 100 bp  
\* 7401 8134: contig of 734 bp in length  
\* 8135 8234: gap of 100 bp  
\* 8235 8966: contig of 732 bp in length  
\* 8967 9066: gap of 100 bp  
\* 9067 9714: contig of 648 bp in length  
\* 9715 9814: gap of 100 bp  
\* 9815 10534: contig of 720 bp in length  
\* 10535 10634: gap of 100 bp  
\* 10635 11348: contig of 714 bp in length  
\* 11349 11448: gap of 100 bp  
\* 11449 12160: contig of 712 bp in length  
\* 12161 12260: gap of 100 bp  
\* 12261 12986: contig of 726 bp in length  
\* 12987 13086: gap of 100 bp  
\* 13087 13816: contig of 730 bp in length  
\* 13817 13916: gap of 100 bp  
\* 13917 14633: contig of 717 bp in length  
\* 14634 14733: gap of 100 bp  
\* 14734 15446: contig of 713 bp in length  
\* 15447 15546: gap of 100 bp  
\* 15547 16272: contig of 726 bp in length  
\* 16273 16372: gap of 100 bp  
\* 16373 17115: contig of 743 bp in length  
\* 17116 17215: gap of 100 bp  
\* 17216 17930: contig of 715 bp in length  
\* 17931 18030: gap of 100 bp  
\* 18031 18748: contig of 718 bp in length  
\* 18749 18848: gap of 100 bp  
\* 18849 19574: contig of 726 bp in length  
\* 19575 19674: gap of 100 bp  
\* 19675 20393: contig of 719 bp in length  
\* 20394 20493: gap of 100 bp  
\* 20494 21206: contig of 713 bp in length  
\* 21207 21306: gap of 100 bp  
\* 21307 22020: contig of 714 bp in length  
\* 22021 22120: gap of 100 bp  
\* 22121 22852: contig of 732 bp in length  
\* 22853 22952: gap of 100 bp  
\* 22953 23692: contig of 740 bp in length  
\* 23693 23792: gap of 100 bp  
\* 23793 24520: contig of 728 bp in length  
\* 24521 24620: gap of 100 bp  
\* 24621 25368: contig of 748 bp in length  
\* 25369 25468: gap of 100 bp  
\* 25469 26186: contig of 718 bp in length  
\* 26187 26286: gap of 100 bp  
\* 26287 27015: contig of 729 bp in length  
\* 27016 27115: gap of 100 bp  
\* 27116 27837: contig of 722 bp in length  
\* 27838 27937: gap of 100 bp  
\* 27938 28649: contig of 712 bp in length  
\* 28650 28749: gap of 100 bp  
\* 28750 29479: contig of 730 bp in length  
\* 29480 29579: gap of 100 bp  
\* 29580 30264: contig of 685 bp in length  
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\* 30365 31103: contig of 739 bp in length  
\* 31104 31203: gap of 100 bp  
\* 31204 31943: contig of 740 bp in length  
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\* 32044 32786: contig of 743 bp in length  
\* 32787 32886: gap of 100 bp  
\* 32887 33595: contig of 709 bp in length  
\* 33596 33695: gap of 100 bp  
\* 33696 34433: contig of 738 bp in length  
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\* 34534 35276: contig of 743 bp in length  
\* 35277 35376: gap of 100 bp

\* 35377 36124: contig of 748 bp in length  
\* 36125 36224: gap of 100 bp  
\* 36225 36946: contig of 722 bp in length  
\* 36947 37046: gap of 100 bp  
\* 37047 37776: contig of 730 bp in length  
\* 37777 37876: gap of 100 bp  
\* 37877 38577: contig of 701 bp in length  
\* 38578 38677: gap of 100 bp  
\* 38678 39398: contig of 721 bp in length  
\* 39399 39498: gap of 100 bp  
\* 39499 40210: contig of 712 bp in length  
\* 40211 40310: gap of 100 bp  
\* 40311 41043: contig of 733 bp in length  
\* 41044 41143: gap of 100 bp  
\* 41144 41859: contig of 716 bp in length  
\* 41860 41959: gap of 100 bp  
\* 41960 42683: contig of 724 bp in length  
\* 42684 42783: gap of 100 bp  
\* 42784 43521: contig of 738 bp in length  
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\* 43622 44359: contig of 738 bp in length  
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\* 44460 45198: contig of 739 bp in length  
\* 45199 45298: gap of 100 bp  
\* 45299 46011: contig of 713 bp in length  
\* 46012 46111: gap of 100 bp  
\* 46112 46840: contig of 729 bp in length  
\* 46841 46940: gap of 100 bp

Query Match 100.0%; Score 15; DB 2; Length 65851;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTCTCGCCCTGTT 15

Db 63511 CTTCTCGCCCTGTT 63525

# RESULT 11

LOCUS AC130797 80669 bp DNA linear HTG 14-AUG-2002  
DEFINITION Chlamydomonas reinhardtii clone cr-1j6, WORKING DRAFT SEQUENCE, 1  
ordered piece.  
ACCESSION AC130797  
VERSION AC130797.1 GI:22218470  
KEYWORDS HTG; HTGS\_PHASE2; HTGS\_DRAFT.  
SOURCE Chlamydomonas reinhardtii.  
ORGANISM Chlamydomonas reinhardtii  
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
Chlamydomonadaceae; Chlamydomonas.  
REFERENCE 1 (bases 1 to 80669)  
AUTHORS Wu, H., Lin, S., Jia, H., Dutcher, S. and Roe, B. A.  
TITLE Chlamydomonas reinhardtii BAC Clone cr-1j6  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 80669)  
AUTHORS Wu, H., Lin, S., Jia, H., Dutcher, S. and Roe, B. A.  
TITLE Direct Submission  
JOURNAL Submitted (14-AUG-2002) Department Of Chemistry And Biochemistry,  
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,  
OK 73019, USA  
COMMENT ----- Genome Center  
Center: Department Of Chemistry And Biochemistry  
The University Of Oklahoma  
Center code: UOKNOR  
-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 1 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* been provided by the submitter.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and



\* the accession number will be preserved.  
\* 1 80669: contig of 80669 bp in length.  
FEATURES  
source Location/Qualifiers  
1..80669  
/organism="Chlamydomonas reinhardtii"  
/db\_xref="taxon:3055"  
/clone\_lib="cr-lj6"  
/clone\_lib="cr-lj6"  
/note="This is one of two clones in the same well cr-lj6"  
BASE COUNT 14154 a 25825 c 24793 g 15894 t 3 others  
ORIGIN  
  
Query Match 100.0%; Score 15; DB 2; Length 80669;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CCTTCGCGCCTGTT 15  
|||||  
Db 70450 CCTTCGCGCCTGTT 70464  
  
RESULT 12  
AC009031/c  
LOCUS  
DEFINITION Homo sapiens chromosome 16 clone RP11-13M21, LOW-PASS SEQUENCE  
ACCESSION AC009031  
VERSION AC009031.2 GI:6758938  
KEYWORDS HTG; HTGS\_PHASE0.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1: (bases 1 to 90280)  
DOE Joint Genome Institute.  
TITLE Sequencing of Human Chromosome 16  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 90280)  
DOE Joint Genome Institute.  
TITLE Direct Submission  
JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint  
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
On Jan 26, 2000 this sequence version replaced gi:5686044.  
-----Genome Center  
Center: Joint Genome Institute  
Center Code: JGI  
Web site: http://www.jgi.doe.gov  
-----  
\* NOTE: This record contains 87 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.  
\* 1 649: contig of 649 bp in length  
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\* 650 1313: contig of 664 bp in length  
\* gap of unknown length  
\* 1314 1981: contig of 668 bp in length  
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\* 1982 2621: contig of 640 bp in length  
\* gap of unknown length  
\* 2622 3298: contig of 677 bp in length  
\* gap of unknown length  
\* 3299 3768: contig of 470 bp in length  
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\* 3769 4417: contig of 649 bp in length  
\* gap of unknown length  
  
\* 4418 5058: contig of 641 bp in length  
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\* 5059 5706: contig of 648 bp in length  
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\* 5707 6273: contig of 567 bp in length  
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\* 6274 6962: contig of 689 bp in length  
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\* 6963 7734: contig of 772 bp in length  
\* gap of unknown length  
\* 7735 8478: contig of 744 bp in length  
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\* 8479 9239: contig of 761 bp in length  
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\* 9240 9982: contig of 743 bp in length  
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\* 11389 12220: contig of 832 bp in length  
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\* 12221 12989: contig of 769 bp in length  
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\* 12990 13644: contig of 655 bp in length  
\* gap of unknown length  
\* 13645 14446: contig of 802 bp in length  
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\* 14447 15320: contig of 874 bp in length  
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\* 15321 15914: contig of 594 bp in length  
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\* 15915 16670: contig of 756 bp in length  
\* gap of unknown length  
\* 16671 17491: contig of 821 bp in length  
\* gap of unknown length  
\* 17492 18135: contig of 644 bp in length  
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\* 18136 18738: contig of 603 bp in length  
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\* 18739 19363: contig of 625 bp in length  
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\* 19364 20076: contig of 713 bp in length  
\* gap of unknown length  
\* 20077 20849: contig of 773 bp in length  
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\* 20850 22064: contig of 1215 bp in length  
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\* 22065 23060: contig of 996 bp in length  
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\* 24345 24969: contig of 625 bp in length  
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\* 24970 25267: contig of 298 bp in length  
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\* 25268 25891: contig of 624 bp in length  
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\* 25892 26674: contig of 783 bp in length  
\* gap of unknown length  
\* 26675 27382: contig of 708 bp in length  
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\* 27383 27459: contig of 77 bp in length  
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\* 27460 28325: contig of 866 bp in length  
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\* 28326 29243: contig of 918 bp in length  
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\* 29244 30009: contig of 766 bp in length  
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\* 30010 30770: contig of 761 bp in length  
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\* 30771 gap of unknown length  
\* 31472: contig of 702 bp in length  
\* 31473 gap of unknown length  
\* 32518: contig of 1046 bp in length  
\* 32519 gap of unknown length  
\* 33729: contig of 1211 bp in length  
\* 33730 gap of unknown length  
\* 33804: contig of 75 bp in length  
\* 33805 gap of unknown length  
\* 34775: contig of 971 bp in length  
\* 34776 gap of unknown length  
\* 35568: contig of 793 bp in length  
\* 35569 gap of unknown length  
\* 36526: contig of 958 bp in length  
\* 36527 gap of unknown length  
\* 37178: contig of 652 bp in length  
\* 37179 gap of unknown length  
\* 38597: contig of 1419 bp in length  
\* 38598 gap of unknown length  
\* 39399: contig of 802 bp in length  
\* 39400 gap of unknown length  
\* 40532: contig of 1133 bp in length  
\* 40533 gap of unknown length  
\* 41611: contig of 1079 bp in length  
\* 41612 gap of unknown length  
\* 42657: contig of 1046 bp in length  
\* 42658 gap of unknown length  
\* 43644: contig of 987 bp in length  
\* 43645 gap of unknown length  
\* 44808: contig of 1164 bp in length  
\* 44809 gap of unknown length  
\* 46147: contig of 1339 bp in length  
\* 46148 gap of unknown length  
\* 47217: contig of 1070 bp in length  
\* 47218 gap of unknown length  
\* 48521: contig of 1304 bp in length  
\* 48522 gap of unknown length  
\* 49309: contig of 788 bp in length  
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\* 52193: contig of 1350 bp in length  
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\* 53317: contig of 1124 bp in length  
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\* 54463: contig of 1146 bp in length  
\* 54464 gap of unknown length  
\* 55711: contig of 1248 bp in length  
\* 55712 gap of unknown length  
\* 56683: contig of 972 bp in length  
\* 56684 gap of unknown length  
\* 58209: contig of 1526 bp in length  
\* 58210 gap of unknown length  
\* 59763: contig of 1554 bp in length  
\* 59764 gap of unknown length  
\* 61209: contig of 1446 bp in length  
\* 61210 gap of unknown length  
\* 62915: contig of 1706 bp in length  
\* 62916 gap of unknown length  
\* 64134: contig of 1219 bp in length  
\* 64135 gap of unknown length  
\* 65998: contig of 1864 bp in length  
\* 67325: contig of 1327 bp in length  
\* 67326 gap of unknown length  
\* 68610: contig of 1285 bp in length  
\* 68611 gap of unknown length  
\* 70086: contig of 1476 bp in length  
\* 71288: gap of unknown length  
\* 70087 contig of 1202 bp in length  
\* 71289 gap of unknown length  
\* 73310: contig of 2022 bp in length  
\* gap of unknown length

\* 73311 74258: contig of 948 bp in length  
\* gap of unknown length  
\* 74259 75836: contig of 1578 bp in length  
\* gap of unknown length

Query Match 100.0%; Score 15; DB 2; Length 90280;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15

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Db 63309 CCTTCTCGCCCTGTT 63295

#### RESULT 13

LMFLCHR12\_1

#### WPCOMMENT

Sequence split into 8 fragments LOCUS LMFLCHR12 Accession AL390114

Fragment Name	Begin	End
LMFLCHR12_0	1	110000
LMFLCHR12_1	100001	210000
LMFLCHR12_2	200001	310000
LMFLCHR12_3	300001	410000
LMFLCHR12_4	400001	510000
LMFLCHR12_5	500001	610000
LMFLCHR12_6	600001	710000
LMFLCHR12_7	700001	757191

Continuation (2 of 8) of LMFLCHR12 from base 100001 (AL390114 Leishmania major chromosome)

Query Match 100.0%; Score 15; DB 2; Length 110000;

Best Local Similarity 100.0%; Pred. No. 38;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15

|||||

Db 46567 CCTTCTCGCCCTGTT 46581

#### RESULT 14

AC094766

LOCUS

DEFINITION Rattus norvegicus clone CH230-5L5, \*\*\* SEQUENCING IN PROGRESS \*\*\*,  
65 unordered pieces.

ACCESSION AC094766

VERSION AC094766.2 GI:17941546

KEYWORDS HTG: HTGS\_PHASE1.

SOURCE Rattus norvegicus.

ORGANISM

Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

#### REFERENCE

AUTHORS

1 (bases 1 to 150765)  
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,  
Albrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbara,J.,  
Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.,  
Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,  
Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,  
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,  
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,  
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,  
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,  
Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,  
Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,  
Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,  
Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,  
Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,  
Hernandez,J., Hernandez,O., Hodgson,A., Hoques,M., Holloway,C.,  
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Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,  
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Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.,
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Weinstock,G., and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 150765)
Worley,K.C.
Direct Submission
Submitted (15-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:15624602.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GBID
Center clone name: CH230-5L5
----- Summary Statistics
Assembly program: Phrap; version 0.990329First call to
findPhrapList
Consensus quality: 115371 bases at least Q40
Consensus quality: 123148 bases at least Q30
Consensus quality: 129020 bases at least Q20
Estimated insert size: 114258; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 1.6x in Q20 bases; sum-of-contigs estimation
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 65 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

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VERSION AX195074.1 GI:15385721  
KEYWORDS human.  
SOURCE Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 160755)  
AUTHORS Chu, T., Blumenfeld, M. and Cohen, D.  
TITLE Biallelic markers derived from genomic regions carrying genes  
involved in central nervous system disorders  
JOURNAL Patent: WO 0151659-A 544 19-JUL-2001;  
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Job time : 1834 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 15:29:02 ; Search time 213 Seconds  
(without alignments)  
158.591 Million cell updates/sec

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Searched: 2185239 seqs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

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c 19	14	93.3	349980	22	AAH68525	C glutamicum codin
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23	13	86.7	324	19	AAV27204	Homo sapiens TSH r
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88	13	86.7	4558	22	AAK52850	Genomic sequence #	c 161	12	80.0	396	22	ABA24926	Probe #3392 for ge
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101	13	86.7	7149	23	ABLI19614	Drosophila melanog	c 174	12	80.0	445	22	ABA52057	Human foetal liver
102	13	86.7	7430	23	AAK59509	Propionibacterium	c 175	12	80.0	445	22	ABA21871	Probe #337 for gen
103	13	86.7	7829	23	ABLI02642	Drosophila melanog	c 176	12	80.0	445	22	AAK00340	Human brain expres
104	13	86.7	8115	22	AAK32860	Human genomic DNA	c 177	12	80.0	445	22	AAK25783	Human bone marrow
105	13	86.7	8116	22	AAK32861	Human genomic DNA	c 178	12	80.0	445	22	AAI10412	Probe #345 for gen
106	13	86.7	9320	22	AAH45588	DNA encoding hydro	c 179	12	80.0	445	22	AAI31664	Probe #350 used to
107	13	86.7	9785	17	AAT44457	DNA encoding tolue	c 180	12	80.0	445	22	AAI00347	Probe #338 used to
108	13	86.7	10726	23	ABL06616	Drosophila melanog	c 181	12	80.0	445	24	ABS00363	Human genome-deriv
109	13	86.7	11992	23	ABL03712	Drosophila melanog	c 182	12	80.0	447	20	AAK27717	Human DNA marker c
110	13	86.7	12313	23	ABLI1964	Drosophila melanog	c 183	12	80.0	447	23	AAK83716	DNA encoding novel
111	13	86.7	35100	19	AAV20441	Human c-fms oncoge	c 184	12	80.0	453	21	AAK64576	Elmeria tenella PK
112	13	86.7	38258	24	AAK98633	DNA encoding colon	c 185	12	80.0	461	24	ABL63543	Breast cancer rela
113	13	86.7	349980	22	AAH41224	Pyrococcus abyssi	c 186	12	80.0	463	22	AAK79697	Human immune/haema
114	12	80.0	18	24	ABK87886	Midkine (MK) expre	c 187	12	80.0	475	22	AAI92355	Human polynucleoti
115	12	80.0	19	21	ABK87887	Midkine (MK) expre	c 188	12	80.0	478	23	ABV46244	Human prostate exp
116	12	80.0	19	21	AAK83529	cdk-we-hu ribozyme	c 189	12	80.0	485	21	AAK02660	Human colon cancer
117	12	80.0	19	21	AAK83530	cdk-we-hu ribozyme	c 190	12	80.0	486	24	ABL82663	Human ovarian canc
118	12	80.0	19	21	AAH83531	cdk-we-hu ribozyme	c 191	12	80.0	494	24	ABQ56572	Human colon cancer
119	12	80.0	19	21	AAH85691	cdk-we-hu ribozyme	c 192	12	80.0	503	22	AAK63333	Human immune/haema
120	12	80.0	19	22	AAH58692	cdk-we-hu ribozyme	c 193	12	80.0	509	22	AAH09380	Human cDNA clone (
121	12	80.0	19	22	AAH58693	cdk-we-hu ribozyme	c 194	12	80.0	522	23	AAK85412	DNA encoding novel
122	12	80.0	24	24	ABN86828	Human fructose-6-p	c 195	12	80.0	523	20	AAV86036	EST clone B227. H
123	12	80.0	30	24	ABG97855	Oligonucleotide ME	c 196	12	80.0	537	24	ABL83088	Human ovarian canc
124	12	80.0	49	22	AAK10683	PCR primer oOH011	c 197	12	80.0	539	22	AAH13272	Human cDNA clone (
125	12	80.0	51	22	AAAL27462	Human SNP oligonuc	c 198	12	80.0	550	22	AAK505612	Mammalian gossypii AG
126	12	80.0	152	22	ABA46826	Human breast cell	c 199	12	80.0	576	24	AAI8065	Human colon cancer
127	12	80.0	152	22	ABA64706	Human foetal liver	c 200	12	80.0	607	24	ABQ57802	Human prostate exp
128	12	80.0	152	22	ABA31830	Probe #10296 for g	c 201	12	80.0	611	23	ABV46802	Oligonucleotide fo
129	12	80.0	152	22	AAK13141	Human brain expres	c 202	12	80.0	611	24	ABQ19264	Oligonucleotide fo
130	12	80.0	152	22	AAK38872	Human bone marrow	c 203	12	80.0	611	24	ABQ19265	Oligonucleotide fo
131	12	80.0	152	22	AAI19680	Probe #9613 for ge	c 204	12	80.0	612	24	ABQ15078	Oligonucleotide fo
132	12	80.0	152	22	AAI44875	Probe #13561 used	c 205	12	80.0	612	24	ABQ15079	Oligonucleotide fo
133	12	80.0	152	22	AAI05399	Probe #5390 used t	c 206	12	80.0	615	21	AAFI1528	Aspergillus niger
134	12	80.0	152	24	ABS12953	Human genome-deriv	c 207	12	80.0	619	24	ABQ44298	Oligonucleotide fo
135	12	80.0	173	24	ABK79902	Bacillus clausii g	c 208	12	80.0	619	24	ABQ44299	Oligonucleotide fo
136	12	80.0	180	22	AAK64796	Human immune/haema	c 209	12	80.0	626	21	AAK09531	Fusarium venenatum
137	12	80.0	187	21	AAK313925	Human secreted pro	c 210	12	80.0	631	21	AAFI3423	Aspergillus oryzae
138	12	80.0	237	21	AAK31359	Human secreted pro	c 211	12	80.0	657	21	AAK50247	Maize heat shock p
139	12	80.0	245	22	AAK67522	Human immune/haema	c 212	12	80.0	657	22	AAH26480	Maize heat shock p
140	12	80.0	252	23	ABLI14549	Drosophila melanog	c 213	12	80.0	659	21	AAFI2907	Aspergillus oryzae
141	12	80.0	257	20	AAK23310	Human l-alpha-Ohas	c 214	12	80.0	660	21	AAK07969	Fusarium venenatum
142	12	80.0	261	21	AAK31684	Human secreted pro	c 215	12	80.0	662	21	AAA01928	Human colon cancer
143	12	80.0	279	22	AAI199217	Human secreted re	c 216	12	80.0	667	21	AAK79649	Eucalyptus grandis
144	12	80.0	279	22	AAI63567	Human kidney relat	c 217	12	80.0	674	24	ABK63167	Rat sequence diffe
145	12	80.0	285	16	AAI25664	Human gene signatu	c 218	12	80.0	674	24	ABQ13506	Oligonucleotide fo
146	12	80.0	294	22	AAI199215	Human excretory re	c 219	12	80.0	674	24	ABQ13507	Oligonucleotide fo
147	12	80.0	294	22	AAI63565	Human kidney relat	c 220	12	80.0	681	23	ABL26035	Drosophila melanog
148	12	80.0	300	21	AAA00253	Human colon cancer	c 221	12	80.0	711	21	AAK294085	Haematopoietic ste
149	12	80.0	309	21	AAA42072	Human secreted exp	c 222	12	80.0	751	22	AAI94531	Human neuroblastom
150	12	80.0	334	24	ABN24354	Human OREF polynuc	c 223	12	80.0	761	20	AAK20473	Human secreted pro
151	12	80.0	337	23	AAK86961	DNA encoding novel	c 224	12	80.0	762	21	AAK08886	Fusarium venenatum
152	12	80.0	350	22	AAK64318	Novel human polynu	c 225	12	80.0	768	23	ABL27737	Drosophila melanog
153	12	80.0	354	21	AAK03111	Human secreted pro	c 226	12	80.0	774	22	AAH68308	C glutamicum codin
154	12	80.0	355	21	AAK28671	Human secreted pro	c 227	12	80.0	787	24	AAK33829	Human secreted pro
155	12	80.0	357	21	AAK242551	Human 5' EST isola	c 228	12	80.0	792	22	AAI97289	Human neuroblastom



c 229	12	80.0	797	22	AAI97388	Human neuroblastom	302	12	80.0	1671	20	AAZ30705	Rat neuronal immed
c 230	12	80.0	801	23	AAS80358	DNA encoding novel	c 303	12	80.0	1695	24	ABQ40322	Oligonucleotide fo
c 231	12	80.0	809	24	ABQ33820	Oligonucleotide fo	304	12	80.0	1695	24	ABQ40323	Oligonucleotide fo
c 232	12	80.0	809	24	ABQ33821	Oligonucleotide fo	305	12	80.0	1746	22	AAH23097	Osteoarthritis tis
c 233	12	80.0	824	22	AAS22636	Human cDNA encodin	306	12	80.0	1746	24	ABN84120	Human cDNA differe
c 234	12	80.0	829	21	AA505050	Maize heat shock p	307	12	80.0	1746	24	ABN95923	Gene #2421 used to
c 235	12	80.0	829	22	AAH26478	Maize heat shock p	308	12	80.0	1746	24	ABK64552	Human benign prost
c 236	12	80.0	837	22	AAH68310	C glutamicum codin	309	12	80.0	1746	24	ABK12141	Human zinc finger
c 237	12	80.0	840	23	AAS88313	DNA encoding novel	310	12	80.0	1746	24	ABL69359	Prostate cancer re
c 238	12	80.0	846	22	AAF54823	Corn glutamate 1-s	311	12	80.0	1764	23	ABL04855	Drosophila melanog
c 239	12	80.0	879	24	AAD33862	Human secreted pro	312	12	80.0	1770	23	ABL22915	DNA encoding novel
c 240	12	80.0	902	22	AAI97794	Human neuroblastom	313	12	80.0	1797	23	AAS86812	Lung cancer associ
c 241	12	80.0	903	23	ABL06853	Drosophila melanog	314	12	80.0	1806	21	AAF18258	cDNA sequence from
c 242	12	80.0	904	18	AAI64849	Myceliophthora the	315	12	80.0	1820	11	AAQ04731	Novel human coding
c 243	12	80.0	960	22	AAI71350	Corynebacterium gl	c 316	12	80.0	1846	24	ABN59602	Human human coding
c 244	12	80.0	972	23	ABL28095	Drosophila melanog	c 317	12	80.0	1878	22	AAH51962	Mycobacterium tube
c 245	12	80.0	974	21	AAI21745	Human breast and o	c 318	12	80.0	1878	22	AAS02609	M. tuberculosis he
c 246	12	80.0	981	24	ABA97002	Human ZFP36 coding	c 319	12	80.0	1879	22	AAH17119	Human cDNA sequenc
c 247	12	80.0	984	19	AAV16105	Fusarium oxysporum	c 320	12	80.0	1954	22	ABA46112	Human breast cell
c 248	12	80.0	987	19	AAV54011	Nucleotide sequenc	c 321	12	80.0	1974	24	ABQ50596	Oligonucleotide fo
c 249	12	80.0	1011	22	AAH68290	C glutamicum codin	c 322	12	80.0	1974	24	ABQ50597	Oligonucleotide fo
c 250	12	80.0	1014	21	AAC56329	Pinus radiata tran	c 323	12	80.0	1992	23	ABL15361	Drosophila melanog
c 251	12	80.0	1020	21	AAA94032	Mycobacterium auru	c 324	12	80.0	2013	24	ABN89466	Abeta42-tsp70 fusi
c 252	12	80.0	1020	21	AAA94040	Mycobacterium auru	c 325	12	80.0	2077	22	AAK94927	Human full-length
c 253	12	80.0	1022	24	ABQ40746	Oligonucleotide fo	c 326	12	80.0	2079	23	ABL24645	Drosophila melanog
c 254	12	80.0	1022	24	ABQ40747	Oligonucleotide fo	c 327	12	80.0	2085	24	ABK80509	Bacillus clausii g
c 255	12	80.0	1028	21	AA505251	Maize heat shock p	c 328	12	80.0	2104	14	AAQ43722	Sequence of DNA cl
c 256	12	80.0	1028	22	AAH26477	Maize heat shock p	c 329	12	80.0	2109	24	ABA90378	Drosophila cell cy
c 257	12	80.0	1038	24	ABL87981	DNA polymerase III	c 330	12	80.0	2122	24	ABN95249	Gene #1747 used to
c 258	12	80.0	1038	24	ABL87982	DNA polymerase III	c 331	12	80.0	2136	22	AAF25028	Nucleotide sequenc
c 259	12	80.0	1080	24	ABN84013	Human oestrogen do	c 332	12	80.0	2172	22	AAS02618	Chimeric immunogen
c 260	12	80.0	1116	23	AAS85415	DNA encoding novel	c 333	12	80.0	2175	22	AAF25031	Nucleotide sequenc
c 261	12	80.0	1116	23	AAS91079	DNA encoding novel	c 334	12	80.0	2178	22	AAH18098	Human cDNA sequenc
c 262	12	80.0	1124	21	AAA95776	Human immune syste	c 335	12	80.0	2199	19	AAV82778	Clone bp783_3 isol
c 263	12	80.0	1128	24	ABQ090902	M. capsulatus gene	c 336	12	80.0	2199	24	ABQ92015	Human polynucleoti
c 264	12	80.0	1134	22	AAI71711	Corynebacterium gl	c 337	12	80.0	2220	23	AAS82863	DNA encoding novel
c 265	12	80.0	1143	23	AA574919	DNA encoding novel	c 338	12	80.0	2225	23	AAS83717	Human DNA sequenc
c 266	12	80.0	1145	22	AAH29291	Drosophila melanog	c 339	12	80.0	2247	24	AA595016	Human secreted pro
c 267	12	80.0	1152	24	AQ668857	Listeria monocytog	c 340	12	80.0	2249	20	AAV84511	Human secreted pro
c 268	12	80.0	1161	19	AAV69538	Thymosin beta 4, Y	c 341	12	80.0	2249	22	ABA83294	Drosophila melanog
c 269	12	80.0	1161	22	AAI63752	Drosophila gustato	c 342	12	80.0	2252	23	ABL14548	Drosophila melanog
c 270	12	80.0	1163	21	AA505252	Maize heat shock p	c 343	12	80.0	2268	23	ABL24186	Drosophila melanog
c 271	12	80.0	1163	22	AAH26479	Maize heat shock p	c 344	12	80.0	2280	21	AAC59224	Human secreted pro
c 272	12	80.0	1200	23	AAS80309	DNA encoding novel	c 345	12	80.0	2281	23	ABL07965	Drosophila melanog
c 273	12	80.0	1230	23	ABL20857	Drosophila melanog	c 346	12	80.0	2334	22	AAF81369	Quorum sensing con
c 274	12	80.0	1242	23	ABL25337	Drosophila melanog	c 347	12	80.0	2349	24	ABQ90069	M. capsulatus gene
c 275	12	80.0	1252	24	ABN86826	Human fructose-6-p	c 348	12	80.0	2349	24	ABQ90651	Human 1-alpha-hydr
c 276	12	80.0	1260	22	AA510677	Mycobacterium tube	c 349	12	80.0	2362	20	AAH02929	Multiple drug resi
c 277	12	80.0	1263	23	AAS85416	DNA encoding novel	c 350	12	80.0	2375	17	AAI38233	Lung cancer associ
c 278	12	80.0	1393	23	ABL24629	Drosophila melanog	c 351	12	80.0	2383	21	AAF18298	Human polynucleoti
c 279	12	80.0	1401	23	ABL07745	Fusarium oxysporum	c 352	12	80.0	2389	22	AAK51748	Human polynucleoti
c 280	12	80.0	1473	12	AAQ14857	Fusarium oxysporum	c 353	12	80.0	2403	23	ABL03183	Drosophila melanog
c 281	12	80.0	1473	13	AAQ26407	Fusarium oxysporum	c 354	12	80.0	2409	21	AAZ30341	Partial sequence o
c 282	12	80.0	1473	13	AAQ26382	Endoglucanase #2.	c 355	12	80.0	2434	22	AAL36971	Human musculoskele
c 283	12	80.0	1473	13	AAQ25933	Cellulase containe	c 356	12	80.0	2446	22	AAS27610	DNA encoding novel
c 284	12	80.0	1473	13	AAQ29935	Endoglucanase gene	c 357	12	80.0	2446	22	AAS27747	DNA encoding novel
c 285	12	80.0	1473	14	AAQ41733	Dye transfer inhib	c 358	12	80.0	2451	20	AAZ07543	Human lalpa hydro
c 286	12	80.0	1473	14	AAQ49942	Endoglucanase enzy	c 359	12	80.0	2454	24	AAS94853	Human DNA sequenc
c 287	12	80.0	1473	16	AAZ60179	F. oxysporum endog	c 360	12	80.0	2456	23	ABL24188	Drosophila melanog
c 288	12	80.0	1473	19	AAV16103	Fusarium oxysporum	c 361	12	80.0	2464	24	ABA95855	Human flavoprotein
c 289	12	80.0	1506	22	AAH65250	C glutamicum codin	c 362	12	80.0	2465	21	AAZ94203	Human transferrase
c 290	12	80.0	1524	20	AAV82433	Human 25-hydroxyvi	c 363	12	80.0	2465	23	ABL05921	Drosophila melanog
c 291	12	80.0	1524	22	AAI76977	Human 25-hydroxyvi	c 364	12	80.0	2468	22	AAH99132	Human EST-derived
c 292	12	80.0	1527	20	AA559352	Human secreted pro	c 365	12	80.0	2469	20	AAV82438	Human 25-hydroxyvi
c 293	12	80.0	1527	22	AAS59233	Human cDNA encodin	c 366	12	80.0	2469	22	AAF76979	Human 25-hydroxyvi
c 294	12	80.0	1527	24	ABA90902	Human polynucleoti	c 367	12	80.0	2484	22	AAF80536	Receptor #24 parti
c 295	12	80.0	1543	24	ABN95910	Gene #2408 used to	c 368	12	80.0	2484	23	AAS83500	DNA encoding novel
c 296	12	80.0	1590	24	ABA96173	Human immunoavidin	c 369	12	80.0	2520	21	AAH78420	Human secreted pro
c 297	12	80.0	1603	22	AAI70989	C. glutamicum SRT	c 370	12	80.0	2528	22	AAH99142	Human EST-derived
c 298	12	80.0	1608	22	AAI88315	Human polynucleoti	c 371	12	80.0	2543	23	ABL26038	Drosophila melanog
c 299	12	80.0	1609	23	ABL12379	Drosophila melanog	c 372	12	80.0	2589	23	ABL11069	Drosophila melanog
c 300	12	80.0	1647	23	ABV21334	Human prostate exp	c 373	12	80.0	2627	24	ABL64775	Lung cancer relate
c 301	12	80.0	1647	23	ABV27153	Human prostate exp	c 374	12	80.0	2627	24	ABL65409	Lung cancer relate

375	12	80.0	2627	24	ABL66513	Lung cancer relate	448	12	80.0	4417	12	AAQ12163	Sequence encoding
376	12	80.0	2627	24	ABL68130	Ovary cancer relat	c 449	12	80.0	4457	23	ABLI1360	Drosophila melanog
377	12	80.0	2627	24	ABL69119	Kidney cancer rela	c 450	12	80.0	4462	23	ABL03182	Drosophila melanog
378	12	80.0	2638	11	AAQ03741	Human myb related	451	12	80.0	4531	22	AAI199538	Human polynucleoti
379	12	80.0	2638	19	RAV20468	Human B-myb oncoge	452	12	80.0	4566	23	ABL21404	Drosophila melanog
380	12	80.0	2641	22	AAI61175	Human polynucleoti	453	12	80.0	4600	23	ABL22914	Drosophila melanog
c 381	12	80.0	2652	22	AAH26468	Ancestral HIV-1 gr	c 454	12	80.0	4859	22	AA540336	DNA encoding human
c 382	12	80.0	2652	22	AAH26470	Semi-optmised anc	c 455	12	80.0	4859	22	AAU03936	Human reproductive
c 383	12	80.0	2652	22	AAH81451	Escherichia coli p	c 456	12	80.0	4916	23	ABL18373	Drosophila melanog
c 384	12	80.0	2656	24	AAH94947	Human DNA sequence	c 457	12	80.0	4925	23	ABL04854	Drosophila melanog
385	12	80.0	2661	22	AAI59389	Human polynucleoti	458	12	80.0	4967	22	AAK80212	Human immune/haema
386	12	80.0	2662	17	AAI08977	Actual shortened B	c 459	12	80.0	5140	23	ABLO7744	Drosophila melanog
387	12	80.0	2735	23	AAAS5641	DNA encoding novel	c 460	12	80.0	5154	23	AA504859	DNA encoding novel
388	12	80.0	2749	22	AAK94479	Human full-length	c 461	12	80.0	5186	16	AAO84967	E. coli PEPC gene
c 389	12	80.0	2793	24	ABK63722	Rat sequence diffe	c 462	12	80.0	5342	23	ABL24644	Drosophila melanog
c 390	12	80.0	2821	24	ABN80292	Human chemically m	c 463	12	80.0	5369	20	AAW78080	Drosophila melanog
c 391	12	80.0	2870	24	ABQ73050	Human GPRC5B-like	c 464	12	80.0	5410	23	ABL11068	Drosophila melanog
c 392	12	80.0	2888	23	ABLI16825	Drosophila melanog	c 465	12	80.0	5535	24	ABL92216	Chemically treated
c 393	12	80.0	2902	22	AAQ90433	Murine Lymph node	c 466	12	80.0	5535	24	ABL49317	Human immune syste
c 394	12	80.0	2979	23	ABL06852	Drosophila melanog	c 467	12	80.0	5572	23	ABL05920	Human polynucleoti
c 395	12	80.0	2993	22	AAI29134	Mouse full length	c 468	12	80.0	5676	15	AAQ64556	Streptomyces sp. c
c 396	12	80.0	3018	24	ABK15653	Rice lipoxigenase	c 469	12	80.0	5692	22	AAF32248	Drosophila melanog
c 397	12	80.0	3038	23	ABL13842	Drosophila melanog	470	12	80.0	5740	23	ABL21400	Human immune/haema
398	12	80.0	3149	22	AAI61108	Human polynucleoti	471	12	80.0	5742	22	AAK85933	Human immune/haema
399	12	80.0	3210	23	ABL13846	Drosophila melanog	c 472	12	80.0	5815	22	AAK71205	Human exostosin-4
c 400	12	80.0	3254	23	ABL10587	Drosophila melanog	c 473	12	80.0	5854	20	AAV72378	Drosophila melanog
c 401	12	80.0	3266	23	ABL16043	Drosophila melanog	c 474	12	80.0	5944	23	ABL06781	Drosophila melanog
c 402	12	80.0	3306	22	AAF87438	Corynebacterium th	c 475	12	80.0	5972	23	ABL05920	Chemically treated
c 403	12	80.0	3362	21	AAK77294	Human OREF ORF2849	c 476	12	80.0	6040	24	ABL92301	Human polynucleoti
c 404	12	80.0	3387	23	AA586456	DNA encoding novel	c 477	12	80.0	6040	24	ABL49370	Human polynucleoti
c 405	12	80.0	3402	23	AA588406	DNA encoding novel	c 478	12	80.0	6134	22	AA528462	Genomic sequence #
c 406	12	80.0	3416	23	ABL20856	Drosophila melanog	c 479	12	80.0	6172	21	AAAI2734	cDNA encoding huma
c 407	12	80.0	3479	21	AAAI2733	cDNA encoding mous	c 480	12	80.0	6189	24	ABR83455	Human cDNA differe
c 408	12	80.0	3496	24	ABK75331	Bacillus lichenifo	c 481	12	80.0	6223	23	AA578879	DNA encoding novel
c 409	12	80.0	3522	23	AA54200	Pseudomonas aerugi	c 482	12	80.0	6349	23	ABL20858	Drosophila melanog
c 410	12	80.0	3535	22	AAH47802	Chimeric CBD-fused	c 483	12	80.0	6412	23	ABL19284	Drosophila melanog
c 411	12	80.0	3536	22	AAI03917	Human caspase-10 D	c 484	12	80.0	6462	24	ABK83473	Human cDNA differe
c 412	12	80.0	3565	24	ABK83577	Human cDNA differe	c 485	12	80.0	6594	23	ABLI5639	Drosophila melanog
c 413	12	80.0	3590	21	AAZ94124	Haematopoietic ste	c 486	12	80.0	6690	23	ABL16769	Drosophila melanog
c 414	12	80.0	3701	16	AAQ79914	Cytochrome-P450-ox	c 487	12	80.0	6871	22	AA532589	Human genomic DNA
c 415	12	80.0	3761	23	ABL05157	Drosophila melanog	c 488	12	80.0	7045	23	ABL26034	Drosophila melanog
c 416	12	80.0	3779	22	AAK79402	Human immune/haema	c 489	12	80.0	7053	23	ABL29767	Drosophila melanog
c 417	12	80.0	3786	22	AAH73323	Human cervical can	c 490	12	80.0	7105	22	AAI37450	Human musculoskele
c 418	12	80.0	3820	23	ABL12378	Drosophila melanog	c 491	12	80.0	7507	22	AAK87178	Human immune/haema
c 419	12	80.0	3821	15	AAQ56609	Human PGF-2/NT-3 5	c 492	12	80.0	7734	22	AA527657	DNA encoding novel
c 420	12	80.0	3821	20	AA334365	Human nerve growth	c 493	12	80.0	7734	22	AAK72311	Human immune/haema
c 421	12	80.0	3821	24	AAAD30143	Human nerve growth	c 494	12	80.0	8284	22	AAI26526	Human breast cance
c 422	12	80.0	3821	24	ARA92502	Human nerve growth	c 495	12	80.0	8284	22	AAI26526	Human breast cance
c 423	12	80.0	3852	20	AAZ20298	Human G-protein co	c 496	12	80.0	8284	22	AAI26600	Human immune/haema
c 424	12	80.0	3889	24	ABA97001	Human ZFP36 gene.	c 497	12	80.0	8450	22	AAK71204	Human immune/haema
c 425	12	80.0	3901	22	AA561042	Human cancer agent	c 498	12	80.0	8467	23	ABL10586	Drosophila melanog
c 426	12	80.0	3901	23	ABV22740	Human prostate exp	c 499	12	80.0	8588	22	AAH26896	Human androgen rec
c 427	12	80.0	3901	23	ABV28568	Human prostate exp	500	12	80.0	8601	13	AAQ24828	AFP-1. Homo sapie
c 428	12	80.0	3921	22	AAH18220	Human cDNA sequenc	501	12	80.0	8601	13	AAQ24829	AFP-1 (C 7508 T).
c 429	12	80.0	3922	23	ABL28094	Drosophila melanog	502	12	80.0	9339	22	AAI02697	Human reproductive
c 430	12	80.0	3953	22	AAK85377	Human immune/haema	c 503	12	80.0	9447	23	ABL29766	Drosophila melanog
c 431	12	80.0	3973	20	AAV65326	Human neuronatin g	c 504	12	80.0	9450	23	AAK06780	Drosophila melanog
c 432	12	80.0	4031	18	AAI84485	Mouse alpha-1 coll	c 505	12	80.0	9905	24	AAK98324	Human purinergic-r
c 433	12	80.0	4117	22	AAI77276	Rat cDNA encoding	c 506	12	80.0	10036	23	ABL10488	Drosophila melanog
c 434	12	80.0	4138	7	AAI06683	Sequence of premel	c 507	12	80.0	10117	22	AAK87179	Human immune/haema
c 435	12	80.0	4160	22	AA527609	DNA encoding novel	c 508	12	80.0	10468	23	ABL05156	Drosophila melanog
c 436	12	80.0	4160	22	AA527746	DNA encoding novel	c 509	12	80.0	10514	24	ABK10772	Human small induci
c 437	12	80.0	4160	22	AAK77304	Human immune/haema	510	12	80.0	10515	24	AAK66446	Human immune/haema
c 438	12	80.0	4163	23	ABL24628	Drosophila melanog	511	12	80.0	11125	22	AAK74606	Human immune/haema
c 439	12	80.0	4185	22	AA527611	DNA encoding novel	c 512	12	80.0	11244	22	AAK74606	Kidney cancer rela
c 440	12	80.0	4185	22	AA527748	DNA encoding novel	513	12	80.0	11893	24	ABL68924	Drosophila melanog
c 441	12	80.0	4185	22	AAK77305	Human immune/haema	514	12	80.0	13549	23	ABL07964	Drosophila melanog
c 442	12	80.0	4200	23	AA551542	Pseudomonas aerugi	c 515	12	80.0	14333	23	ABL28579	Mouse ischaemic co
c 443	12	80.0	4238	24	ABK84776	Human cDNA differe	516	12	80.0	14775	24	ABI99535	Human box-dependen
c 444	12	80.0	4238	24	ABL69127	Kidney cancer rela	517	12	80.0	14985	17	AAI3574	Human Bin1 gene.
c 445	12	80.0	4262	21	AA645577	E. tenella cGMP de	518	12	80.0	14985	19	AAI3574	Human Bin1 gene.
c 446	12	80.0	4285	23	ABL25336	Drosophila melanog	c 519	12	80.0	15296	22	AAK74605	Human immune/haema
c 447	12	80.0	4413	23	AA583715	DNA encoding novel	c 520	12	80.0	15606	23	ABL16881	Drosophila melanog

c 521	12	80.0	17269	23	ABL14506	Drosophila melanog	594	11	73.3	15	17	AAT49764	Human CETP HH ribo
c 522	12	80.0	17677	22	AAK70506	Human immune/haema	595	11	73.3	15	17	AAT49766	Human CETP HH ribo
c 523	12	80.0	17677	22	AAK84095	Human immune/haema	596	11	73.3	15	17	AAT49762	Human CETP HH ribo
c 524	12	80.0	17949	22	AAH89228	Human signal trans	597	11	73.3	24	16	AAT00183	Hepatitis GB virus
c 525	12	80.0	18132	22	AAK67033	Human immune/haema	598	11	73.3	24	21	AAAS5451	Hepatitis GB virus
c 526	12	80.0	18132	22	AAK79622	Human immune/haema	c 599	11	73.3	30	22	AAAD10246	Human fibrinogen (
c 527	12	80.0	18522	23	AAAS59560	Propionibacterium	c 600	11	73.3	31	21	AAA78804	Human genomic DNA
c 528	12	80.0	18533	22	AAK75941	Human immune/haema	c 601	11	73.3	35	21	AAZ49995	Bacteriophage T7 p
c 529	12	80.0	18647	21	AAF21059	Human low adenosin	c 602	11	73.3	40	24	AAAL48381	Cytohesin binding
c 530	12	80.0	18648	21	AAK34937	Human adenosine re	c 603	11	73.3	41	22	AAAH49741	Human amylase 8 co
c 531	12	80.0	18648	24	ABL65840	Lung cancer relate	c 604	11	73.3	41	22	AAAH49742	Human amylase 8 co
c 532	12	80.0	18648	24	ABL69114	Kidney cancer rela	c 605	11	73.3	50	19	AAV95556	Human c-fos hairpi
c 533	12	80.0	19861	22	AAK71206	Human immune/haema	c 606	11	73.3	50	22	AAI75275	Human silent SNP c
c 534	12	80.0	19942	22	AAK87416	Human immune/haema	c 607	11	73.3	51	18	AAAT69953	Human silent SNP c
c 535	12	80.0	20015	22	ABA20740	Human nervous syst	c 608	11	73.3	51	22	AAI75274	PCR primer RG749
c 536	12	80.0	20097	22	AAAS32695	Human genomic DNA	c 609	11	73.3	54	18	AAAT69954	Human silent SNP c
c 537	12	80.0	20097	22	AAAS42142	Genomic sequence #	c 610	11	73.3	60	20	AAAX36609	PCR primer RG750
c 538	12	80.0	20366	23	ABL28578	Drosophila melanog	c 611	11	73.3	60	22	AAAF5488	Mammalian CETP imm
c 539	12	80.0	20645	22	AAI05355	Human reproductive	c 612	11	73.3	60	22	AAAF5488	Nucleotide sequenc
c 540	12	80.0	20645	23	ABL98224	Human testicular a	c 613	11	73.3	60	24	ABN59243	Human spliced tran
c 541	12	80.0	21010	22	AAI05888	Human reproductive	c 614	11	73.3	60	24	ABN59339	Human spliced tran
c 542	12	80.0	21010	22	AAK89247	Human digestive sy	c 615	11	73.3	65	24	ABN55183	Human spliced tran
c 543	12	80.0	21010	23	ABL98452	Human testicular a	c 616	11	73.3	70	13	AAQ35815	Mouse spliced tran
c 544	12	80.0	21024	22	AAI05889	Human reproductive	c 617	11	73.3	70	13	AAQ35816	Annealing oligonuc
c 545	12	80.0	21024	22	AAK89248	Human digestive sy	c 618	11	73.3	70	24	ABH98923	Oligonucleotide RW
c 546	12	80.0	21024	23	ABL98453	Human testicular a	c 619	11	73.3	70	24	ABH98924	Oligonucleotide RW
c 547	12	80.0	21185	21	AAK63350	Streptomyces globi	c 620	11	73.3	91	24	ABL71090	Corn tassell-deri
c 548	12	80.0	21606	22	AAAS36233	Human cardiovascular	c 621	11	73.3	94	24	AAAL48339	Cytohesin binding
c 549	12	80.0	21606	23	ABL28639	Drosophila melanog	c 622	11	73.3	139	22	ABA50440	Human breast cell
c 550	12	80.0	22253	23	ABL16042	Drosophila melanog	c 623	11	73.3	139	22	ABA68390	Human foetal liver
c 551	12	80.0	22401	22	AAK71911	Human immune/haema	c 624	11	73.3	139	22	ABA35385	Probe #13951 for g
c 552	12	80.0	22402	22	AAK71912	Human immune/haema	c 625	11	73.3	139	22	AAK16763	Human brain expres
c 553	12	80.0	23452	22	AAAS42122	Genomic sequence #	c 626	11	73.3	139	22	AAK42540	Human bone marrow
c 554	12	80.0	23457	22	AAAS42121	Genomic sequence #	c 627	11	73.3	139	22	AAI23286	Probe #13219 for g
c 555	12	80.0	23458	22	AAAS42120	Genomic sequence #	c 628	11	73.3	139	22	AAI23286	Probe #17292 used
c 556	12	80.0	23580	22	AAAS28556	Genomic sequence #	c 629	11	73.3	139	22	AAI08927	Probe #8918 used t
c 557	12	80.0	23580	22	AAK87248	Human immune/haema	c 630	11	73.3	139	24	ABS16584	Human genome-deriv
c 558	12	80.0	23677	20	AAI16323	Partial human geno	c 631	11	73.3	150	22	AAK70658	Human immune/haema
c 559	12	80.0	24236	23	ABL16880	Drosophila melanog	c 632	11	73.3	151	22	AAK85943	Human immune/haema
c 560	12	80.0	24593	6	AAAS50226	Sequence of opine	c 633	11	73.3	160	24	AAAD27054	Plasmid pGN1 DNA f
c 561	12	80.0	24596	6	AAAS50182	Complete nucleotid	c 634	11	73.3	161	21	AAAC13763	Human secreted pro
c 562	12	80.0	25956	23	ABL28638	Drosophila melanog	c 635	11	73.3	162	21	AAAC13766	Human secreted pro
c 563	12	80.0	32012	22	AAI05864	Human reproductive	c 636	11	73.3	162	21	AAAC13344	Human secreted pro
c 564	12	80.0	32012	23	ABL98428	Human testicular a	c 637	11	73.3	164	21	AAK86934	Human immune/haema
c 565	12	80.0	32190	22	AAAS36709	Human cardiovascular	c 638	11	73.3	169	21	AAK14237	Human secreted pro
c 566	12	80.0	36336	23	ABL08764	Drosophila melanog	c 639	11	73.3	170	21	AAAC14237	Human secreted pro
c 567	12	80.0	41335	22	AAK86202	Human immune/haema	c 640	11	73.3	183	21	AAAC12186	Human secreted pro
c 568	12	80.0	47670	23	ABL16824	Drosophila melanog	c 641	11	73.3	183	24	ABN18469	Human OREF polynuc
c 569	12	80.0	50368	23	ABL16768	Drosophila melanog	c 642	11	73.3	199	22	ABA16948	Human nervous syst
c 570	12	80.0	62944	24	ABL66947	Lung cancer relate	c 643	11	73.3	214	21	AAAC13975	Human secreted pro
c 571	12	80.0	62944	24	ABL68262	Kidney cancer rela	c 644	11	73.3	228	22	ABA50316	Human breast cell
c 572	12	80.0	63164	21	AAK63348	Streptomyces globi	c 645	11	73.3	228	22	ABA35269	Probe #13735 for g
c 573	12	80.0	73465	24	ABQ88161	Human osteoblast d	c 646	11	73.3	228	22	AAK16638	Human brain expres
c 574	12	80.0	86080	24	ABQ88164	Human osteoblast d	c 647	11	73.3	228	22	AAK42397	Human bone marrow
c 575	12	80.0	86080	24	AAK83561	Human cDNA differe	c 648	11	73.3	228	22	AAI08815	Probe #8806 used t
c 576	12	80.0	89328	24	ABL61995	Colon adenocarcino	c 649	11	73.3	230	24	AAAD27060	Plasmid pGN1 DNA f
c 577	12	80.0	97835	24	AAK84796	Human cDNA differe	c 650	11	73.3	234	22	ABA70545	Human foetal liver
c 578	12	80.0	110608	24	AAK83572	Human cDNA differe	c 651	11	73.3	234	22	ABA71408	Human foetal liver
c 579	12	80.0	129722	24	ABQ88117	Human osteoblast d	c 652	11	73.3	234	22	ABA37148	Probe #15614 for g
c 580	12	80.0	149480	24	ABL61947	Colon adenocarcino	c 653	11	73.3	234	22	AAK18790	Probe #16095 for g
c 581	12	80.0	149480	24	ABL61947	Colon adenocarcino	c 654	11	73.3	234	22	AAK19728	Human brain expres
c 582	12	80.0	149480	24	ABL61948	Colon adenocarcino	c 655	11	73.3	234	22	AAK44727	Human bone marrow
c 583	12	80.0	149480	24	ABL61948	Colon adenocarcino	c 656	11	73.3	234	22	AAK45748	Human bone marrow
c 584	12	80.0	149480	24	ABL68365	Kidney cancer rela	c 657	11	73.3	234	22	AAI24990	Probe #14923 for g
c 585	12	80.0	149480	24	ABL68365	Kidney cancer rela	c 658	11	73.3	234	22	AAI25381	Probe #15314 for g
c 586	12	80.0	167343	24	ABL64403	Stomach cancer rel	c 659	11	73.3	234	22	AAI50705	Probe #19391 used
c 587	12	80.0	167343	24	ABL67239	Thyroid cancer rel	c 660	11	73.3	234	22	AAI51674	Probe #20360 used
c 588	12	80.0	302250	24	ABL67703	Oesophagus cancer	c 661	11	73.3	234	22	ABS18965	Human genome-deriv
c 589	12	80.0	309400	22	AAH68534	C glutamicum codin	c 662	11	73.3	234	24	ABS20026	Human genome-deriv
c 590	12	80.0	309400	22	AAH68534	C glutamicum codin	c 663	11	73.3	243	22	AAK67346	Human immune/haema
c 591	12	80.0	325791	22	AAH68534	Human oestrogen re	c 664	11	73.3	243	22	AAK67348	Human immune/haema
c 592	12	80.0	349980	22	AAH41226	Pyrococcus abyssi	c 665	11	73.3	243	22	AAK67349	Human immune/haema
c 593	12	80.0	349980	22	AAH64966	C glutamicum codin	c 666	11	73.3	245	21	AAAC27911	Human secreted pro

c 667	11	73.3	246	24	ABK74699	Bacillus lichenifo	c 740	11	73.3	389	21	AAC00960	Human secreted pro
c 668	11	73.3	248	21	AAA45247	Human secreted exp	c 741	11	73.3	390	22	AAS40332	DNA encoding human
c 669	11	73.3	251	21	AAC04345	Human secreted pro	c 742	11	73.3	390	22	AAO03932	Human reproductive
c 670	11	73.3	263	22	ABA16947	Human nervous syst	c 743	11	73.3	390	24	ABK39017	cDNA encoding lung
671	11	73.3	267	24	ABN19830	Human ORFX polynuc	c 744	11	73.3	391	22	AAI86822	Human polynucleoti
672	11	73.3	269	21	AAA31621	Plant microsatelli	745	11	73.3	393	21	AAC28592	Human secreted pro
673	11	73.3	274	16	AAT20999	Human gene signatu	c 746	11	73.3	393	22	AAS40330	DNA encoding human
674	11	73.3	276	21	AAC03087	Human secreted pro	c 747	11	73.3	393	22	AAO03930	Human reproductive
675	11	73.3	280	21	AAC23009	Human secreted pro	c 748	11	73.3	393	24	ABK80520	Bacillus clausii g
c 676	11	73.3	283	24	ABL40182	Phanerochaete chry	749	11	73.3	396	22	ABK94968	Human ovarian cnc
c 677	11	73.3	284	21	AAC48086	Zea mays DNA fragm	750	11	73.3	396	22	ABT03235	Human ovarian carc
678	11	73.3	285	23	ABV55515	Human prostate exp	751	11	73.3	396	24	ABL48918	Ovarian carcinoma
c 679	11	73.3	286	14	AAQ00018	Human brain Expres	c 752	11	73.3	397	21	AAC02453	Novel human polynu
c 680	11	73.3	286	24	ABL73864	Corn tassal-deriv	c 753	11	73.3	397	22	ABF65137	Human prostate exp
681	11	73.3	300	20	AAZ14730	Human gene express	754	11	73.3	397	23	ABV35913	Human prostate exp
682	11	73.3	301	24	ABK76169	Bacillus lichenifo	755	11	73.3	397	23	ABV44976	Human prostate exp
683	11	73.3	308	22	AAS47033	Human breast cnc	756	11	73.3	405	24	ABN79264	Human transport pr
684	11	73.3	308	22	AAFI7603	Human breast cnc	c 757	11	73.3	409	21	AAA63745	DNA encoding a pol
685	11	73.3	308	24	ABK95068	Human breast tumou	758	11	73.3	410	22	AAS60195	Human cancer agent
686	11	73.3	312	22	ABA18819	Human nervous syst	759	11	73.3	410	23	AAS64312	DNA encoding novel
c 687	11	73.3	315	23	ABL14057	Drosophila melanog	c 760	11	73.3	411	22	AAF64900	Novel human polynu
688	11	73.3	319	24	ABL66236	Lung cancer relate	c 761	11	73.3	416	21	AAFI8000	Lung cancer associ
c 689	11	73.3	322	22	AAI82727	Human polynucleoti	762	11	73.3	420	21	AAC01121	Human secreted pro
c 690	11	73.3	323	24	ABN18578	Human ORFX polynuc	763	11	73.3	420	21	AAZ42745	Human 5' EST isola
691	11	73.3	324	16	AAT19143	Human gene signatu	c 764	11	73.3	420	24	ABK64308	Human benign prost
c 692	11	73.3	324	17	AAT13728	ACNPV ORF 149, res	765	11	73.3	422	22	AAI16610	Human novel protei
c 693	11	73.3	329	24	ABO56111	Human ovarian anti	766	11	73.3	422	23	ABK43938	DNA encoding novel
694	11	73.3	330	24	ABN24989	Human ORFX polynuc	767	11	73.3	424	22	AAK56301	Human immune/haema
c 695	11	73.3	335	23	ABV47908	Human prostate exp	c 768	11	73.3	424	23	ABV22622	Human prostate exp
c 696	11	73.3	336	20	AAAX0691	Human secreted pro	c 769	11	73.3	424	23	ABV28444	Human prostate exp
c 697	11	73.3	338	22	AAS37594	Novel human diagno	770	11	73.3	426	21	AAC12329	Human secreted pro
698	11	73.3	340	20	AAAX57202	Porcine Oct-4 exon	771	11	73.3	427	22	AAI20935	Human breast cnc
c 699	11	73.3	342	24	ABN24124	Human ORFX polynuc	772	11	73.3	428	22	AAI12050	Human breast cnc
700	11	73.3	343	21	AAC56650	Eucalyptus grandis	c 773	11	73.3	428	24	ABL84237	Human ovarian cnc
701	11	73.3	345	21	AAC56063	Eucalyptus grandis	c 774	11	73.3	429	23	ABV46777	Human prostate exp
702	11	73.3	345	21	AAS56644	M. tuberculosis an	775	11	73.3	435	13	AAV03986	Human prostate exp
703	11	73.3	348	20	AAZ19425	M. tuberculosis re	c 776	11	73.3	438	22	AAK55779	Human immune/haema
704	11	73.3	348	20	AAZ19213	Human immune/haema	777	11	73.3	438	24	ABQ90685	M. capsulatus gene
705	11	73.3	349	22	AAK68365	Human immune/haema	c 778	11	73.3	439	23	ABV13206	Human prostate exp
706	11	73.3	349	22	AAK82408	Human prostate exp	779	11	73.3	441	22	ABA42616	Human breast cell
707	11	73.3	349	23	ABV15112	Streptomyces sp. c	780	11	73.3	441	22	ABA53045	Human foetal liver
708	11	73.3	350	24	ABN88915	Human polynucleoti	781	11	73.3	441	22	ABA22819	Probe #1285 for ge
c 709	11	73.3	351	22	AAI89605	Human nervous syst	782	11	73.3	441	22	AAK01293	Human brain expres
710	11	73.3	354	22	ABA19471	Human secreted pro	783	11	73.3	441	22	AAK26753	Human bone marrow
711	11	73.3	358	21	AAC22938	Human secreted pro	784	11	73.3	441	22	AAI11381	Probe #1314 for ge
c 712	11	73.3	358	22	AAK78857	Human immune/haema	785	11	73.3	441	22	AAI32649	Probe #1335 used t
c 713	11	73.3	358	22	AAK78858	Human immune/haema	786	11	73.3	441	22	AAI01297	Probe #1288 used t
c 714	11	73.3	360	21	AAZ50397	Human interferon-i	c 787	11	73.3	441	22	ABK92846	Bacillus DNA encod
715	11	73.3	361	13	AAQ27208	PDGF-B7, Syntheti	788	11	73.3	441	24	ABS01348	Human genome-deriv
716	11	73.3	361	20	AAAX41031	Human secreted pro	789	11	73.3	441	24	ABL83271	Human ovarian cnc
717	11	73.3	362	22	ABA45180	Human breast cell	790	11	73.3	442	23	AAS68611	DNA encoding novel
718	11	73.3	362	22	ABA23357	Probe #3823 for ge	791	11	73.3	442	24	ABN64468	Human cancer relat
719	11	73.3	362	22	ABA09648	Human bone marrow	792	11	73.3	443	24	ABN62530	Human cancer relat
720	11	73.3	362	22	AAK03688	Human brain expres	c 793	11	73.3	446	21	AAF08137	Fusarium venenatum
721	11	73.3	362	22	AAK29357	Human bone marrow	c 794	11	73.3	447	22	AAI93786	Human polynucleoti
722	11	73.3	362	22	AAI03812	Probe #3803 used t	795	11	73.3	450	22	AAS60194	Human cancer agent
c 723	11	73.3	369	22	AAAS9183	Human cancer relat	796	11	73.3	451	21	AAF08070	Fusarium venenatum
724	11	73.3	370	22	ABA45307	Human breast cell	c 797	11	73.3	451	23	ABV04037	Human prostate exp
725	11	73.3	370	22	ABA55796	Human foetal liver	798	11	73.3	454	22	AAAS1644	cDNA encoding nove
726	11	73.3	370	22	ABA25477	Probe #3943 for ge	c 799	11	73.3	456	21	AAC74976	Human ORFX ORF531
727	11	73.3	370	22	ABA04017	Human brain expres	c 800	11	73.3	458	23	ABV34325	Human prostate exp
728	11	73.3	370	22	AAK29504	Human bone marrow	c 801	11	73.3	458	23	ABV43186	Human genome-deriv
729	11	73.3	370	22	AAI14074	Probe #4007 for ge	802	11	73.3	458	24	ABV23895	Human prostate exp
730	11	73.3	370	22	AAI35454	Probe #4140 used t	c 803	11	73.3	459	23	ABV52949	Human prostate exp
731	11	73.3	370	22	AAI03927	Probe #3918 used t	804	11	73.3	459	24	ABN65832	Human cancer relat
732	11	73.3	370	22	ABS04052	Human genome-deriv	c 805	11	73.3	461	22	AAK01575	Human brain expres
c 733	11	73.3	373	22	AAAS9182	Human cancer relat	c 806	11	73.3	461	22	AAK61455	Human immune/haema
c 734	11	73.3	375	22	ABA11654	Human nervous syst	c 807	11	73.3	461	22	AAI01547	Probe #1538 used t
735	11	73.3	379	22	AAAS60648	Human cancer agent	c 808	11	73.3	461	23	ABV09422	Human prostate exp
c 736	11	73.3	381	21	AAK97347	Helicobacter pylor	c 809	11	73.3	462	20	AAV84302	Wheat geminivirus
c 737	11	73.3	383	22	AAF64677	Novel human polynu	810	11	73.3	462	23	AAAS74211	DNA encoding novel
c 738	11	73.3	384	22	AAI91239	Human polynucleoti	c 811	11	73.3	464	22	AAH99201	Human protein enco
c 739	11	73.3	386	22	AAF64412	Novel human polynu	c 812	11	73.3	467	24	ABL87387	Human ovarian cnc

c 813	11	73.3	470	21	AAC53876	Arabidopsis thalia	886	11	73.3	547	24	ABQ19219	Oligonucleotide fo
814	11	73.3	471	22	ABA57882	Human foetal liver	c 887	11	73.3	550	23	ABV57531	Human prostate exp
815	11	73.3	471	22	ABA27213	Probe #5679 for ge	c 888	11	73.3	552	24	ABQ16336	Oligonucleotide fo
816	11	73.3	471	22	AAK05955	Human brain expres	c 889	11	73.3	552	24	ABQ16337	Oligonucleotide fo
817	11	73.3	471	22	AAK31596	Human bone marrow	890	11	73.3	553	22	ABA63348	Human foetal liver
818	11	73.3	471	22	AAI15744	Probe #5677 for ge	891	11	73.3	553	22	ABA30552	Human bone marrow
819	11	73.3	471	22	AAI37475	Probe #6161 used t	892	11	73.3	553	22	AAK37590	Human bone marrow
820	11	73.3	471	24	ABSO6350	Human genome-deriv	893	11	73.3	553	22	AAI18347	Probe #8280 for ge
821	11	73.3	474	24	ABO91381	M. capsulatus gene	894	11	73.3	553	22	AAI43462	Probe #12148 used
c 822	11	73.3	474	24	ABY199634	Mouse ischaemic co	895	11	73.3	553	22	ABS11576	Human genome-deriv
c 823	11	73.3	476	22	AAI93440	Human polynucleoti	c 896	11	73.3	555	21	AAA39473	Human RBP 11 DNA.
824	11	73.3	478	24	ABM94180	Gene #678 used to	c 897	11	73.3	555	24	ABQ56320	Human colon cancer
825	11	73.3	478	24	ABL63371	Breast cancer rela	c 898	11	73.3	559	22	ABA60540	Human foetal liver
826	11	73.3	478	24	ABL63783	Breast cancer rela	c 899	11	73.3	559	22	AAK08821	Human brain expres
c 827	11	73.3	479	21	AAC41321	Zea mays DNA fragm	c 900	11	73.3	559	22	AAK34708	Human bone marrow
c 828	11	73.3	480	20	AAAX24499	Human SR-BI gene e	c 901	11	73.3	559	22	AAI40429	Probe #9115 used t
c 829	11	73.3	480	20	AAAX24591	Human SR-BI gene e	c 902	11	73.3	560	24	ABQ34672	Oligonucleotide fo
c 830	11	73.3	483	22	AAI86667	Human polynucleoti	903	11	73.3	560	24	ABQ34673	Oligonucleotide fo
c 831	11	73.3	483	22	AAK30682	Human bone marrow	904	11	73.3	561	21	AACT6986	Human ORFX ORF2541
c 832	11	73.3	483	24	ABL91792	Human polynucleoti	c 905	11	73.3	562	23	ABV59302	Human prostate exp
c 833	11	73.3	484	23	ABV00253	Human prostate exp	c 906	11	73.3	568	21	AACT6527	Human ORFX ORF2082
c 834	11	73.3	484	22	ABA20246	Human nervous syst	c 907	11	73.3	572	21	AAF10180	Fusarium venenatum
c 835	11	73.3	488	22	AAAL0200	Human breast cancer	c 908	11	73.3	572	22	AAH13292	Human cDNA clone (
c 836	11	73.3	488	22	AAAL19780	Human breast cancer	c 909	11	73.3	573	23	ABV16982	Human prostate exp
c 837	11	73.3	488	22	AAI18187	Human polynucleoti	910	11	73.3	574	22	ABA88607	Escherichia coli p
c 838	11	73.3	489	22	ABA43763	Human breast cell	911	11	73.3	575	22	ABA61146	Human foetal liver
c 839	11	73.3	489	22	ABA54220	Human foetal liver	912	11	73.3	575	22	AAK09441	Human brain expres
c 840	11	73.3	489	22	ABA57936	Human foetal liver	913	11	73.3	575	22	AAK35333	Human bone marrow
c 841	11	73.3	489	22	ABA23968	Probe #2434 for ge	914	11	73.3	575	22	AAI41046	Probe #9732 used t
c 842	11	73.3	489	22	ABA27240	Probe #5706 for ge	915	11	73.3	575	22	AAH09628	Human cDNA clone (
c 843	11	73.3	489	22	AAK02497	Human brain expres	c 916	11	73.3	577	24	ABQ46256	Oligonucleotide fo
c 844	11	73.3	489	22	AAK06009	Human brain expres	917	11	73.3	577	24	ABQ46257	Oligonucleotide fo
c 845	11	73.3	489	22	AAK31653	Human bone marrow	c 918	11	73.3	578	24	ABQ38468	Oligonucleotide fo
c 846	11	73.3	489	22	AAI15771	Probe #5704 for ge	919	11	73.3	578	24	ABQ38469	Oligonucleotide fo
c 847	11	73.3	489	22	AAI37530	Probe #6216 used t	c 920	11	73.3	581	24	ABQ46608	Oligonucleotide fo
c 848	11	73.3	489	22	AAI02422	Probe #2413 used t	921	11	73.3	581	24	ABQ46609	Oligonucleotide fo
c 849	11	73.3	489	24	ABSO2394	Human genome-deriv	922	11	73.3	582	24	AAAS42487	Human cDNA encodin
c 850	11	73.3	489	24	ABSO6408	Human genome-deriv	c 923	11	73.3	582	24	ABQ49072	Oligonucleotide fo
c 851	11	73.3	494	24	ABO60169	Human colon cancer	924	11	73.3	582	24	ABQ49073	Oligonucleotide fo
852	11	73.3	500	24	ABQ73194	C. glutanicum tran	c 925	11	73.3	584	24	ABQ25760	Oligonucleotide fo
c 853	11	73.3	502	21	ABQ79286	Human lung tumour-	926	11	73.3	584	24	ABQ25761	Oligonucleotide fo
c 854	11	73.3	502	23	AAAD23362	Human lung tumour-	c 927	11	73.3	584	24	AAF09369	Fusarium venenatum
c 855	11	73.3	507	22	ABA60120	Human foetal liver	c 928	11	73.3	584	24	AAI15299	Human breast cancer
c 856	11	73.3	507	22	ABA28478	Probe #6944 for ge	c 929	11	73.3	590	22	AAAD08504	Human secreted pro
c 857	11	73.3	507	22	AAK08396	Human brain expres	c 930	11	73.3	599	23	AAAS83950	DNA encoding novel
c 858	11	73.3	507	22	AAK34276	Human bone marrow	c 931	11	73.3	606	23	ABV50586	Human prostate exp
c 859	11	73.3	507	22	AAI39999	Probe #8685 used t	c 932	11	73.3	607	24	ABK83886	Human cDNA differe
c 860	11	73.3	507	24	ABSO9003	Human genome-deriv	c 933	11	73.3	612	21	AAF07825	Fusarium venenatum
c 861	11	73.3	507	24	ABQ56838	Human colon cancer	c 934	11	73.3	612	21	AACT77160	Human ORFX ORF2715
c 862	11	73.3	508	22	ABA13728	Human nervous syst	c 935	11	73.3	612	22	AAAD08528	Human secreted pro
863	11	73.3	508	22	AAK62580	Human immune/haema	936	11	73.3	617	22	AAK82842	Human immune/haema
864	11	73.3	508	24	ABL79848	Human ovarian canc	937	11	73.3	617	22	AAK82843	Human immune/haema
865	11	73.3	510	22	AAAS60609	Human cancer agent	c 938	11	73.3	618	23	AAAS84878	DNA encoding novel
866	11	73.3	510	22	AAK92676	Human cDNA 3'-end	939	11	73.3	619	24	ABN61608	Human cancer relat
867	11	73.3	514	13	AAQ27204	Synthetic PDGF-B g	940	11	73.3	625	22	ABA08653	Human zn finger pr
868	11	73.3	514	13	AAQ27205	Synthetic PDGF-B g	c 941	11	73.3	625	22	ABQ41922	Oligonucleotide fo
c 869	11	73.3	515	24	ABQ44524	Oligonucleotide fo	942	11	73.3	625	24	ABQ41923	Oligonucleotide fo
c 870	11	73.3	515	24	ABQ44525	Oligonucleotide fo	c 943	11	73.3	625	24	ABQ47864	Oligonucleotide fo
871	11	73.3	516	24	ABN62480	Human cancer relat	944	11	73.3	625	24	ABQ47865	Oligonucleotide fo
c 872	11	73.3	519	22	AAF85226	Nucleotide sequenc	945	11	73.3	627	23	AAAS87080	Oligonucleotide fo
c 873	11	73.3	519	22	AAH29605	Drosophila melanog	946	11	73.3	629	23	AAAS87081	N. meningitidis pa
874	11	73.3	520	24	ABK54836	Human colon cancer	c 947	11	73.3	633	23	ABL04069	Drosophila melanog
c 875	11	73.3	528	24	ABL87359	Human ovarian canc	c 948	11	73.3	634	24	ABQ57032	Human colon cancer
c 876	11	73.3	538	24	ABN59715	Novel human coding	949	11	73.3	638	21	AAF14136	Aspergillus oryzae
c 877	11	73.3	539	22	AAH11837	Human cDNA clone (	950	11	73.3	639	22	AAH65877	c glutamicum codin
878	11	73.3	540	22	AAH10637	Human cDNA clone (	c 951	11	73.3	641	24	ABQ33134	Oligonucleotide fo
c 879	11	73.3	541	23	ABV52199	Human prostate exp	952	11	73.3	641	24	ABQ33135	Oligonucleotide fo
880	11	73.3	543	24	ABS11537	Human genome-deriv	c 953	11	73.3	646	24	ABQ42450	Oligonucleotide fo
881	11	73.3	544	19	AAV69687	Human glial cell l	954	11	73.3	646	24	ABQ42451	Oligonucleotide fo
c 882	11	73.3	546	23	ABV30598	Human prostate exp	955	11	73.3	647	22	AAH07347	Human cDNA clone (
c 883	11	73.3	546	23	ABV39567	Human prostate exp	c 956	11	73.3	650	24	ABK36109	cDNA sequence #500
c 884	11	73.3	546	24	ABK63776	Rat sequence diffe	c 957	11	73.3	654	24	ABQ44552	Oligonucleotide fo
c 885	11	73.3	547	24	ABQ19218	Oligonucleotide fo	958	11	73.3	654	24	ABQ44553	Oligonucleotide fo

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c 959 11 73.3 656 24 ABQ22194- Oligonucleotide fo
960 11 73.3 656 24 ABQ22195- Oligonucleotide fo
961 11 73.3 659 24 AAS62648 cDNA sequence #435
c 962 11 73.3 661 22 AAL24145 Human breast cance
963 11 73.3 662 13 AAQ32354 MAGE-21 gene. Hom
964 11 73.3 662 15 AAQ72479 Tumour rejection a
965 11 73.3 662 20 AAX84115 MAGE-21 gene. Hom
c 966 11 73.3 669 24 ABQ41786 Oligonucleotide fo
967 11 73.3 669 24 ABQ41787 Oligonucleotide fo
c 968 11 73.3 671 24 ABN73729 Bovine embryonic g
969 11 73.3 673 19 AAV42305 HCV core protein c
c 970 11 73.3 673 22 AAF25492 Nucleotide sequenc
c 971 11 73.3 690 24 ABQ21698 Oligonucleotide fo
972 11 73.3 690 24 ABQ21699 Oligonucleotide fo
c 973 11 73.3 692 22 AAH04686 Human cDNA clone (
974 11 73.3 693 17 AAT08703 Partial human OCT-
c 975 11 73.3 697 21 AAC03865 Human secreted pro
c 976 11 73.3 705 24 ABQ36860 Oligonucleotide fo
977 11 73.3 705 24 ABQ36861 Oligonucleotide fo
c 978 11 73.3 707 22 AAK58487 Human immune/haema
c 979 11 73.3 711 20 AAX34231 Mycobacterium spec
c 980 11 73.3 714 21 AAF13004 Aspergillus oryzae
981 11 73.3 714 22 AAH98816 Human ESI-derived
982 11 73.3 720 22 AAK91837 Human cDNA 5'-end
c 983 11 73.3 720 22 AAK93239 Human cDNA clone r
c 984 11 73.3 720 24 ABK77214 Bacillus clausii g
985 11 73.3 724 24 ABQ88914 Human prostate exp
c 986 11 73.3 724 24 RAD31158 Human Alzheimer's
c 987 11 73.3 724 24 ABQ43744 Oligonucleotide fo
988 11 73.3 724 24 ABQ43745 Oligonucleotide fo
c 989 11 73.3 725 24 ABK34436 Human cDNA for nov
990 11 73.3 730 24 ABN87190 Lolium perenne LpO
c 991 11 73.3 736 21 AAF21773 Human breast and o
c 992 11 73.3 738 24 ABQ43318 Oligonucleotide fo
993 11 73.3 738 24 ABQ43319 Oligonucleotide fo
c 994 11 73.3 739 20 AAZ24832 Human secreted pro
c 995 11 73.3 739 22 AAF44795 Cysteine protease
c 996 11 73.3 740 24 ABQ41086 Oligonucleotide fo
997 11 73.3 740 24 ABQ41087 Oligonucleotide fo
c 998 11 73.3 741 21 AAC03863 Human secreted pro
c 999 11 73.3 744 22 AAH68357 C. glutamicum codin
c1000 11 73.3 747 24 ABQ25166 Oligonucleotide fo
```

## ALIGNMENTS

```
RESULT 1
AAH28084 standard; DNA; 15 BP.
XX AAH28084;
AC
XX
XX 05-SEP-2001 (first entry)
DT
XX
DE Probe for human norepinephrine transporter gene wild type allele.
XX
KW Norepinephrine transporter; orthostatic intolerance; gene therapy;
KW mental illness; hypertension; heart disease; stimulant abuse; cocaine;
KW amphetamine abuse; probe; ss.
XX
OS Homo sapiens.
XX
XX WO200148246-A1.
PN
XX
PD 05-JUL-2001.
XX
XX 28-DEC-2000; 2000WO-US35491.
XX
XX 29-DEC-1999; 99US-0173682.
XX
XX 11-JAN-2000; 2000US-0175456.
XX
XX (UYVA-) UNIV VANDERBILT.
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XX Robertson D, Blakely RD;
PI
XX WPI; 2001-425681/45.
DR
XX
PT Screening for susceptibility to sub-optimal norepinephrine transport,
PT particularly orthostatic intolerance in a subject by detecting a
PT polymorphism of norepinephrine transporter gene
XX
XX Claim 15; Page 69; 133pp; English.
PS
XX
CC The present sequence represents a probe for the wild type allele of
CC a human norepinephrine transporter gene. The specification a method
CC for screening for susceptibility to sub-optimal norepinephrine transport
CC in a subject. The method comprises obtaining a biological sample from
CC the subject and detecting a polymorphism of a norepinephrine transporter
CC gene in the sample from the subject, the presence of the polymorphism
CC indicating the susceptibility of the subject to sub-optimal
CC norepinephrine transport. The method is useful for screening for
CC susceptibility of a subject to orthostatic intolerance. Norepinephrine
CC transporter genes are useful for gene therapy for modulating
CC norepinephrine transport in a target cell and treating susceptibility
CC to impaired norepinephrine transporter function, orthostatic intolerance
CC or other relevant diseases in humans and animals such as mental illness,
CC hypertension, heart disease, psycho stimulant abuse e.g. cocaine or
CC amphetamine abuse.
XX
SQ Sequence 15 BP; 0 A; 7 C; 2 G; 6 T; 0 other;
Query Match 100.0%; Score 15; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTTCTCGCCCTGTT 15
Db 1 CCTTCTCGCCCTGTT 15
|||||
RESULT 2
AAH88259
ID AAH88259 standard; DNA; 920 BP.
XX
XX AAH88259;
XX
XX 26-FEB-2002 (first entry)
DT
XX
DE CNS disorder-related biallelic marker #10 from NET gene.
XX
KW Single nucleotide polymorphism; SNP; biallelic marker; human; ds;
KW central nervous system disorder; CNS; NET; norepinephrine transporter.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH misc_feature 95
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN WO200151659-A2.
XX
XX 19-JUL-2001.
XX
XX 11-JAN-2001; 2001WO-IB00116.
XX
XX 13-JAN-2000; 2000US-0175854.
XX
XX (GEST ) GENSET.
XX
XX Chu T, Blumenfeld M, Cohen D;
XX WPI; 2001-483085/52.
XX
XX Isolated polynucleotides, useful for genotyping nucleic acids for
PT
```

PT biallelic markers for the diagnosis of depression, comprises central  
PT nervous system disorder related biallelic marker -  
XX  
XX  
PS Claim 1; Page 248; 519pp; English.  
XX  
CC The present invention relates to biallelic markers derived from human  
CC genes involved in central nervous system (CNS) disorders. The present  
CC sequence is one such biallelic marker derived from human norepinephrine  
CC transporter (NET) gene. This marker has a single nucleotide polymorphism  
CC (SNP) and is useful in determining the genetic predisposition of  
CC individuals to CNS disorders, by identifying the nucleotides at a set of  
CC genetic markers in a biological sample, where the markers comprise at  
CC least one CNS disorder related marker.  
XX  
XX  
SQ Sequence 920 BP; 204 A; 260 C; 225 G; 227 T; 4 other;  
Query Match 100.0%; Score 15; DB 23; Length 920;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 CCTTCTCGCCCTGTT 15  
IIIIIIIIIIIIIIII  
Db 170 CCTTCTCGCCCTGTT 184  
RESULT 3  
AAH88264  
ID AAH88264 standard; DNA; 920 BP.  
XX  
XX  
AC AAH88264;  
XX  
XX  
DT 26-FEB-2002 (first entry)  
DE  
DE  
DE  
XX CNS disorder-related biallelic marker #15 from NET gene.  
XX  
KW Single nucleotide polymorphism; SNP; biallelic marker; human; ds;  
KW central nervous system disorder; CNS; NET; norepinephrine transporter.  
XX  
XX  
OS Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 206  
FT /\*tag= a  
FT /\*standard\_name= "single nucleotide polymorphism"  
XX  
XX  
PN WO200151659-A2.  
XX  
XX  
PD 19-JUL-2001.  
XX  
XX  
PF 11-JAN-2001; 2001WO-IB00116.  
XX  
XX  
PR 13-JAN-2000; 2000US-0175854.  
XX  
XX  
PA (GEST ) GENSET.  
XX  
XX  
PI Chu T, Blumenfeld M, Cohen D;  
XX  
XX  
DR WPI; 2001-483085/52.  
XX  
XX  
PT Isolated polynucleotides, useful for genotyping nucleic acids for  
PT biallelic markers for the diagnosis of depression, comprises central  
PT nervous system disorder related biallelic marker -  
XX  
XX  
PS Claim 1; Pages 251-252; 519pp; English.  
XX  
XX  
CC The present invention relates to biallelic markers derived from human  
CC genes involved in central nervous system (CNS) disorders. The present  
CC sequence is one such biallelic marker derived from human norepinephrine  
CC transporter (NET) gene. This marker has a single nucleotide polymorphism  
CC (SNP) and is useful in determining the genetic predisposition of  
CC individuals to CNS disorders, by identifying the nucleotides at a set of  
CC genetic markers in a biological sample, where the markers comprise at  
CC least one CNS disorder related marker.

XX  
SQ Sequence 920 BP; 204 A; 260 C; 225 G; 227 T; 4 other;  
Query Match 100.0%; Score 15; DB 23; Length 920;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 CCTTCTCGCCCTGTT 15  
IIIIIIIIIIIIIIII  
Db 170 CCTTCTCGCCCTGTT 184  
RESULT 4  
AAH28088  
ID AAH28088 standard; DNA; 980 BP.  
XX  
XX  
AC AAH28088;  
XX  
XX  
DT 05-SEP-2001 (first entry)  
DE  
DE  
DE  
XX Nucleotide sequence of a exon 9 of norepinephrine transporter gene.  
XX  
KW Norepinephrine transporter; orthostatic intolerance; gene therapy;  
KW mental illness; hypertension; heart disease; stimulant abuse; cocaine;  
KW amphetamine abuse; ss.  
XX  
XX  
OS Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT exon 129..257  
FT /\*tag= a  
FT intron 257..700  
FT /\*tag= b  
FT exon 701..802  
FT /\*tag= c  
XX  
XX  
PN WO200148246-A1.  
XX  
XX  
PD 05-JUL-2001.  
XX  
XX  
PF 28-DEC-2000; 2000WO-US35491.  
XX  
XX  
PR 29-DEC-1999; 990US-0173682.  
PR 11-JAN-2000; 2000US-0175456.  
XX  
XX  
PA (UYVA-) UNIV VANDERBILT.  
XX  
XX  
PI Robertson D, Blakely RD;  
XX  
XX  
DR WPI; 2001-425681/45.  
XX  
XX  
PT Screening for susceptibility to sub-optimal norepinephrine transport,  
PT particularly orthostatic intolerance in a subject by detecting a  
PT polymorphism of norepinephrine transporter gene -  
XX  
XX  
PS Disclosure; Page 125; 133pp; English.  
XX  
XX  
CC The present sequence represents exon 9 of the human norepinephrine  
CC transporter gene. The specification a method for screening for  
CC susceptibility to sub-optimal norepinephrine (NE) transport in a  
CC subject. The method comprises obtaining a biological sample from the  
CC subject and detecting a polymorphism of a norepinephrine transporter  
CC gene in the sample from the subject, the presence of the polymorphism  
CC indicating the susceptibility of the subject to sub-optimal  
CC norepinephrine transport. The method is useful for screening for  
CC susceptibility of a subject to orthostatic intolerance. Norepinephrine  
CC transporter genes are useful for gene therapy for modulating  
CC norepinephrine transport in a target cell and treating susceptibility  
CC to impaired norepinephrine transporter function, orthostatic intolerance  
CC or other relevant diseases in humans and animals such as mental illness,  
CC hypertension, heart disease, psycho stimulant abuse e.g. cocaine or  
CC amphetamine abuse.  
XX

SQ Sequence 980 BP; 218 A; 275 C; 246 G; 238 T; 3 other;

Query Match 100.0%; Score 15; DB 22; Length 980;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15  
|||||  
Db 230 CCTTCTCGCCCTGTT 244

RESULT 5  
AAS80746/c  
ID AAS80746 standard; cDNA; 1044 BP.

XX AC AAS80746;  
XX DT 13-FEB-2002 (first entry)  
XX DE DNA encoding novel human diagnostic protein #16550.  
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX OS Homo sapiens.  
XX FN WO200175067-A2.  
XX PD 11-OCT-2001.  
XX PF 30-MAR-2001; 2001WO-US08631.  
XX PR 31-MAR-2000; 2000US-0540217.  
XX PR 23-AUG-2000; 2000US-0649167.  
XX PA (HYSE-) HYSEQ INC.  
XX PI Drmanac RT, Liu C, Tang YT;  
XX DR WPI; 2001-639362/73.  
XX DR P-PSDB; ABG16559.  
XX PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity -  
XX PS Claim 1; SEQ ID No 16550; 103pp; English.  
XX CC The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptides and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AAS84197-AAS94564 represent novel human  
CC diagnostic coding sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX SQ Sequence 1044 BP; 229 A; 303 C; 258 G; 254 T; 0 other;

Query Match 100.0%; Score 15; DB 23; Length 1044;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15  
|||||  
Db 97 CCTTCTCGCCCTGTT 83

RESULT 6  
AAH28082  
ID AAH28082 standard; DNA; 1854 BP.

XX AC AAH28082;  
XX DT 05-SEP-2001 (first entry)  
XX DE Nucleotide sequence of a human norepinephrine transporter.  
XX KW Norepinephrine transporter; orthostatic intolerance; gene therapy;  
KW mental illness; hypertension; heart disease; stimulant abuse; cocaine;  
KW amphetamine abuse; ss.  
XX OS Homo sapiens.  
XX FN Key Location/Qualifiers  
FT CDS 1..1854  
FT FT /\*tag= a  
FT FT /product= "norepinephrine transporter"  
XX PN WO200148246-A1.  
XX PD 05-JUL-2001.  
XX PF 28-DEC-2000; 2000WO-US35491.  
XX PR 29-DEC-1999; 99US-0173682.  
XX PR 11-JAN-2000; 2000US-0175456.  
XX PA (UYVA-) UNIV VANDERBILT.  
XX PI Robertson D, Blakely RD;  
XX DR WPI; 2001-425681/45.  
XX DR P-PSDB; AAB84532.  
XX PT Screening for susceptibility to sub-optimal norepinephrine transport,  
PT particularly orthostatic intolerance in a subject by detecting a  
PT polymorphism of norepinephrine transporter gene -  
XX PS Claim 75; Page 98-101; 133pp; English.  
XX CC The present sequence encodes a human norepinephrine transporter. The  
CC specification a method for screening for susceptibility to sub-optimal  
CC norepinephrine (NE) transport in a subject. The method comprises  
CC obtaining a biological sample from the subject and detecting a  
CC polymorphism of a norepinephrine transporter gene in the sample from  
CC the subject, the presence of the polymorphism indicating the  
CC susceptibility of the subject to sub-optimal norepinephrine transport.  
CC The method is useful for screening for susceptibility of a subject to  
CC orthostatic intolerance. Norepinephrine transporter genes are useful  
CC for gene therapy for modulating norepinephrine transport in a target  
CC cell and treating susceptibility to impaired norepinephrine transporter  
CC function, orthostatic intolerance or other relevant diseases in humans  
CC and animals such as mental illness, hypertension, heart disease, psycho  
CC stimulant abuse e.g. cocaine or amphetamine abuse.  
XX SQ Sequence 1854 BP; 356 A; 554 C; 494 G; 450 T; 0 other;

Query Match 100.0%; Score 15; DB 22; Length 1854;  
Best Local Similarity 100.0%; Pred. No. 9.9;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



```
OY 1 CCTTCTCGCCCTGTT 15
Db 1362 CCTTCTCGCCCTGTT 1376

RESULT 7
AAH28086
ID AAH28086 standard; DNA; 1854 BP.
XX
AC AAH28086;
XX
DT 05-SEP-2001 (first entry)
XX
DE Nucleotide sequence of a human norepinephrine transporter.
KW Norepinephrine transporter; orthostatic intolerance; gene therapy;
KW mental illness; hypertension; heart disease; stimulant abuse; cocaine;
KW amphetamine abuse; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1854
FT /*tag= a
FT /product= "norepinephrine transporter"
XX
PN WO200148246-A1.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US35491.
XX
PR 29-DEC-1999; 99US-0173682.
PR 11-JAN-2000; 2000US-0175456.
XX
PA (UYVA-) UNIV VANDERBILT.
XX
PI Robertson D, Blakely RD;
DR WPI: 2001-425681/45.
DR P-PSDB; AAB84534.
XX
PT Screening for susceptibility to sub-optimal norepinephrine transport,
PT particularly orthostatic intolerance in a subject by detecting a
PT polymorphism of norepinephrine transporter gene
XX
PS Claim 75; Page 112-115; 133pp; English.
XX
CC The present sequence encodes a human norepinephrine transporter. The
CC specification a method for screening for susceptibility to sub-optimal
CC norepinephrine (NE) transport in a subject. The method comprises
CC obtaining a biological sample from the subject and detecting a
CC polymorphism of a norepinephrine transporter gene in the sample from
CC the subject, the presence of the polymorphism indicating the
CC susceptibility of the subject to sub-optimal norepinephrine transport.
CC The method is useful for screening for susceptibility of a subject to
CC orthostatic intolerance. Norepinephrine transporter genes are useful
CC for gene therapy for modulating norepinephrine transport in a target
CC cell and treating susceptibility to impaired norepinephrine transporter
CC function, orthostatic intolerance or other relevant diseases in humans
CC and animals such as mental illness, hypertension, heart disease, psycho
CC stimulant abuse e.g. cocaine or amphetamine abuse.
XX
SQ Sequence 1854 BP; 357 A; 553 C; 494 G; 450 T; 0 other;

Query Match 100.0%; Score 15; DB 22; Length 1854;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCTTCTCGCCCTGTT 15
Db 1362 CCTTCTCGCCCTGTT 1376
```

```
RESULT 8
AAQ28118
ID AAQ28118 standard; cDNA; 1983 BP.
XX
AC AAQ28118;
XX
DT 15-MAR-1993 (first entry)
XX
DE Human norepinephrine transporter protein cDNA clone.
XX
KW NT; noradrenaline; neuroblastoma; neurotransmitter; antidepressant;
KW ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 61..1914
FT /*tag= a
XX
PN WO9217568-A.
XX
PD 15-OCT-1992.
XX
PF 20-FEB-1992; 92WO-US01376.
XX
PR 28-MAR-1991; 91US-0676980.
XX
PA (UYOR-) UNIV OREGON HEALTH SCI.
XX
PI Amara SG, Blakely RD, Pacholczyk T;
DR WPI: 1992-366242/44.
DR P-PSDB; AAR26416.
XX
PT Complementary DNA clone encoding human norepinephrine transporter
PT protein - isolated from human neuroblastoma cells and useful for
PT determining action of e.g. antidepressant drugs
XX
PS Claim 3; Fig 1; 37pp; English.
XX
CC Pools of clones from a human SK-N-SH cell (a human neuroblastoma
CC cell line) cDNA library were transfected into COS-1 cells. The
CC transfected clones were in the form of expression vectors (pXM)
CC having an SV-40 replication origin to enable amplification.
CC Transfectants of these cells expressing the norepinephrine
CC transporter were identified by employing an assay exploiting the
CC fact that the norepinephrine analogue m-iodobenzylguanidine (m-IBG)
CC is accumulated intracellularly by SK-N-SH cells expressing the
CC intact NT. The accumulated radiolabelled m-IBG allows direct
CC autoradiographic visualisation of transporter expressing
CC transfectants. DNA was rescued from positive colonies and the
CC resulting plasmid pools rescreened and subdivided until a single
CC clone was obtd. Transfected cells become capable of norepinephrine
CC uptake, which may be inhibited by various drugs, e.g. cocaine, to
CC a degree similar to the effect of such drugs on noradrenergic
CC neurons. The cloned cDNA makes possible well-controlled studies
CC of neurotransmitter transporter function in non-neuronal cells
CC without the abfuscating influence of other transporters in the
CC same cell. Such studies include the relative effects of various
CC (psychotropic) drugs such as antidepressants.
XX
SQ Sequence 1983 BP; 384 A; 602 C; 529 G; 468 T; 0 other;

Query Match 100.0%; Score 15; DB 13; Length 1983;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCTTCTCGCCCTGTT 15
Db 1422 CCTTCTCGCCCTGTT 1436
```

## RESULT 9

ABK8362/c  
ID ABK8362 standard; cDNA; 5161 BP.  
XX  
AC ABK8362;  
DT  
XX 14-AUG-2002 (first entry)  
DE Human cDNA differentially expressed in granulocytic cells #433.  
XX  
KW Human; ss; granulocytic cell; DNA chip; bacterial infection;  
KW viral infection; parasitic infection; protozoal infection;  
KW fungal infection; sterile inflammatory disease; psoriasis;  
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;  
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;  
KW adult respiratory distress syndrome; inflammatory bowel disease;  
KW Crohn's disease; ulcerative colitis; periodontal disease;  
KW granulocyte activation; chronic inflammation; allergy.  
XX  
OS Homo sapiens.  
XX  
XX WO200228999-A2.  
PN  
XX  
PD 11-APR-2002.  
XX  
PF 03-OCT-2001; 2001WO-US30821.  
XX  
XX 03-OCT-2000; 2000US-237189P.  
PR  
XX (GENE-) GENE LOGIC INC.  
PA  
XX  
PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;  
XX  
XX WPI; 2002-435328/46.  
DR  
XX  
PT Detecting granulocyte activation by detecting differential expression  
PT of genes associated with granulocyte activation, which serves as  
PT diagnostic markers that is useful for monitoring disease states and  
PT drug toxicity -  
XX  
PS Claim 1; SEQ ID No 433; 114pp; English.  
XX  
CC The invention relates to detecting (M1) granulocyte (GC) activation  
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by  
CC DNA chip analysis as given in the specification, and comparing  
CC the expression level to an expression level in an unactivated  
CC GC, where differential expression of Gs is indicative of GCA.  
CC Also included are modulating (M2) GA by contacting GC with an agent  
CC that alters the expression of at least one gene in Gs; (2) screening (M3)  
CC for an agent capable of modulating GCA or an inflammation (especially  
CC chronic) in a tissue, an allergic response in a subject, exposure of a  
CC subject to a pathogen or sterile inflammatory disease using the  
CC gene expression profile; (3) detecting (M4) an inflammation (especially  
CC chronic) in a tissue, an allergic response in a subject, exposure of a  
CC subject to a pathogen or sterile inflammatory disease, by detecting the  
CC level of expression in a sample of the tissue of gene(s) from Gs, where  
CC the level of expression of the gene is indicative of inflammation;  
CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,  
CC an allergic response in a subject, exposure of a subject to a pathogen  
CC or sterile inflammatory disease, by contacting a tissue having  
CC inflammation with an agent that modulates the expression of gene(s)  
CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for  
CC modulating GA; M3 is useful for screening an agent capable of modulating  
CC GCA preferably in an inflammation in a tissue; M4 is useful for  
CC detecting an inflammation (especially chronic) in a tissue, an allergic  
CC response in a subject, exposure of a subject to a pathogen or sterile  
CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,  
CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal  
CC reperfusion injury, ARDS, adult respiratory distress syndrome,  
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,  
CC periodontal disease; also bacterial infection, viral infection,  
CC parasitic infection, protozoal infection, fungal infection, and M5 is  
CC useful for treating one of the above conditions. The present

CC sequence represents a gene differentially expressed in granulocytes.  
CC Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic  
CC format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX

SQ Sequence 5161 BP; 1254 A; 1420 C; 1363 G; 1124 T; 0 other;

Query Match 100.0%; Score 15; DB 24; Length 5161;  
Best Local Similarity 100.0%; Pred. No. 9.6;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15  
|||||

Db 2673 CCTTCTCGCCCTGTT 2659  
|||||

## RESULT 10

AAH88704  
ID AAH88704 standard; DNA; 160755 BP.

XX AC AAH88704;

XX 26-FEB-2002 (first entry)

XX Human DNA sequence SEQ ID 544.

XX Single nucleotide polymorphism; SNP; biallelic marker; human;  
KW central nervous system disorder; CNS; ds.

XX Homo sapiens.

XX WO200151659-A2.

XX 19-JUL-2001.

XX 11-JAN-2001; 2001WO-IB00116.

XX 13-JAN-2000; 2000US-0175854.

XX (GEST ) GENSET.

XX Chu T, Blumenfeld M, Cohen D;

XX WPI; 2001-483085/52.

XX Isolated polynucleotides, useful for genotyping nucleic acids for  
PT biallelic markers for the diagnosis of depression, comprises central  
PT nervous system disorder related biallelic marker -

XX Disclosure; Page 476-519; 519pp; English.

XX The present invention relates to biallelic markers derived from human  
CC genes involved in central nervous system (CNS) disorders (see  
CC AAH88161-AAH88702). The markers have a single nucleotide polymorphism  
CC (SNP) and are useful in determining the genetic predisposition of  
CC individuals to CNS disorders, by identifying the nucleotides at a set of  
CC genetic markers in a biological sample, where the markers comprise at  
CC least one CNS disorder related marker. The present sequence was used  
CC to illustrate the invention.

SQ Sequence 160755 BP; 43057 A; 36601 C; 38189 G; 42727 T; 181 other;

Query Match 100.0%; Score 15; DB 23; Length 160755;

Best Local Similarity 100.0%; Pred. No. 8.7;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15  
|||||

Db 63345 CCTTCTCGCCCTGTT 63359  
|||||

## RESULT 11



CC identification of individuals and in forensic analysis, and the  
CC polypeptides may be used as food additives or to prepare antibodies  
CC useful in disease diagnosis, drug targeting and phenotyping. The present  
CC sequence represents cDNA encoding a human ovarian antigen of the  
CC invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 655 BP; 182 A; 168 C; 177 G; 116 T; 12 other;  
  
Query Match 93.3%; Score 14; DB 24; Length 655;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 CTTCTCGCCCTGTT 15  
DB 556 CTTCTCGCCCTGTT 543  
|||||  
  
RESULT 13  
AAH63499/c  
ID AAH65499 standard; DNA; 708 BP.  
XX  
AC AAH65499;  
XX  
DT 26-SEP-2001 (first entry)  
XX  
DE C glutamicum coding sequence fragment SEQ ID NO: 534.  
XX  
KW Corynebacterium; amino acid synthesis; vitamin; saccharide;  
KW organic acid synthesis; ds.  
XX  
OS Corynebacterium glutamicum.  
XX  
PN EP1108790-A2.  
XX  
PI 20-JUN-2001.  
XX  
PF 18-DEC-2000; 2000EP-0127688.  
XX  
PR 16-DEC-1999; 99JP-0377484.  
PR 07-APR-2000; 2000JP-0159162.  
PR 03-AUG-2000; 2000JP-0280988.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;  
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;  
XX  
WPI; 2001-376931/40.  
DR P-PSDB; AAG90280.  
XX  
Novel polynucleotides derived from Coryneform bacteria, for identifying  
PT mutation point of a gene, measuring expression of a gene, analysing  
PT expression profile or pattern of a gene and identifying homologous gene  
PT  
PT  
PT  
XX  
PS Claim 8; SEQ ID NO: 534; 246pp + Sequence Listing; English.  
XX  
The present invention provides a number of nucleotide and protein  
CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These  
CC are useful for identifying the mutation point of a gene derived from a  
CC mutant of coryneform bacterium, measuring expression amount and  
CC analysing the expression profile or expression pattern of a gene derived  
CC from Coryneform bacterium, and identifying a homologue of a gene derived  
CC from coryneform bacterium. Coryneform bacteria are useful for producing  
CC amino acids, nucleic acids, vitamins, saccharides and organic acids,  
CC particularly L-lysine. The present sequence is a nucleic acid described  
CC in the exemplification of the invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from the  
CC European Patent Office.

XX  
SQ Sequence 708 BP; 152 A; 212 C; 196 G; 148 T; 0 other;  
  
Query Match 93.3%; Score 14; DB 22; Length 708;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CCTTCTCGCCCTGT 14  
DB 250 CCTTCTCGCCCTGT 237  
|||||  
  
RESULT 14  
ABL11823/c  
ID ABL11823 standard; cDNA; 2036 BP.  
XX  
AC ABL11823;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 29951.  
XX  
KW Drosophila; developmental biology; cell signalling; insecticide;  
KW pharmaceutical; gene; ss.  
XX  
OS Drosophila melanogaster.  
XX  
PN WO200171042-A2.  
XX  
PD 27-SEP-2001.  
XX  
PF 23-MAR-2001; 2001WO-US09231.  
XX  
PR 23-MAR-2000; 2000US-191637P.  
PR 11-JUL-2000; 2000US-0614150.  
XX  
PA (PEKE ) PE CORP NY.  
XX  
PI Venter JC, Adams M, Li PWD, Myers EW;  
XX  
WPI; 2001-656860/75.  
DR P-PSDB; ABB67720.  
XX  
New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signalling and cell-cell  
PT interactions -  
XX  
PS Claim 1; SEQ ID NO 29951; 21pp + Sequence Listing; English.  
XX  
The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins  
CC (ABB57737-ABB72072).  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 2036 BP; 552 A; 513 C; 553 G; 418 T; 0 other;  
  
Query Match 93.3%; Score 14; DB 23; Length 2036;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CCTTCTCGCCCTGT 14  
DB 326 CCTTCTCGCCCTGT 313  
|||||  
  
RESULT 15

AAQ14533  
ID AAQ14533 standard; DNA; 2397 BP.  
XX  
AC AAQ14533;  
XX  
DT 29-JAN-1992 (first entry)  
XX  
DE Tea gene (cDNA 20.5).  
XX  
KW Multiple membrane spanning protein; T cell; development; ss.  
XX  
OS Mus musculus.  
XX  
FH Key Location/Qualifiers  
FT CDS 410..1767  
FT /\*tag= a  
XX  
PN W09116430-A.  
XX  
PD 31-OCT-1991.  
XX  
PF 12-APR-1990; 90WO-U002518.  
XX  
PR 13-APR-1990; 90US-0509684.  
XX  
PA (REDE-) RES DEV FOUND.  
XX  
PI Macleod CL;  
XX  
WPI; 1991-339818/46.  
DR P-PSDB; AAR14645.  
XX  
PT New recombinant polypeptide comprising a T-cell protein - used to  
PT regulate T-cell development and tumorigenic phenotype and to  
PT block T-cell activation in auto-immune disease  
XX  
PS Disclosure; Fig 13; 98pp; English.  
XX  
CC The 23 Ns in the sequence represent bases illegible in the  
CC specification.  
CC The 20.5 gene, also referred to as Tea, identifies transcripts  
CC found in only a limited number of tissues. Tea transcripts are  
CC induced in splenocytes activated with the T cell mitogen ConA.  
CC Unlike other known genes expressed in activated T cells, the Tea gene  
CC appears to encode a protein which traverses the membrane multiple times,  
CC whereas the large number of known integral membrane protein which are  
CC induced in T cell activation are single membrane spanning proteins.  
CC See also AAQ14530-34.  
XX  
SQ Sequence 2397 BP; 541 A; 570 C; 579 G; 684 T; 23 other;  
Query Match 93.3%; Score 14; DB 12; Length 2397;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 CTTCTCGCCCTGTT 15  
Db 1379 CTTCTCGCCCTGTT 1392  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	14	93.3	2397	1 US-07-686-322A-5	Sequence 5, Appli
2	14	93.3	2397	1 US-08-002-999-5	Sequence 5, Appli
3	14	93.3	2397	2 US-08-132-990A-5	Sequence 5, Appli
4	14	93.3	2397	5 PCT-US92-09382-5	Sequence 5, Appli
5	13	86.7	485	4 US-09-400-208B-22	Sequence 22, Appl
6	13	86.7	491	4 US-09-400-208B-23	Sequence 23, Appl
7	13	86.7	497	4 US-09-400-208B-24	Sequence 24, Appl
8	13	86.7	2001	4 US-09-400-208B-4	Sequence 4, Appli
9	13	86.7	2023	4 US-09-491-522-6	Sequence 6, Appli
10	13	86.7	2450	4 US-09-491-522-2	Sequence 2, Appli
11	13	86.7	3240	4 US-09-171-337A-4	Sequence 4, Appli
12	13	86.7	3748	1 US-08-261-206A-76	Sequence 76, Appl
13	13	86.7	4657	3 US-09-254-325-1	Sequence 1, Appli
14	13	86.7	6692	4 US-09-491-522-1	Sequence 1, Appli
15	13	86.7	9785	1 US-08-319-387-1	Sequence 1, Appli
16	13	86.7	35100	5 US-08-306-691B-19	Sequence 19, Appl
17	13	86.7	35100	5 PCT-US93-06251-19	Sequence 19, Appl
18	12	80.0	257	3 US-08-906-791-4	Sequence 4, Appli
19	12	80.0	358	1 US-07-925-920-1	Sequence 1, Appli
20	12	80.0	447	4 US-09-018-584A-17	Sequence 17, Appl
21	12	80.0	476	4 US-09-625-188-15	Sequence 15, Appl
22	12	80.0	576	4 US-09-249-180-7	Sequence 7, Appli
23	12	80.0	657	4 US-09-249-180-4	Sequence 4, Appli
24	12	80.0	829	4 US-09-249-180-4	Sequence 4, Appli
25	12	80.0	984	4 US-09-230-665-7	Sequence 7, Appli
26	12	80.0	1020	4 US-09-527-522-2	Sequence 2, Appli
27	12	80.0	1028	4 US-09-249-180-1	Sequence 1, Appli
28	12	80.0	1161	3 US-09-058-489-26	Sequence 26, Appl

1163	80.0	1163	4	US-09-249-180-5	Sequence 5, Appli
1173	80.0	1173	6	5248670-6	Patent No. 5248670
1292	80.0	1292	1	US-08-503-133A-7	Sequence 7, Appli
1292	80.0	1292	2	US-08-576-775A-7	Sequence 7, Appli
1292	80.0	1292	3	US-08-972-498-7	Sequence 7, Appli
1292	80.0	1292	3	US-08-899-545-7	Sequence 7, Appli
1473	80.0	1473	1	US-08-090-013-3	Sequence 3, Appli
1473	80.0	1473	1	US-08-081-328-3	Sequence 3, Appli
1473	80.0	1473	1	US-08-232-249-3	Sequence 3, Appli
1473	80.0	1473	2	US-08-833-642A-3	Sequence 3, Appli
1473	80.0	1473	2	US-08-389-423-3	Sequence 3, Appli
1473	80.0	1473	4	US-09-230-665-3	Sequence 3, Appli
1473	80.0	1473	4	US-09-189-028-3	Sequence 3, Appli
1524	80.0	1524	4	US-09-111-730-4	Sequence 4, Appli
2310	80.0	2310	2	US-08-476-062A-41	Sequence 41, Appli
2310	80.0	2310	5	PCT-US96-01314-41	Sequence 41, Appli
2376	80.0	2376	1	US-08-394-880B-1	Sequence 1, Appli
2409	80.0	2409	4	US-09-293-322C-8	Sequence 8, Appli
2469	80.0	2469	4	US-09-111-730-6	Sequence 6, Appli
2484	80.0	2484	4	US-09-276-531-46	Sequence 46, Appli
2638	80.0	2638	1	US-08-306-691B-46	Sequence 46, Appli
2662	80.0	2662	3	US-08-750-357-8	Sequence 8, Appli
2976	80.0	2976	4	US-09-221-017B-36	Sequence 36, Appli
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3701	80.0	3701	1	US-08-553-279-1	Sequence 1, Appli
3973	80.0	3973	2	US-08-602-093-6	Sequence 6, Appli
4031	80.0	4031	1	US-08-159-784-1	Sequence 1, Appli
4417	80.0	4417	4	US-07-741-453A-57	Sequence 57, Appli
5186	80.0	5186	2	US-08-596-366-1	Sequence 1, Appli
5186	80.0	5186	2	US-08-967-104-1	Sequence 1, Appli
5369	80.0	5369	3	US-09-212-247C-3	Sequence 3, Appli
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8078	80.0	8078	4	US-09-445-247-12	Sequence 12, Appli
14985	80.0	14985	1	US-08-652-972A-6	Sequence 6, Appli
14985	80.0	14985	5	PCT-US96-06231A-6	Sequence 6, Appli
17656	80.0	17656	4	US-09-433-579-3	Sequence 3, Appli
17949	80.0	17949	4	US-09-087-465-3	Sequence 3, Appli
24595	80.0	24595	6	5428147-1	Patent No. 5428147
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112132	80.0	112132	4	US-08-363-240A-121	Sequence 121, App
112132	80.0	112132	4	US-08-459-260A-677	Sequence 677, App
112132	80.0	112132	4	US-09-321-831-8	Sequence 8, Appli
112132	80.0	112132	5	US-08-998-099-296	Sequence 296, App
112132	80.0	112132	5	US-08-566-398-6	Sequence 6, Appli
112132	80.0	112132	5	US-08-566-398-7	Sequence 7, Appli
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112132	80.0	112132	7	US-08-224-657-89	Sequence 90, Appl
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112132	80.0	112132	7	US-08-709-209-407	Sequence 407, App
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112132	80.0	112132	7	US-08-257-073-45	Sequence 45, Appl
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112132	80.0	112132	7	US-08-303-275-113	Sequence 113, App
112132	80.0	112132	7	US-08-458-101-406	Sequence 406, App
112132	80.0	112132	7	US-08-458-101-407	Sequence 407, App
112132	80.0	112132	7	US-08-658-665-129	Sequence 129, App
112132	80.0	112132	7	US-08-658-665-130	Sequence 130, App
112132	80.0	112132	7	US-08-675-566-71	Sequence 71, Appl
112132	80.0	112132	7	US-08-675-566-72	Sequence 72, Appl
112132	80.0	112132	7	US-08-796-101-105	Sequence 105, App
112132	80.0	112132	7	US-08-796-101-106	Sequence 106, App
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112132	80.0	112132	7	US-09-085-273-130	Sequence 130, App
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112132	80.0	112132	7	US-09-354-138-90	Sequence 90, Appl
112132	80.0	112132	7	PCT-US96-00547-42	Sequence 42, Appl
112132	80.0	112132	7	PCT-US96-00547-43	Sequence 43, Appl
112132	80.0	112132	7	US-08-184-009-100	Sequence 100, App
112132	80.0	112132	7	US-08-458-356-100	Sequence 100, App

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102	11	73.3	306	2	US-08-624-797-10	Sequence 10, Appl	175	11	73.3	1723	4	US-09-199-637A-135	Sequence 135, App
103	11	73.3	308	4	US-09-222-575-88	Sequence 88, Appl	c 176	11	73.3	1777	4	US-09-064-411A-5	Sequence 5, Appl
104	11	73.3	348	4	US-09-072-596-308	Sequence 308, App	177	11	73.3	1839	4	US-09-516-914-6	Sequence 6, Appl
105	11	73.3	361	1	US-08-094-079-12	Sequence 12, Appl	c 178	11	73.3	1879	3	US-08-403-852D-5	Sequence 5, Appl
106	11	73.3	361	1	US-08-094-079-18	Sequence 18, Appl	c 179	11	73.3	1879	3	US-08-510-646B-5	Sequence 5, Appl
107	11	73.3	361	1	US-08-094-079-20	Sequence 20, Appl	c 180	11	73.3	1879	4	US-09-231-818-5	Sequence 5, Appl
108	11	73.3	361	1	US-08-094-079-22	Sequence 22, Appl	181	11	73.3	1882	4	US-08-540-650B-11	Sequence 11, Appl
c 109	11	73.3	479	2	US-08-890-980-6	Sequence 6, Appl	182	11	73.3	1885	3	US-08-501-572-5	Sequence 5, Appl
c 110	11	73.3	479	3	US-08-890-979-6	Sequence 6, Appl	183	11	73.3	1885	3	US-09-040-444-5	Sequence 5, Appl
c 111	11	73.3	479	3	US-09-032-894-6	Sequence 6, Appl	c 184	11	73.3	1892	5	PCI-US96-00547-41	Sequence 41, Appl
c 112	11	73.3	479	4	US-09-031-626-6	Sequence 6, Appl	c 185	11	73.3	1954	3	US-08-922-635-2	Sequence 2, Appl
113	11	73.3	514	1	US-08-094-079-6	Sequence 6, Appl	c 186	11	73.3	1981	3	US-08-747-574-1	Sequence 1, Appl
114	11	73.3	514	1	US-08-094-079-10	Sequence 10, Appl	c 187	11	73.3	2020	2	US-08-417-210A-138	Sequence 138, App
c 115	11	73.3	555	3	US-08-705-771-4	Sequence 4, Appl	c 188	11	73.3	2028	2	US-08-417-210A-138	Sequence 141, App
116	11	73.3	662	1	US-07-807-043B-10	Sequence 10, Appl	c 189	11	73.3	2060	2	US-08-417-210A-141	Sequence 404, App
117	11	73.3	662	1	US-08-299-849B-10	Sequence 10, Appl	c 190	11	73.3	2073	4	US-09-221-017B-404	Sequence 3, Appl
118	11	73.3	662	2	US-08-142-368A-10	Sequence 10, Appl	c 191	11	73.3	2179	2	US-08-551-356-3	Sequence 1, Appl
119	11	73.3	662	2	US-08-967-727-10	Sequence 10, Appl	c 192	11	73.3	2179	5	PCI-US93-12687-3	Sequence 3, Appl
120	11	73.3	662	4	US-08-037-230D-10	Sequence 10, Appl	193	11	73.3	2242	3	US-09-400-742-1	Sequence 1, Appl
c 121	11	73.3	739	4	US-09-325-932A-100	Sequence 100, App	194	11	73.3	2242	3	US-08-618-651A-1	Sequence 1, Appl
122	11	73.3	759	1	US-08-685-660A-4	Sequence 4, Appl	195	11	73.3	2242	3	US-09-215-252-1	Sequence 1, Appl
123	11	73.3	759	2	US-08-974-196-4	Sequence 4, Appl	c 196	11	73.3	2507	4	US-09-605-785-332	Sequence 332, App
c 124	11	73.3	796	1	US-08-104-073-2	Sequence 2, Appl	c 197	11	73.3	2507	4	US-09-439-313-332	Sequence 332, App
125	11	73.3	847	4	US-08-998-416-545	Sequence 545, App	c 198	11	73.3	2507	4	US-09-352-616A-332	Sequence 332, App
126	11	73.3	867	1	US-08-181-471-3	Sequence 3, Appl	c 199	11	73.3	2507	4	US-09-232-149A-332	Sequence 332, App
127	11	73.3	897	2	US-08-486-663A-19	Sequence 19, Appl	c 200	11	73.3	2511	2	US-08-680-326-116	Sequence 116, App
128	11	73.3	897	3	US-08-767-942A-24	Sequence 24, Appl	201	11	73.3	2565	1	US-08-619-554-5	Sequence 5, Appl
c 129	11	73.3	965	2	US-08-158-009-79	Sequence 79, Appl	c 202	11	73.3	2566	4	US-09-270-542-124	Sequence 124, App
c 130	11	73.3	965	2	US-08-458-356-79	Sequence 79, Appl	c 203	11	73.3	2568	6	5196526-3	Patent No. 5196526
c 131	11	73.3	965	4	US-08-460-736-79	Sequence 79, Appl	204	11	73.3	2605	2	US-08-680-395-4	Sequence 4, Appl
c 132	11	73.3	1001	4	US-09-641-638-319	Sequence 319, App	c 205	11	73.3	2630	2	US-08-890-980-1	Sequence 1, Appl
c 133	11	73.3	1086	3	US-08-464-400-1	Sequence 1, Appl	c 206	11	73.3	2630	3	US-08-890-979-1	Sequence 1, Appl
c 134	11	73.3	1086	3	US-08-875-273A-1	Sequence 1, Appl	c 207	11	73.3	2630	3	US-09-032-894-1	Sequence 1, Appl
c 135	11	73.3	1086	4	US-09-123-386-1	Sequence 1, Appl	c 208	11	73.3	2630	4	US-09-031-626-1	Sequence 1, Appl
c 136	11	73.3	1086	5	PCI-US95-01827A-1	Sequence 1, Appl	209	11	73.3	2681	4	US-09-373-157-5	Sequence 5, Appl
c 137	11	73.3	1094	2	US-08-184-009-109	Sequence 109, App	c 210	11	73.3	2700	3	US-08-928-213B-7	Sequence 7, Appl
c 138	11	73.3	1094	2	US-08-458-356-109	Sequence 109, App	c 211	11	73.3	2700	3	US-08-815-809-4	Sequence 4, Appl
c 139	11	73.3	1094	4	US-08-460-736-109	Sequence 109, App	c 212	11	73.3	2749	1	US-07-717-331B-4	Sequence 4, Appl
c 140	11	73.3	1139	3	US-09-124-758-5	Sequence 5, Appl	213	11	73.3	2750	2	US-08-136-277-1	Sequence 1, Appl
c 141	11	73.3	1257	1	US-08-487-748A-11	Sequence 11, Appl	214	11	73.3	2750	2	US-08-479-403-1	Sequence 1, Appl
c 142	11	73.3	1257	3	US-08-480-070C-11	Sequence 11, Appl	c 215	11	73.3	2750	3	US-08-835-734-1	Sequence 1, Appl
c 143	11	73.3	1257	3	US-08-829-525-11	Sequence 11, Appl	c 216	11	73.3	2784	1	US-08-104-073-3	Sequence 3, Appl
c 144	11	73.3	1257	4	US-08-609-583A-11	Sequence 11, Appl	c 217	11	73.3	2784	1	US-08-351-413-10	Sequence 10, Appl
c 145	11	73.3	1257	4	US-08-937-399-11	Sequence 11, Appl	c 218	11	73.3	2784	2	US-09-025-583-10	Sequence 10, Appl
c 146	11	73.3	1257	4	US-09-310-367-11	Sequence 11, Appl	219	11	73.3	2868	4	US-09-228-986-4	Sequence 4, Appl
c 147	11	73.3	1257	4	US-09-032-337-11	Sequence 11, Appl	220	11	73.3	2935	1	US-09-041-075A-13	Sequence 13, Appl
c 148	11	73.3	1313	1	US-08-198-446B-7	Sequence 7, Appl	221	11	73.3	2935	4	US-08-716-873-12	Sequence 12, Appl
c 149	11	73.3	1313	2	US-08-870-693-7	Sequence 7, Appl	c 222	11	73.3	2935	4	US-09-368-431-12	Sequence 12, Appl
c 150	11	73.3	1394	4	US-09-504-445-3	Sequence 3, Appl	c 223	11	73.3	2945	6	5196526-2	Patent No. 5196526
c 151	11	73.3	1413	4	US-09-504-445-1	Sequence 1, Appl	224	11	73.3	2959	1	US-09-041-075A-15	Sequence 15, Appl
152	11	73.3	1419	3	US-09-354-129-1	Sequence 1, Appl	225	11	73.3	2989	2	US-08-566-398-9	Sequence 9, Appl
153	11	73.3	1419	4	US-09-504-357-1	Sequence 1, Appl	c 226	11	73.3	3043	4	US-09-008-271A-14	Sequence 14, Appl
154	11	73.3	1428	4	US-09-171-969-3	Sequence 3, Appl	227	11	73.3	3083	4	US-08-693-308-1	Sequence 1, Appl
c 155	11	73.3	1428	4	US-09-171-969-3	Sequence 3, Appl	c 228	11	73.3	3176	2	US-08-425-299A-3	Sequence 3, Appl
156	11	73.3	1441	1	US-08-136-277-18	Sequence 18, Appl	229	11	73.3	3176	2	US-08-486-663A-14	Sequence 14, Appl
157	11	73.3	1441	3	US-08-479-403-18	Sequence 18, Appl	230	11	73.3	3176	2	US-08-247-904B-13	Sequence 13, Appl
158	11	73.3	1441	3	US-08-835-734-18	Sequence 18, Appl	231	11	73.3	3176	2	US-08-767-942A-14	Sequence 14, Appl
159	11	73.3	1458	4	US-09-105-537-9	Sequence 9, Appl	232	11	73.3	3177	2	US-09-070-060-10	Sequence 10, Appl
c 160	11	73.3	1483	4	US-08-796-101-44	Sequence 44, Appl	233	11	73.3	3177	3	US-09-357-746-10	Sequence 10, Appl
c 161	11	73.3	1484	2	US-08-184-009-103	Sequence 103, App	234	11	73.3	3250	3	US-08-617-860B-1	Sequence 1, Appl
c 162	11	73.3	1484	2	US-08-458-356-103	Sequence 103, App	c 235	11	73.3	3318	3	US-08-650-766-3	Sequence 3, Appl
c 163	11	73.3	1484	4	US-08-460-736-103	Sequence 103, App	c 236	11	73.3	3318	3	US-08-922-635-3	Sequence 3, Appl
c 164	11	73.3	1511	4	US-08-796-101-168	Sequence 168, App	c 237	11	73.3	3323	2	US-07-624-299-14	Sequence 14, Appl
c 165	11	73.3	1512	2	US-08-184-009-99	Sequence 99, Appl	c 238	11	73.3	3385	3	US-08-650-766-1	Sequence 1, Appl
c 166	11	73.3	1512	2	US-08-458-356-99	Sequence 99, Appl	c 239	11	73.3	3385	3	US-08-922-635-1	Sequence 1, Appl
c 167	11	73.3	1512	4	US-08-460-736-99	Sequence 99, Appl	c 240	11	73.3	3460	2	US-08-658-665-57	Sequence 57, Appl
c 168	11	73.3	1565	3	US-09-320-878-24	Sequence 24, Appl	c 241	11	73.3	3460	4	US-08-796-101-21	Sequence 21, Appl
c 169	11	73.3	1600	4	US-09-325-932A-98	Sequence 98, Appl	c 242	11	73.3	3460	4	US-09-085-273-57	Sequence 57, Appl
c 170	11	73.3	1610	4	US-09-013-896A-1	Sequence 1, Appl	c 243	11	73.3	3579	3	US-08-674-168-15	Sequence 15, Appl
c 171	11	73.3	1678	2	US-08-650-766-2	Sequence 2, Appl	c 244	11	73.3	3579	3	US-08-985-908-18	Sequence 18, Appl
c 172	11	73.3	1700	2	US-08-428-131-1	Sequence 1, Appl	c 245	11	73.3	3579	3	US-08-852-730-3	Sequence 3, Appl
c 173	11	73.3	1700	2	US-08-602-846-1	Sequence 1, Appl	c 246	11	73.3	3579	4	US-08-985-916-10	Sequence 10, Appl



c 247	11	73.3	3622	2	US-08-658-665-60	Sequence 60, Appl	c 320	11	73.3	8147	4	US-09-514-247A-9	Sequence 9, Appl
c 248	11	73.3	3622	4	US-08-796-101-24	Sequence 24, Appl	c 321	11	73.3	9034	4	US-08-469-260A-397	Sequence 397, Appl
c 249	11	73.3	3622	4	US-09-085-273-60	Sequence 60, Appl	c 322	11	73.3	9122	2	US-08-417-629B-1	Sequence 1, Appl
c 250	11	73.3	3668	2	US-08-792-055-2	Sequence 2, Appl	c 323	11	73.3	9126	1	US-08-580-038-26	Sequence 26, Appl
c 251	11	73.3	3695	1	US-08-091-569-1	Sequence 1, Appl	c 324	11	73.3	9126	2	US-08-639-857-3	Sequence 3, Appl
c 252	11	73.3	3695	1	US-08-203-676-1	Sequence 1, Appl	c 325	11	73.3	10962	2	US-08-816-155B-6	Sequence 6, Appl
c 253	11	73.3	3695	2	US-08-822-238-1	Sequence 1, Appl	c 326	11	73.3	10962	3	US-09-079-587-6	Sequence 6, Appl
c 254	11	73.3	3770	4	US-09-221-017B-807	Sequence 807, App	c 327	11	73.3	11492	4	US-08-991-840A-1	Sequence 1, Appl
c 255	11	73.3	3825	4	US-09-332-295-1	Sequence 1, Appl	c 328	11	73.3	11531	1	US-08-068-945A-1	Sequence 1, Appl
c 256	11	73.3	3825	4	US-09-709-979-1	Sequence 1, Appl	c 329	11	73.3	11531	1	US-08-442-806-1	Sequence 1, Appl
c 257	11	73.3	4002	2	US-08-996-545-1	Sequence 1, Appl	c 330	11	73.3	11672	4	US-09-441-340-2	Sequence 2, Appl
c 258	11	73.3	4002	2	US-08-996-545-3	Sequence 3, Appl	c 331	11	73.3	13613	4	US-09-105-537-3	Sequence 3, Appl
c 259	11	73.3	4002	2	US-09-328-320-1	Sequence 1, Appl	c 332	11	73.3	13953	4	US-09-738-884-3	Sequence 3, Appl
c 260	11	73.3	4002	4	US-09-328-320-3	Sequence 3, Appl	c 333	11	73.3	14272	4	US-09-516-914-23	Sequence 23, Appl
c 261	11	73.3	4027	4	US-08-551-356-5	Sequence 5, Appl	c 334	11	73.3	15202	3	US-08-922-635-21	Sequence 21, Appl
c 262	11	73.3	4027	5	PCT-US93-12687-5	Sequence 5, Appl	c 335	11	73.3	15602	4	US-09-844-634-17	Sequence 17, Appl
c 263	11	73.3	4047	2	US-08-612-734B-1	Sequence 1, Appl	c 336	11	73.3	16595	4	US-09-146-053-7	Sequence 7, Appl
c 264	11	73.3	4157	1	US-07-807-043B-9	Sequence 9, Appl	c 337	11	73.3	16595	2	US-08-816-155B-8	Sequence 8, Appl
c 265	11	73.3	4157	1	US-08-299-849B-9	Sequence 9, Appl	c 338	11	73.3	19877	3	US-09-079-587-8	Sequence 8, Appl
c 266	11	73.3	4157	2	US-08-142-368A-9	Sequence 9, Appl	c 339	11	73.3	25165	4	US-09-453-702B-39	Sequence 39, Appl
c 267	11	73.3	4157	3	US-08-967-727-9	Sequence 9, Appl	c 340	11	73.3	30001	1	US-08-125-468-1	Sequence 1, Appl
c 268	11	73.3	4157	4	US-08-037-230D-9	Sequence 9, Appl	c 341	11	73.3	30001	2	US-08-474-933-1	Sequence 1, Appl
c 269	11	73.3	4162	4	US-09-453-702B-259	Sequence 259, App	c 342	11	73.3	35081	2	US-08-752-760A-1	Sequence 1, Appl
c 270	11	73.3	4204	2	US-08-928-615-1	Sequence 1, Appl	c 343	11	73.3	35100	2	US-08-770-379-17	Sequence 17, Appl
c 271	11	73.3	4204	4	US-09-056-105-6	Sequence 6, Appl	c 344	11	73.3	35100	4	US-08-757-669A-17	Sequence 17, Appl
c 272	11	73.3	4204	4	US-09-166-448-1	Sequence 1, Appl	c 345	11	73.3	35100	4	US-09-230-371A-17	Sequence 17, Appl
c 273	11	73.3	4204	4	US-09-348-933-1	Sequence 1, Appl	c 346	11	73.3	35100	2	US-08-804-227C-1	Sequence 1, Appl
c 274	11	73.3	4204	4	US-09-697-884-1	Sequence 1, Appl	c 347	11	73.3	36899	1	US-08-471-119A-1	Sequence 1, Appl
c 275	11	73.3	4343	1	US-08-224-657-93	Sequence 93, Appl	c 348	11	73.3	84495	4	US-09-797-906-3	Sequence 3, Appl
c 276	11	73.3	4343	1	US-09-354-138-93	Sequence 93, Appl	c 349	11	73.3	87350	3	US-08-781-891-79	Sequence 79, Appl
c 277	11	73.3	4427	2	US-08-658-665-48	Sequence 48, Appl	c 350	11	73.3	87543	4	US-09-791-211-3	Sequence 3, Appl
c 278	11	73.3	4427	4	US-08-796-101-12	Sequence 12, Appl	c 351	11	73.3	111282	4	US-09-754-250-3	Sequence 3, Appl
c 279	11	73.3	4427	4	US-09-085-273-48	Sequence 48, Appl	c 352	11	73.3	168575	4	US-09-426-290-1	Sequence 1, Appl
c 280	11	73.3	4463	2	US-08-760-489-1	Sequence 1, Appl	c 353	11	73.3	169998	4	US-09-676-610B-24	Sequence 24, Appl
c 281	11	73.3	4463	2	US-08-760-489-3	Sequence 3, Appl	c 354	11	73.3	4403765	4	US-09-103-840A-2	Sequence 2, Appl
c 282	11	73.3	4463	4	US-09-185-373-1	Sequence 1, Appl	c 355	11	73.3	4403765	4	US-09-103-840A-2	Sequence 2, Appl
c 283	11	73.3	4463	4	US-09-185-373-3	Sequence 3, Appl	c 356	11	73.3	4411529	4	US-09-103-840A-1	Sequence 1, Appl
c 284	11	73.3	4559	4	US-09-056-105-5	Sequence 5, Appl	c 357	11	73.3	4411529	4	US-09-103-840A-1	Sequence 1, Appl
c 285	11	73.3	4584	2	US-08-901-200A-15	Sequence 15, Appl	c 358	11	66.7	17	6	5202428-6	Patent No. 5202428
c 286	11	73.3	4584	3	US-09-219-391-15	Sequence 15, Appl	c 359	10	66.7	18	2	US-08-359-705B-38	Sequence 38, Appl
c 287	11	73.3	4604	1	US-08-224-657-96	Sequence 96, Appl	c 360	10	66.7	18	2	US-08-286-846A-38	Sequence 38, Appl
c 288	11	73.3	4604	4	US-09-354-138-96	Sequence 96, Appl	c 361	10	66.7	18	2	US-08-457-880A-38	Sequence 38, Appl
c 289	11	73.3	4635	2	US-08-404-531B-27	Sequence 27, Appl	c 362	10	66.7	18	3	US-09-255-911-20	Sequence 20, Appl
c 290	11	73.3	4635	2	US-08-476-900A-27	Sequence 27, Appl	c 363	10	66.7	18	3	US-08-444-622A-38	Sequence 38, Appl
c 291	11	73.3	4635	3	US-08-488-546A-27	Sequence 27, Appl	c 364	10	66.7	18	3	US-09-156-923-38	Sequence 38, Appl
c 292	11	73.3	4800	2	US-08-612-734B-3	Sequence 3, Appl	c 365	10	66.7	19	4	US-08-815-795-2	Sequence 2, Appl
c 293	11	73.3	4857	2	US-08-566-398-16	Sequence 16, Appl	c 366	10	66.7	20	4	US-09-517-467B-107	Sequence 107, App
c 294	11	73.3	4931	4	US-08-726-320-2	Sequence 2, Appl	c 367	10	66.7	21	5	PCT-US94-06331A-29	Sequence 29, Appl
c 295	11	73.3	4931	4	US-09-208-715-2	Sequence 2, Appl	c 368	10	66.7	27	2	US-08-937-102-5	Sequence 5, Appl
c 296	11	73.3	5091	4	US-08-469-260A-668	Sequence 668, App	c 369	10	66.7	27	4	US-09-439-616-8	Sequence 8, Appl
c 297	11	73.3	5110	2	US-08-404-531B-4	Sequence 4, Appl	c 370	10	66.7	27	4	US-08-584-040-4829	Sequence 4829, Ap
c 298	11	73.3	5110	2	US-08-404-531B-5	Sequence 5, Appl	c 371	10	66.7	29	3	US-09-066-597-9	Sequence 9, Appl
c 299	11	73.3	5110	3	US-08-476-900A-4	Sequence 4, Appl	c 372	10	66.7	35	4	US-09-475-460A-12	Sequence 12, Appl
c 300	11	73.3	5110	3	US-08-476-900A-5	Sequence 5, Appl	c 373	10	66.7	35	4	US-09-748-061A-12	Sequence 12, Appl
c 301	11	73.3	5110	3	US-08-488-546A-5	Sequence 4, Appl	c 374	10	66.7	36	2	US-09-988-128-11	Sequence 11, Appl
c 302	11	73.3	5110	3	US-08-488-546A-5	Sequence 5, Appl	c 375	10	66.7	36	3	US-09-124-758-30	Sequence 30, Appl
c 303	11	73.3	5630	2	US-08-937-931-1	Sequence 1, Appl	c 376	10	66.7	39	1	US-08-324-977-27	Sequence 27, Appl
c 304	11	73.3	5630	4	US-09-285-502-1	Sequence 1, Appl	c 377	10	66.7	39	2	US-08-384-616-27	Sequence 27, Appl
c 305	11	73.3	5630	4	US-09-709-126-1	Sequence 1, Appl	c 378	10	66.7	39	2	US-08-904-886A-27	Sequence 27, Appl
c 306	11	73.3	5630	4	US-09-871-385A-1	Sequence 1, Appl	c 379	10	66.7	39	4	US-09-315-850-27	Sequence 27, Appl
c 307	11	73.3	5943	1	US-08-206-176-1	Sequence 1, Appl	c 380	10	66.7	41	2	US-08-464-257-8	Sequence 8, Appl
c 308	11	73.3	6344	1	US-08-843-417-1	Sequence 1, Appl	c 381	10	66.7	41	2	US-09-062-375-8	Sequence 8, Appl
c 309	11	73.3	6418	1	US-08-480-528A-11	Sequence 11, Appl	c 382	10	66.7	41	3	US-09-203-796A-8	Sequence 8, Appl
c 310	11	73.3	6418	1	US-08-479-666-11	Sequence 11, Appl	c 383	10	66.7	45	2	US-08-937-102-3	Sequence 3, Appl
c 311	11	73.3	6418	5	PCT-US93-10520-11	Sequence 11, Appl	c 384	10	66.7	47	4	US-08-849-602C-4	Sequence 4, Appl
c 312	11	73.3	6524	4	US-08-669-656A-1	Sequence 1, Appl	c 385	10	66.7	54	1	US-08-373-124A-2182	Sequence 2182, Ap
c 313	11	73.3	6527	4	US-08-669-656A-7	Sequence 7, Appl	c 386	10	66.7	54	1	US-08-363-240A-1039	Sequence 1039, Ap
c 314	11	73.3	6678	3	US-08-816-617A-1	Sequence 1, Appl	c 387	10	66.7	54	1	US-08-363-240A-1162	Sequence 1162, Ap
c 315	11	73.3	7052	4	US-09-194-905-7	Sequence 7, Appl	c 388	10	66.7	54	1	US-08-435-628-2182	Sequence 2182, Ap
c 316	11	73.3	7052	4	US-08-669-656A-5	Sequence 5, Appl	c 389	10	66.7	54	4	US-08-584-040-8248	Sequence 8248, Ap
c 317	11	73.3	7326	1	US-08-194-468-1	Sequence 1, Appl	c 390	10	66.7	54	4	US-08-584-040-8256	Sequence 8256, Ap
c 318	11	73.3	7326	4	US-09-514-247A-7	Sequence 7, Appl	c 391	10	66.7	54	4	US-08-679-645-594	Sequence 594, App
c 319	11	73.3	7344	3	US-08-961-739-1	Sequence 1, Appl	c 392	10	66.7	68	1	US-08-095-481-1	Sequence 1, Appl

C 393	10	66.7	70	1	US-08-487-141B-107	Sequence 107, App	466	10	66.7	501	2	US-08-483-695-30	Sequence 30, Appl
C 394	10	66.7	70	2	US-08-927-561-107	Sequence 107, App	467	10	66.7	501	2	US-07-965-285-28	Sequence 28, Appl
C 395	10	66.7	70	5	PCT-US96-09388-107	Sequence 107, App	468	10	66.7	501	2	US-07-965-285-30	Sequence 30, Appl
C 396	10	66.7	98	1	US-08-472-255A-38	Sequence 38, Appl	469	10	66.7	501	2	US-08-487-231-28	Sequence 28, Appl
C 397	10	66.7	98	1	US-08-479-724A-38	Sequence 38, Appl	470	10	66.7	501	2	US-08-487-231-30	Sequence 30, Appl
C 398	10	66.7	98	3	US-08-472-256B-38	Sequence 38, Appl	471	10	66.7	501	4	US-09-201-912-28	Sequence 28, Appl
C 399	10	66.7	98	4	US-08-952-793-38	Sequence 38, Appl	472	10	66.7	501	4	US-09-201-912-30	Sequence 30, Appl
C 400	10	66.7	98	5	PCT-US96-09455A-38	Sequence 38, Appl	c 473	10	66.7	504	4	US-09-149-476-98	Sequence 98, Appl
C 401	10	66.7	120	4	US-09-347-504-13	Sequence 13, Appl	474	10	66.7	505	4	US-09-221-017B-376	Sequence 376, App
C 402	10	66.7	122	5	PCT-US95-04910-7	Sequence 7, Appl	475	10	66.7	507	4	US-09-257-894-5	Sequence 5, Appl
C 403	10	66.7	132	4	US-09-309-487-30	Sequence 30, Appl	476	10	66.7	510	3	US-08-441-971-66	Sequence 66, Appl
C 404	10	66.7	132	4	US-09-309-487-31	Sequence 31, Appl	477	10	66.7	510	4	US-08-221-653-66	Sequence 66, Appl
C 405	10	66.7	180	4	US-09-214-278-10	Sequence 10, Appl	478	10	66.7	510	4	US-08-442-144A-66	Sequence 66, Appl
C 406	10	66.7	190	1	US-08-478-808-1	Sequence 1, Appl	479	10	66.7	519	4	US-08-441-970-66	Sequence 66, Appl
C 407	10	66.7	201	1	US-08-470-892-2	Sequence 2, Appl	c 480	10	66.7	519	4	US-08-580-031A-12	Sequence 12, Appl
C 408	10	66.7	201	4	US-08-485-069-2	Sequence 2, Appl	481	10	66.7	534	4	US-09-296-284-69	Sequence 69, Appl
C 409	10	66.7	228	4	US-09-122-171D-2	Sequence 2, Appl	482	10	66.7	535	1	US-08-318-193-11	Sequence 11, Appl
C 410	10	66.7	240	4	US-09-189-060B-52	Sequence 52, Appl	c 483	10	66.7	537	4	US-08-874-102-40	Sequence 40, Appl
C 411	10	66.7	247	3	US-08-934-946A-2	Sequence 2, Appl	c 484	10	66.7	537	4	US-08-984-919A-40	Sequence 40, Appl
C 412	10	66.7	247	4	US-09-231-594-2	Sequence 2, Appl	c 485	10	66.7	543	4	US-09-513-007-3	Sequence 3, Appl
C 413	10	66.7	247	4	US-09-404-879A-316	Sequence 316, App	486	10	66.7	543	6	5200327-4	Patent No. 5200327
C 414	10	66.7	295	4	US-09-060-756-448	Sequence 448, App	487	10	66.7	551	3	US-08-994-946A-5	Sequence 5, Appl
C 415	10	66.7	298	4	US-09-071-035-147	Sequence 147, App	488	10	66.7	551	4	US-09-291-994-5	Sequence 5, Appl
C 416	10	66.7	300	3	US-08-676-818-7	Sequence 7, Appl	c 489	10	66.7	552	1	US-08-266-311-4	Sequence 4, Appl
C 417	10	66.7	300	4	US-09-407-549-7	Sequence 7, Appl	c 490	10	66.7	552	1	US-08-467-527A-4	Sequence 4, Appl
C 418	10	66.7	306	4	US-09-147-935A-45	Sequence 45, Appl	c 491	10	66.7	552	4	US-08-467-528-4	Sequence 4, Appl
C 419	10	66.7	325	4	US-09-060-756-216	Sequence 216, App	c 492	10	66.7	566	1	US-08-266-311-12	Sequence 12, Appl
C 420	10	66.7	333	4	US-09-060-756-723	Sequence 723, App	c 493	10	66.7	566	1	US-08-467-527A-12	Sequence 12, Appl
C 421	10	66.7	339	2	US-08-263-911-1	Sequence 1, Appl	c 494	10	66.7	566	1	US-08-467-528-12	Sequence 12, Appl
C 422	10	66.7	348	4	US-09-072-596-308	Sequence 308, App	c 495	10	66.7	573	2	US-08-290-665A-134	Sequence 134, App
C 423	10	66.7	356	4	US-08-483-533-14	Sequence 14, Appl	c 496	10	66.7	573	5	PCT-US95-10398-134	Sequence 134, App
C 424	10	66.7	356	4	US-08-483-533-19	Sequence 19, Appl	497	10	66.7	576	1	US-08-086-428B-10	Sequence 10, Appl
C 425	10	66.7	356	4	US-09-283-471A-14	Sequence 14, Appl	498	10	66.7	576	1	US-08-086-428B-12	Sequence 12, Appl
C 426	10	66.7	356	4	US-09-283-471A-19	Sequence 19, Appl	499	10	66.7	576	1	US-08-086-428B-13	Sequence 13, Appl
C 427	10	66.7	368	4	US-08-483-533-8	Sequence 8, Appl	500	10	66.7	576	1	US-08-086-428B-14	Sequence 14, Appl
C 428	10	66.7	368	4	US-09-283-471A-8	Sequence 8, Appl	501	10	66.7	576	1	US-08-086-428B-20	Sequence 20, Appl
C 429	10	66.7	384	4	US-09-071-035-353	Sequence 353, App	502	10	66.7	576	1	US-08-086-428B-21	Sequence 21, Appl
C 430	10	66.7	389	4	US-09-060-756-235	Sequence 235, App	503	10	66.7	576	1	US-08-086-428B-24	Sequence 24, Appl
C 431	10	66.7	397	2	US-08-636-597-2	Sequence 2, Appl	504	10	66.7	576	1	US-08-086-428B-25	Sequence 25, Appl
C 432	10	66.7	397	4	US-09-232-063-2	Sequence 2, Appl	505	10	66.7	576	1	US-08-086-428B-42	Sequence 42, Appl
C 433	10	66.7	397	6	5200327-7	Patent No. 5200327	506	10	66.7	576	2	US-08-468-570-10	Sequence 10, Appl
C 434	10	66.7	401	1	US-08-318-193-17	Sequence 17, Appl	507	10	66.7	576	2	US-08-468-570-12	Sequence 12, Appl
C 435	10	66.7	402	5	PCT-US93-07213-14	Sequence 14, Appl	508	10	66.7	576	2	US-08-468-570-13	Sequence 13, Appl
C 436	10	66.7	411	1	US-08-279-058B-39	Sequence 39, Appl	509	10	66.7	576	2	US-08-468-570-14	Sequence 14, Appl
C 437	10	66.7	411	4	US-08-828-323-39	Sequence 39, Appl	510	10	66.7	576	2	US-08-468-570-20	Sequence 20, Appl
C 438	10	66.7	413	3	US-09-188-930-55	Sequence 55, Appl	511	10	66.7	576	2	US-08-468-570-21	Sequence 21, Appl
C 439	10	66.7	417	4	US-09-615-192A-358	Sequence 358, App	512	10	66.7	576	2	US-08-468-570-24	Sequence 24, Appl
C 440	10	66.7	420	4	US-09-060-756-496	Sequence 496, App	513	10	66.7	576	2	US-08-468-570-25	Sequence 25, Appl
C 441	10	66.7	432	5	PCT-US93-07213-10	Sequence 10, Appl	514	10	66.7	576	2	US-08-468-570-42	Sequence 42, Appl
C 442	10	66.7	432	5	PCT-US94-00545-11	Sequence 11, Appl	515	10	66.7	576	2	US-08-290-665A-10	Sequence 10, Appl
C 443	10	66.7	433	2	US-08-967-101-34	Sequence 34, Appl	516	10	66.7	576	2	US-08-290-665A-12	Sequence 12, Appl
C 444	10	66.7	433	2	US-08-592-541-34	Sequence 34, Appl	517	10	66.7	576	2	US-08-290-665A-13	Sequence 13, Appl
C 445	10	66.7	433	3	US-09-124-698-34	Sequence 34, Appl	518	10	66.7	576	2	US-08-290-665A-14	Sequence 14, Appl
C 446	10	66.7	433	4	US-09-127-480-34	Sequence 34, Appl	519	10	66.7	576	2	US-08-290-665A-20	Sequence 20, Appl
C 447	10	66.7	433	4	US-08-496-841C-34	Sequence 34, Appl	520	10	66.7	576	2	US-08-290-665A-21	Sequence 21, Appl
C 448	10	66.7	433	4	US-08-976-259-116	Sequence 116, App	521	10	66.7	576	2	US-08-290-665A-24	Sequence 24, Appl
C 449	10	66.7	433	4	US-09-124-523-34	Sequence 34, Appl	522	10	66.7	576	2	US-08-290-665A-25	Sequence 25, Appl
C 450	10	66.7	441	4	US-09-071-035-145	Sequence 145, App	523	10	66.7	576	2	US-08-290-665A-42	Sequence 42, Appl
C 451	10	66.7	445	4	US-09-060-756-75	Sequence 75, Appl	524	10	66.7	576	5	PCT-US95-10398-10	Sequence 10, Appl
C 452	10	66.7	445	4	US-09-173-300-12	Sequence 12, Appl	525	10	66.7	576	5	PCT-US95-10398-12	Sequence 12, Appl
C 453	10	66.7	455	4	US-09-615-192A-102	Sequence 102, App	526	10	66.7	576	5	PCT-US95-10398-13	Sequence 13, Appl
C 454	10	66.7	462	4	US-09-643-597-289	Sequence 289, App	527	10	66.7	576	5	PCT-US95-10398-14	Sequence 14, Appl
C 455	10	66.7	469	2	US-08-975-316-19	Sequence 19, Appl	528	10	66.7	576	5	PCT-US95-10398-20	Sequence 20, Appl
C 456	10	66.7	469	4	US-09-615-192A-19	Sequence 19, Appl	529	10	66.7	576	5	PCT-US95-10398-21	Sequence 21, Appl
C 457	10	66.7	470	2	US-08-967-101-99	Sequence 99, Appl	530	10	66.7	576	5	PCT-US95-10398-24	Sequence 24, Appl
C 458	10	66.7	470	2	US-08-592-541-99	Sequence 99, Appl	531	10	66.7	576	5	PCT-US95-10398-25	Sequence 25, Appl
C 459	10	66.7	470	3	US-09-124-698-99	Sequence 99, Appl	532	10	66.7	576	5	PCT-US95-10398-42	Sequence 42, Appl
C 460	10	66.7	470	4	US-09-060-756-157	Sequence 157, App	533	10	66.7	584	4	US-09-296-284-68	Sequence 68, Appl
C 461	10	66.7	470	4	US-09-127-480-99	Sequence 99, Appl	c 534	10	66.7	589	4	US-09-470-191-30	Sequence 30, Appl
C 462	10	66.7	470	4	US-08-496-841C-99	Sequence 99, Appl	535	10	66.7	594	1	US-08-324-977-21	Sequence 21, Appl
C 463	10	66.7	470	4	US-09-124-523-99	Sequence 99, Appl	536	10	66.7	594	2	US-08-384-616-21	Sequence 21, Appl
C 464	10	66.7	487	4	US-09-072-596-291	Sequence 291, App	537	10	66.7	594	2	US-08-904-686A-21	Sequence 21, Appl
C 465	10	66.7	501	2	US-08-483-695-28	Sequence 28, Appl	538	10	66.7	594	4	US-09-315-850-21	Sequence 21, Appl

c 543	10	66.7	595	4	US-08-483-533-4	Sequence 4, Appli	612	10	66.7	833	4	US-09-123-492A-4	Sequence 4, Appli
c 544	10	66.7	595	4	US-09-283-471A-4	Sequence 4, Appli	613	10	66.7	834	4	US-09-296-284-62	Sequence 62, Appli
c 545	10	66.7	595	1	US-08-087-772A-6	Sequence 6, Appli	614	10	66.7	837	4	US-09-123-492A-3	Sequence 3, Appli
c 546	10	66.7	612	4	US-09-615-192A-101	Sequence 101, App	615	10	66.7	838	1	US-08-318-193-13	Sequence 13, Appli
c 547	10	66.7	618	4	US-09-703-807-15	Sequence 15, Appli	616	10	66.7	846	6	5200327-5	Patent No. 5200327
c 548	10	66.7	619	4	US-09-328-111-815	Sequence 815, App	c 617	10	66.7	850	4	US-09-449-285A-8	Sequence 8, Appli
c 549	10	66.7	633	4	US-09-703-807-13	Sequence 13, Appli	c 618	10	66.7	856	3	US-08-463-903-16	Sequence 16, Appli
c 550	10	66.7	633	1	US-08-726-136-3	Sequence 3, Appli	c 619	10	66.7	856	4	US-07-935-695-16	Sequence 16, Appli
c 551	10	66.7	633	3	US-09-103-434-3	Sequence 3, Appli	c 620	10	66.7	860	1	US-08-310-416A-19	Sequence 19, Appli
c 552	10	66.7	633	4	US-09-687-594-3	Sequence 3, Appli	c 621	10	66.7	860	2	US-08-888-171-19	Sequence 19, Appli
c 553	10	66.7	634	4	US-09-296-284-67	Sequence 67, Appli	c 622	10	66.7	870	2	US-08-708-858A-3	Sequence 3, Appli
c 554	10	66.7	637	3	US-08-545-196B-23	Sequence 23, Appli	c 623	10	66.7	870	3	US-09-287-375-3	Sequence 3, Appli
c 555	10	66.7	645	4	US-08-998-416-114	Sequence 114, App	c 624	10	66.7	870	4	US-09-455-406-3	Sequence 3, Appli
c 556	10	66.7	652	1	US-08-247-296-1	Sequence 1, Appli	c 625	10	66.7	871	1	US-08-744-026-2	Sequence 2, Appli
c 557	10	66.7	655	1	US-08-471-119A-5	Sequence 5, Appli	c 626	10	66.7	871	2	US-09-102-732-2	Sequence 2, Appli
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c 559	10	66.7	677	5	PCT-US93-07213-6	Sequence 6, Appli	c 628	10	66.7	871	4	US-08-969-987-7	Sequence 7, Appli
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c 995 10 66.7 2539 3 US-08-581-148C-20  
c 996 10 66.7 2543 1 US-08-555-669-11  
c 997 10 66.7 2543 3 US-09-073-663-11  
c 998 10 66.7 2544 4 US-09-302-769-17  
c 999 10 66.7 2559 2 US-08-886-152-4  
c1000 10 66.7 2559 4 US-09-196-222-4

## ALIGNMENTS

RESULT 1  
US-07-686-322A-5  
; Sequence 5, Application US/07686322A  
; Patent No. 5312733  
; GENERAL INFORMATION:  
; APPLICANT: MacLeod Dr., Carol L.  
; TITLE OF INVENTION: No. 5312733el T-cell Lymphoma cDNA Clones  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patent Department, Fulbright & Jaworski  
; STREET: 1301 McKinney, Suit 5100  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77010-3095  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/686.322A  
; FILING DATE: 19910411  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/509684  
; FILING DATE: 13-APR-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Launer, Charlene A.  
; REGISTRATION NUMBER: 33,035  
; REFERENCE/DOCKET NUMBER: D-5232-CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (713) 651-3634  
; TELEFAX: (713) 651-5246  
; TELEX: Western Union 762829  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2397 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; ORIGINAL SOURCE:  
; ORGANISM: Mouse

; STRAIN: AKRI Jackson  
; INDIVIDUAL ISOLATE: SL12 cell line  
; TISSUE TYPE: Lymphoma  
; CELL TYPE: T-cell  
; CELL LINE: SL12.3 and SL12.4  
; IMMEDIATE SOURCE:  
; CLONE: 20.5  
US-07-686-322A-5  
  
Query Match 93.3%; Score 14; DB 1; Length 2397;  
Best Local Similarity 100.0%; Pred. No. 3.5;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 CTCTCGCCCTGTT 15  
|||||  
Db 1379 CTCTCGCCCTGTT 1392  
  
RESULT 2  
US-08-002-999-5  
; Sequence 5, Application US/08002999  
; Patent No. 5440017  
; GENERAL INFORMATION:  
; APPLICANT: MacLeod Dr., Carol L.  
; TITLE OF INVENTION: No. 5440017el T-cell Lymphoma cDNA Clones  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patent Department, Fulbright & Jaworski  
; STREET: 1301 McKinney, Suite 5100  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77010-3095  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/002,999  
; FILING DATE: 19930111  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/686,322  
; FILING DATE: 11-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Adler, Benjamin A.  
; REGISTRATION NUMBER: 35,423  
; REFERENCE/DOCKET NUMBER: D-5232-DIV  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (713) 651-5587  
; TELEFAX: (713) 651-5246  
; TELEX: Western Union 762829  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2397 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; ORIGINAL SOURCE:  
; ORGANISM: Mouse  
; STRAIN: AKRI Jackson  
; INDIVIDUAL ISOLATE: SL12 cell line  
; TISSUE TYPE: Lymphoma  
; CELL TYPE: T-cell  
; CELL LINE: SL12.3 and SL12.4  
; IMMEDIATE SOURCE:  
; CLONE: 20.5  
US-08-002-999-5  
  
Query Match 93.3%; Score 14; DB 1; Length 2397;  
Best Local Similarity 100.0%; Pred. No. 3.5;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 CTTCTCGCCCTGTT 15  
|||||

Db 1379 CTTCTCGCCCTGTT 1392

## RESULT 3

US-08-132-990A-5  
; Sequence 5, Application US/08132990A  
; Patent No. 5834589  
; GENERAL INFORMATION:  
; APPLICANT: MERUELO, DANIEL  
; APPLICANT: YOSHIMOTO, TAKAYUKI  
; TITLE OF INVENTION: Human Retrovirus Receptor and DNA Coding Therefor  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/132,990A  
; FILING DATE: 07-OCT-1993  
; PRIOR APPLICATION NUMBER: 08/084,729  
; FILING DATE: 29-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/05569  
; FILING DATE: 11-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/899,075  
; FILING DATE: 11-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/806,178  
; FILING DATE: 13-DEC-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/627,950  
; FILING DATE: 14-DEC-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 8105-004-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864  
; TELEX: 66441 PENNIE

SEQUENCE CHARACTERISTICS:  
; INFORMATION FOR SEQ ID NO: 5:  
; LENGTH: 2397 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 410..1768  
US-08-132-990A-5

Query Match 93.3%; Score 14; DB 2; Length 2397;

Best Local Similarity 100.0%; Pred. No. 3.5;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 CTTCTCGCCCTGTT 15  
|||||

Db 1379 CTTCTCGCCCTGTT 1392

## RESULT 4

PCT-US92-09382-5  
; Sequence 5, Application PC/TUS9209382  
; GENERAL INFORMATION:  
; APPLICANT: MERUELO, DANIEL  
; APPLICANT: YOSHIMOTO, TAKAYUKI  
; TITLE OF INVENTION: Human Retrovirus Receptor and DNA Coding  
; TITLE OF INVENTION: Therefor  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Browdy and Neimark  
; STREET: 419 Seventh Street, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20004

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/09382  
; FILING DATE: 19921213  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Livnat, Shmuel  
; REGISTRATION NUMBER: 33,949  
; REFERENCE/DOCKET NUMBER: MERUELO-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202 628-5197  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2397 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 410..1768  
PCT-US92-09382-5

Query Match 93.3%; Score 14; DB 5; Length 2397;

Best Local Similarity 100.0%; Pred. No. 3.5;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 CTTCTCGCCCTGTT 15

|||||

Db 1379 CTTCTCGCCCTGTT 1392

## RESULT 5

US-09-400-208B-22/c  
; Sequence 22, Application US/09400208B  
; Patent No. 6271011  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Margie  
; APPLICANT: Sanchez, Susan  
; APPLICANT: Henk, Adam  
; TITLE OF INVENTION: Pasteurella Neureminidase Coding Sequences,  
; TITLE OF INVENTION: Compositions and Diagnostic Methods  
; FILE REFERENCE: 77-96B  
; CURRENT APPLICATION NUMBER: US/09/400,208B  
; CURRENT FILING DATE: 1999-09-21  
; PRIOR APPLICATION NUMBER: US 08/951,984  
; PRIOR FILING DATE: 1997-10-15  
; PRIOR APPLICATION NUMBER: US 60/028,876  
; PRIOR FILING DATE: 1996-10-16  
; PRIOR APPLICATION NUMBER: US 60/028,482  
; PRIOR FILING DATE: 1996-10-15

; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 22  
; LENGTH: 485  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida  
US-09-400-208B-22

Query Match 86.7%; Score 13; DB 4; Length 485;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTCTCGCCCTGT 14  
|||||  
Db 414 CTTCTCGCCCTGT 402

## RESULT 6

US-09-400-208B-23/c  
; Sequence 23, Application US/09400208B  
; Patent No. 6271011

; GENERAL INFORMATION:  
; APPLICANT: Lee, Margie  
; APPLICANT: Sanchez, Susan  
; APPLICANT: Henk, Adam  
; TITLE OF INVENTION: Pasteurella Neuraminidase Coding Sequences,  
; TITLE OF INVENTION: Compositions and Diagnostic Methods  
; FILE REFERENCE: 77-96B  
; CURRENT APPLICATION NUMBER: US/09/400,208B  
; CURRENT FILING DATE: 1999-09-21  
; PRIOR APPLICATION NUMBER: US 08/951,984  
; PRIOR FILING DATE: 1997-10-15  
; PRIOR APPLICATION NUMBER: US 60/028,876  
; PRIOR FILING DATE: 1996-10-16  
; PRIOR APPLICATION NUMBER: US 60/028,482  
; PRIOR FILING DATE: 1996-10-15  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 23  
; LENGTH: 491  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida  
US-09-400-208B-23

Query Match 86.7%; Score 13; DB 4; Length 491;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTCTCGCCCTGT 14  
|||||  
Db 414 CTTCTCGCCCTGT 402

## RESULT 7

US-09-400-208B-24/c  
; Sequence 24, Application US/09400208B  
; Patent No. 6271011

; GENERAL INFORMATION:  
; APPLICANT: Lee, Margie  
; APPLICANT: Sanchez, Susan  
; APPLICANT: Henk, Adam  
; TITLE OF INVENTION: Pasteurella Neuraminidase Coding Sequences,  
; TITLE OF INVENTION: Compositions and Diagnostic Methods  
; FILE REFERENCE: 77-96B  
; CURRENT APPLICATION NUMBER: US/09/400,208B  
; CURRENT FILING DATE: 1999-09-21  
; PRIOR APPLICATION NUMBER: US 08/951,984  
; PRIOR FILING DATE: 1997-10-15  
; PRIOR APPLICATION NUMBER: US 60/028,876  
; PRIOR FILING DATE: 1996-10-16  
; PRIOR APPLICATION NUMBER: US 60/028,482  
; PRIOR FILING DATE: 1996-10-15  
; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 497  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida  
US-09-400-208B-24

Query Match 86.7%; Score 13; DB 4; Length 497;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTCTCGCCCTGT 14  
|||||  
Db 464 CTTCTCGCCCTGT 452

## RESULT 8

US-09-400-208B-4/c  
; Sequence 4, Application US/09400208B  
; Patent No. 6271011

; GENERAL INFORMATION:  
; APPLICANT: Lee, Margie  
; APPLICANT: Sanchez, Susan  
; APPLICANT: Henk, Adam  
; TITLE OF INVENTION: Pasteurella Neuraminidase Coding Sequences,  
; TITLE OF INVENTION: Compositions and Diagnostic Methods  
; FILE REFERENCE: 77-96B  
; CURRENT APPLICATION NUMBER: US/09/400,208B  
; CURRENT FILING DATE: 1999-09-21  
; PRIOR APPLICATION NUMBER: US 08/951,984  
; PRIOR FILING DATE: 1997-10-15  
; PRIOR APPLICATION NUMBER: US 60/028,876  
; PRIOR FILING DATE: 1996-10-16  
; PRIOR APPLICATION NUMBER: US 60/028,482  
; PRIOR FILING DATE: 1996-10-15  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 2001  
; TYPE: DNA  
; ORGANISM: Pasteurella multocida  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (188)..(1486)  
; NAME/KEY: mat.peptide  
; LOCATION: (251)..(1486)  
US-09-400-208B-4

Query Match 86.7%; Score 13; DB 4; Length 2001;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTCTCGCCCTGT 14  
|||||  
Db 1064 CTTCTCGCCCTGT 1052

## RESULT 9

US-09-491-522-6/c  
; Sequence 6, Application US/09491522  
; Patent No. 6428998

; GENERAL INFORMATION:  
; APPLICANT: Colige, Alain  
; APPLICANT: Lapiere, Charles M.  
; APPLICANT: Prockop, Darwin J.  
; TITLE OF INVENTION: RECOMBINANT N-PROTEINASE,  
; TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds, LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY



COUNTRY: USA  
ZIP: 10036-2811  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/491,522  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/886,333  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Abrams, Samuel B  
REGISTRATION NUMBER: 30,605  
REFERENCE/DOCKET NUMBER: 8389-0060-999  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 203 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-491-522-6

Query Match 86.7%; Score 13; DB 4; Length 203;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTG 13  
|||||  
Db 511 CCTTCTCGCCCTG 499

RESULT 10  
US-09-491-522-2/c  
; Sequence 2, Application US/09491522  
; Patent No. 6428998  
; GENERAL INFORMATION:  
; APPLICANT: Colige, Alain  
; APPLICANT: Lapiere, Charles M.  
; APPLICANT: Prockop, Darwin J.  
; TITLE OF INVENTION: RECOMBINANT N-PROTEINASE,  
; TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds, LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/491,522  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/886,333  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Abrams, Samuel B  
; REGISTRATION NUMBER: 30,605  
; REFERENCE/DOCKET NUMBER: 8389-0060-999

TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-493-4935  
; TELEFAX: 650-493-5556  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2450 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-491-522-2

Query Match 86.7%; Score 13; DB 4; Length 2450;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTG 13  
|||||  
Db 511 CCTTCTCGCCCTG 499

RESULT 11  
US-09-171-337A-4/c  
; Sequence 4, Application US/09171337A  
; Patent No. 6300095  
; GENERAL INFORMATION:  
; APPLICANT: BARREDO FUENTE, Jose Luis  
; RODRIGUEZ SAIZ, Marta  
; COLLADOS DE LA VIEJA, Alfonso J.  
; MORENO VALLE, Migueal Angel  
; SALTO MALDONADO, Francisco  
; DIEZ GARCIA, Bruno  
; TITLE OF INVENTION: PROMOTERS OF THE GENES GLUTAMATE  
; DESHYDROGENASE, -N-ACETYLHEXOSAMINIDASE  
; AND -ACTIN AND THEIR USE IN FILAMENTOUS  
; FUNGI EXPRESSION, SECRETION AND ANTISENSE  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LADAS & PARRY  
; STREET: 26 WEST 61 STREET  
; CITY: NEW YORK  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10023  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3-1/4" Disk 1.44MB  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11  
; SOFTWARE: WordPerfect 8 for Windows  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/171,337A  
; FILING DATE: 14-May-1999  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/ES98/00056  
; FILING DATE: 5-MAR-1998  
; APPLICATION NUMBER: ES9700482  
; FILING DATE: 5-MAR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MASS, Clifford J.  
; REGISTRATION NUMBER: 30,086  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 233288  
; INFORMATION FOR SEQ ID NO: 4  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3240 base pairs  
; TYPE: nucleotides  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: genomic DNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO

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; ORIGINAL SOURCE:
; ORGANISM: Penicillium chrysogenum
; IMMEDIATE SOURCE:
; CLONE: <Unknown>
; FEATURE:
; NAME/KEY: intron
; LOCATION: 794...920
; FEATURE:
; NAME/KEY: intron
; LOCATION: 952...1123
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1180...1289
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1321...1410
; FEATURE:
; NAME/KEY: intron
; LOCATION: 2183...2249
; OTHER INFORMATION: act gene
; SEQUENCE DESCRIPTION: SEQ ID NO: 4
US-09-171-337A-4

Query Match      86.7%; Score 13; DB 4; Length 3240;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTGCGCCCTG 13
Db 1238 CCTTCTGCGCCCTG 1226

RESULT 12
US-08-261-206A-76/c
; Sequence 76, Application US/08261206A
; Patent No. 5574007
; GENERAL INFORMATION:
; APPLICANT: Zushi, Mitichitaka
; APPLICANT: Gomi, Komakazu
; APPLICANT: Yamamoto, Shuji
; APPLICANT: Suzuki, Koji
; APPLICANT: Matsuda, Akio
; TITLE OF INVENTION: A Polypeptide Capable of Interacting
; TITLE OF INVENTION: with Thrombin
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 301 N. Washington St.
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/261,206A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/740,492
; FILING DATE: 03-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30330
; REFERENCE/DOCKET NUMBER: 216-275P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 76:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 3748 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Acremonium chrysogenum
; FEATURE:
; NAME/KEY:
; LOCATION: 1..3748
; OTHER INFORMATION: /label= actin_gene
; OTHER INFORMATION: /note= "Nucleotide sequence of region B in Figure
; OTHER INFORMATION: 60. Sequence corresponds to Figure 62."
; Patent No. 5574007
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1294..1300
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1428..1458
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1631..1686
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1797..1827
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1918..2689
; FEATURE:
; NAME/KEY: exon
; LOCATION: 2757..2984
; NAME/KEY: CDS
; LOCATION: join(1294..1300, 1428..1458, 1631..1686, 1797
; LOCATION: ..1827, 1918..2689, 2757..2984)
US-08-261-206A-76

Query Match      86.7%; Score 13; DB 1; Length 3748;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTGCGCCCTG 13
Db 1745 CCTTCTGCGCCCTG 1733

RESULT 13
US-09-254-325-1
; Sequence 1, Application US/09254325
; Patent No. 6090607
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: ENHANCED EXPRESSION OF
; TITLE OF INVENTION: PROTEOLYTIC ENZYMES IN KOJI MOLDS
; NUMBER OF SEQUENCES: 17
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/254,325
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4657 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
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US-09-254-325-1

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Best Local Similarity 100.0%; Pred. No. 14;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 4557 CTCTCGCCCTGT 4569

RESULT 14  
US-09-491-522-1/c  
; Sequence 1, Application US/09491522  
; Patent No. 6428998  
; GENERAL INFORMATION:  
; APPLICANT: Colige, Alain  
; APPLICANT: Lapiere, Charles M.  
; APPLICANT: Prockop, Darwin J.  
; TITLE OF INVENTION: RECOMBINANT N-PROTEINASE,  
; AND THE PRODUCTION, METHODS AND USES THEREOF  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds, LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
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; APPLICATION NUMBER: US/09/491,522  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/886,333  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Adams, Samuel B  
; REGISTRATION NUMBER: 30,605  
; REFERENCE/DOCKET NUMBER: 8389-0060-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-493-4935  
; TELEFAX: 650-493-5556  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6692 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
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Query Match 86.7%; Score 13; DB 4; Length 6692;

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; Sequence 1, Application US/08319387  
; Patent No. 5543317  
; GENERAL INFORMATION:  
; APPLICANT: Shields, Malcolm S.  
; APPLICANT: Francesconi, Stephen C.  
; TITLE OF INVENTION: Microbial Degradation of Trichloroethylene,  
; TITLE OF INVENTION: Dichloroethylenes and Aromatic Pollutants  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
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; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/167,457  
; FILING DATE: 15-DEC-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/694,718  
; FILING DATE: 02-MAY-1991  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Whitlock, Ted W.  
; REGISTRATION NUMBER: 36,965  
; REFERENCE/DOCKET NUMBER: UWF-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 1:  
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Query Match 86.7%; Score 13; DB 1; Length 9785;

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7	12	80.0	173	10 US-09-974-300-7193	Sequence 7193, Ap
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c 97	11	73.3	286	10	US-09-294-0933B-3238	Sequence 3238, Ap	170	11	73.3	945	10	US-09-974-300-3106	Sequence 3106, Ap
c 98	11	73.3	296	10	US-09-867-550-167	Sequence 167, App	171	11	73.3	948	10	US-09-815-242-7678	Sequence 7678, Ap
c 99	11	73.3	296	10	US-09-960-352-14240	Sequence 14240, A	c 172	11	73.3	957	12	US-10-042-417-41	Sequence 41, Appl
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102	11	73.3	308	10	US-09-339-338-88	Sequence 88, Appl	c 175	11	73.3	1023	10	US-09-731-872-168	Sequence 168, Appl
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c 137	11	73.3	471	10	US-09-864-761-5679	Sequence 5679, Ap	c 215	11	73.3	1836	10	US-09-870-162A-6	Sequence 3832, Ap
c 138	11	73.3	478	9	US-09-954-531-641	Sequence 641, App	c 216	11	73.3	1836	10	US-09-880-107-3832	Sequence 15, Appl
c 139	11	73.3	478	9	US-09-954-531-1053	Sequence 1053, Ap	c 217	11	73.3	1936	10	US-09-975-901-15	Sequence 4107, Ap
c 140	11	73.3	483	10	US-09-880-107-678	Sequence 678, App	c 218	11	73.3	1958	10	US-09-938-842A-4107	Sequence 6020, Ap
c 141	11	73.3	483	10	US-09-864-761-16053	Sequence 16053, A	c 219	11	73.3	2000	9	US-09-815-242-6020	Sequence 19, Appl
c 142	11	73.3	489	10	US-09-864-761-2434	Sequence 2434, Ap	c 220	11	73.3	2176	9	US-10-032-159A-19	Sequence 6215, Ap
c 143	11	73.3	489	10	US-09-864-761-5706	Sequence 5706, Ap	c 221	11	73.3	2205	10	US-09-815-242-6215	Sequence 1, Appli
c 144	11	73.3	502	10	US-09-738-973-328	Sequence 328, App	c 222	11	73.3	2242	9	US-09-970-989-1	Sequence 52, Appl
c 145	11	73.3	507	10	US-09-864-761-6944	Sequence 6944, Ap	c 223	11	73.3	2254	10	US-09-800-729-52	Sequence 368, App
c 146	11	73.3	508	10	US-09-867-701-2826	Sequence 2826, Ap	c 224	11	73.3	2281	9	US-09-922-598-368	Sequence 368, App
c 147	11	73.3	510	10	US-09-998-598-2597	Sequence 2597, Ap	c 225	11	73.3	2281	9	US-09-989-293A-368	Sequence 368, App
c 148	11	73.3	512	10	US-09-834-975-610	Sequence 610, App	c 226	11	73.3	2281	10	US-09-989-722-368	Sequence 368, App
c 149	11	73.3	520	10	US-09-783-590-7859	Sequence 7859, Ap	c 227	11	73.3	2281	10	US-09-989-279-368	Sequence 368, App
c 150	11	73.3	520	10	US-09-919-580-306	Sequence 306, App	c 228	11	73.3	2281	10	US-09-989-727-368	Sequence 368, App
c 151	11	73.3	528	10	US-09-867-701-15937	Sequence 15937, A	c 229	11	73.3	2281	10	US-09-989-731-368	Sequence 368, App
c 152	11	73.3	543	10	US-09-864-761-15909	Sequence 15909, A	c 230	11	73.3	2281	10	US-09-989-732-368	Sequence 368, App
c 153	11	73.3	546	10	US-09-917-800A-1683	Sequence 1683, Ap	c 231	11	73.3	2281	10	US-09-991-163-368	Sequence 368, App
c 154	11	73.3	553	10	US-09-864-761-9018	Sequence 9018, Ap	c 232	11	73.3	2281	10	US-09-991-163-368	Sequence 368, App
c 155	11	73.3	554	10	US-09-734-017A-77	Sequence 77, Appl	c 233	11	73.3	2281	10	US-09-991-163-368	Sequence 368, App
c 156	11	73.3	559	10	US-09-864-761-12322	Sequence 12322, A	c 234	11	73.3	2294	12	US-10-052-586-283	Sequence 283, App
c 157	11	73.3	560	10	US-09-887-576-804	Sequence 804, App	c 235	11	73.3	2295	10	US-09-989-721-368	Sequence 253, App
c 158	11	73.3	575	10	US-09-864-761-12618	Sequence 12618, A	c 236	11	73.3	2354	10	US-09-989-721-368	Sequence 1767, Ap
c 159	11	73.3	650	10	US-09-867-550-15907	Sequence 15907, Ap	c 237	11	73.3	2406	10	US-09-764-864-1767	Sequence 300, App
c 160	11	73.3	659	10	US-09-822-830A-435	Sequence 435, App	c 238	11	73.3	2412	9	US-09-967-768A-300	Sequence 1529, Ap
c 161	11	73.3	720	10	US-09-974-300-4505	Sequence 4505, App						US-09-974-300-1529	Sequence 3, Appli
c 162	11	73.3	744	10	US-09-833-381-293	Sequence 293, App							
c 163	11	73.3	757	10	US-09-861-893-71	Sequence 71, Appl							
c 164	11	73.3	758	10	US-09-867-550-1385	Sequence 1385, Ap							
c 165	11	73.3	772	10	US-09-770-445-908	Sequence 908, App							

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c 240	11	73.3	2507	10	US-09-759-143-332	Sequence 332, App	c 313	11	73.3	26928	10	US-09-880-107-2278	Sequence 2278, Ap
c 241	11	73.3	2507	10	US-09-780-669-332	Sequence 332, App	314	11	73.3	32170	10	US-09-764-860-1108	Sequence 1108, Ap
c 242	11	73.3	2507	10	US-09-822-827-332	Sequence 332, App	315	11	73.3	32188	10	US-09-764-860-799	Sequence 799, App
c 243	11	73.3	2604	10	US-09-801-368-97	Sequence 97, Appl	c 316	11	73.3	35100	10	US-09-782-378A-26	Sequence 26, Appl
c 244	11	73.3	2648	9	US-10-112-527-5	Sequence 5, Appl	317	11	73.3	42432	9	US-10-027-806-2	Sequence 2, Appl
c 245	11	73.3	2652	9	US-09-764-868-1388	Sequence 1388, Ap	318	11	73.3	45845	10	US-09-927-091-6	Sequence 6, Appl
c 246	11	73.3	2754	10	US-09-861-801-3	Sequence 3, Appl	319	11	73.3	46718	10	US-09-816-093-3	Sequence 3, Appl
c 247	11	73.3	2760	9	US-09-991-496-126	Sequence 126, App	320	11	73.3	57130	10	US-09-835-081-3	Sequence 3, Appl
c 248	11	73.3	2781	9	US-09-991-496-125	Sequence 125, App	321	11	73.3	58837	10	US-09-982-091A-5	Sequence 5, Appl
c 249	11	73.3	2810	10	US-09-833-381-873	Sequence 873, App	322	11	73.3	62944	10	US-09-954-456-2257	Sequence 2257, Ap
c 250	11	73.3	2844	12	US-10-044-090-813	Sequence 813, App	c 323	11	73.3	110096	10	US-09-880-107-1542	Sequence 1542, Ap
c 251	11	73.3	2875	9	US-09-801-220-1	Sequence 1, Appl	c 324	11	73.3	111282	12	US-10-094-989-3	Sequence 3, Appl
c 252	11	73.3	2894	10	US-09-954-456-691	Sequence 691, App	c 325	11	73.3	116592	10	US-09-818-512-3	Sequence 3, Appl
c 253	11	73.3	2935	10	US-09-742-582-13	Sequence 13, Appl	c 326	11	73.3	126512	10	US-09-804-474A-3	Sequence 3, Appl
c 254	11	73.3	2959	10	US-09-742-582-15	Sequence 15, Appl	c 327	11	73.3	145831	10	US-09-969-708-79	Sequence 79, Appl
c 255	11	73.3	3287	10	US-09-925-297-128	Sequence 128, App	c 328	11	73.3	145831	10	US-09-954-456-2116	Sequence 2116, Ap
c 256	11	73.3	3301	9	US-09-981-876-66	Sequence 66, Appl	c 329	11	73.3	172637	10	US-09-835-232-7	Sequence 7, Appl
c 257	11	73.3	3338	9	US-10-108-605-192	Sequence 192, App	c 330	11	73.3	172637	10	US-09-805-458A-3	Sequence 3, Appl
c 258	11	73.3	3472	10	US-09-925-299-96	Sequence 96, Appl	331	11	73.3	302250	10	US-09-962-832-154	Sequence 154, App
c 259	11	73.3	3669	10	US-09-861-801-1	Sequence 1, Appl	332	11	73.3	397658	10	US-09-813-320-3	Sequence 3, Appl
c 260	11	73.3	3744	10	US-09-815-242-6048	Sequence 6048, Ap	c 333	11	73.3	397658	10	US-09-946-807-1	Sequence 1, Appl
c 261	11	73.3	3825	12	US-10-147-268-1	Sequence 1, Appl	c 334	11	73.3	1503841	10	US-09-795-668-1	Sequence 1, Appl
c 262	11	73.3	3896	10	US-09-927-091-3	Sequence 3, Appl	c 335	11	73.3	1503841	10	US-09-795-668-1	Sequence 1, Appl
c 263	11	73.3	3915	10	US-09-954-456-507	Sequence 507, App	336	10	66.7	15	10	US-09-504-231A-589	Sequence 589, App
c 264	11	73.3	3915	10	US-09-758-828-1	Sequence 1, Appl	337	10	66.7	15	10	US-09-504-231A-591	Sequence 591, App
c 265	11	73.3	4002	9	US-09-758-828-3	Sequence 3, Appl	338	10	66.7	15	10	US-09-274-553D-589	Sequence 589, App
c 266	11	73.3	4119	10	US-09-954-456-729	Sequence 729, App	339	10	66.7	15	10	US-09-274-553D-591	Sequence 591, App
c 267	11	73.3	4139	10	US-09-880-107-2279	Sequence 2279, Ap	340	10	66.7	15	10	US-09-274-553D-591	Sequence 591, App
c 268	11	73.3	4162	10	US-09-861-881-1	Sequence 1, Appl	341	10	66.7	15	10	US-09-866-108-186	Sequence 186, App
c 269	11	73.3	4204	9	US-09-784-199-1	Sequence 1, Appl	342	10	66.7	17	10	US-09-866-108-187	Sequence 187, App
c 270	11	73.3	4204	10	US-09-954-456-747	Sequence 747, App	343	10	66.7	17	10	US-09-866-108-188	Sequence 188, App
c 271	11	73.3	4330	10	US-09-880-107-2361	Sequence 2361, Ap	344	10	66.7	17	10	US-09-866-108-189	Sequence 189, App
c 272	11	73.3	4330	10	US-09-861-881-2	Sequence 2, Appl	345	10	66.7	17	10	US-09-866-108-190	Sequence 190, App
c 273	11	73.3	4744	10	US-09-880-107-3459	Sequence 3459, Ap	346	10	66.7	17	10	US-09-866-108-191	Sequence 191, App
c 274	11	73.3	5091	8	US-08-424-5508-668	Sequence 668, App	347	10	66.7	17	10	US-09-866-108-192	Sequence 192, App
c 275	11	73.3	5512	10	US-09-764-887-522	Sequence 522, App	348	10	66.7	17	10	US-09-866-108-193	Sequence 193, App
c 276	11	73.3	5630	10	US-09-871-388-1	Sequence 1, Appl	349	10	66.7	17	10	US-09-866-108-193	Sequence 193, App
c 277	11	73.3	6336	10	US-09-964-824A-114	Sequence 114, App	350	10	66.7	18	10	US-09-966-147-38	Sequence 38, Appl
c 278	11	73.3	6336	9	US-09-880-107-1537	Sequence 1537, Ap	c 351	10	66.7	20	9	US-09-963-875-35	Sequence 35, Appl
c 279	11	73.3	6560	10	US-09-808-602-76	Sequence 76, Appl	c 352	10	66.7	23	9	US-09-931-007A-10	Sequence 10, Appl
c 280	11	73.3	6651	10	US-09-954-456-178	Sequence 178, App	353	10	66.7	25	10	US-09-866-108-3115	Sequence 3115, Ap
c 281	11	73.3	6651	10	US-09-954-456-1217	Sequence 1217, Ap	354	10	66.7	25	10	US-09-866-108-3116	Sequence 3116, Ap
c 282	11	73.3	6800	10	US-09-764-869-2142	Sequence 2142, Ap	355	10	66.7	25	10	US-09-866-108-3117	Sequence 3117, Ap
c 283	11	73.3	6892	10	US-09-764-877-3770	Sequence 3770, Ap	356	10	66.7	25	10	US-09-866-108-3118	Sequence 3118, Ap
c 284	11	73.3	7326	12	US-10-109-886-7	Sequence 7, Appl	357	10	66.7	25	10	US-09-866-108-3119	Sequence 3119, Ap
c 285	11	73.3	8145	10	US-09-070-927A-386	Sequence 386, App	358	10	66.7	25	10	US-09-866-108-3120	Sequence 3120, Ap
c 286	11	73.3	8147	12	US-10-109-886-9	Sequence 9, Appl	359	10	66.7	25	10	US-09-866-108-3121	Sequence 3121, Ap
c 287	11	73.3	8663	10	US-09-764-878-397	Sequence 397, App	360	10	66.7	25	10	US-09-866-108-3122	Sequence 3122, Ap
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c 289	11	73.3	8797	9	US-09-808-602-77	Sequence 77, Appl	362	10	66.7	25	10	US-09-866-108-3124	Sequence 3124, Ap
c 290	11	73.3	8797	9	US-09-808-602-77	Sequence 77, Appl	363	10	66.7	25	10	US-09-866-108-3125	Sequence 3125, Ap
c 291	11	73.3	8911	10	US-09-764-853-895	Sequence 895, App	364	10	66.7	25	10	US-09-866-108-3126	Sequence 3126, Ap
c 292	11	73.3	9034	8	US-08-424-5508-397	Sequence 397, App	365	10	66.7	25	10	US-09-866-108-3127	Sequence 3127, Ap
c 293	11	73.3	9729	9	US-09-808-602-12	Sequence 12, Appl	366	10	66.7	25	10	US-09-866-108-3128	Sequence 3128, Ap
c 294	11	73.3	9815	10	US-09-764-847-1601	Sequence 1601, Ap	367	10	66.7	25	10	US-09-866-108-3129	Sequence 3129, Ap
c 295	11	73.3	9826	9	US-09-808-602-7	Sequence 7, Appl	368	10	66.7	25	10	US-09-866-108-3130	Sequence 3130, Ap
c 296	11	73.3	10419	9	US-10-027-806-3	Sequence 3, Appl	c 369	10	66.7	27	10	US-09-928-796A-8	Sequence 8, Appl
c 297	11	73.3	10953	10	US-09-764-846-313	Sequence 313, App	c 370	10	66.7	31	10	US-09-801-274-1765	Sequence 1765, Ap
c 298	11	73.3	11298	10	US-09-764-847-1343	Sequence 1343, Ap	371	10	66.7	38	9	US-09-864-785-744	Sequence 744, App
c 299	11	73.3	12822	10	US-09-764-847-1579	Sequence 1579, Ap	372	10	66.7	50	10	US-09-504-231A-2980	Sequence 2980, Ap
c 300	11	73.3	13272	10	US-09-764-846-312	Sequence 312, App	373	10	66.7	50	10	US-09-504-231A-3097	Sequence 3097, Ap
c 301	11	73.3	13337	10	US-09-764-846-312	Sequence 312, App	374	10	66.7	50	10	US-09-274-553D-2980	Sequence 2980, Ap
c 302	11	73.3	13337	10	US-09-764-847-1629	Sequence 1629, Ap	c 375	10	66.7	50	10	US-09-274-553D-3097	Sequence 3097, Ap
c 303	11	73.3	13613	9	US-09-860-846-3	Sequence 3, Appl	376	10	66.7	81	10	US-09-398-473-2	Sequence 2, Appl
c 304	11	73.3	13613	9	US-09-861-289-3	Sequence 3, Appl	377	10	66.7	113	10	US-09-878-574-939	Sequence 939, App
c 305	11	73.3	13953	9	US-10-096-961-3	Sequence 3, Appl	378	10	66.7	114	9	US-09-768-827-19	Sequence 19, Appl
c 306	11	73.3	14272	10	US-09-870-162A-23	Sequence 23, Appl	379	10	66.7	120	8	US-08-902-572-15	Sequence 15, Appl
c 307	11	73.3	15425	10	US-09-764-869-1654	Sequence 1654, Ap	380	10	66.7	120	10	US-09-862-179A-42	Sequence 42, Appl
c 308	11	73.3	15515	10	US-09-822-860-3	Sequence 3, Appl	381	10	66.7	127	10	US-09-864-761-29696	Sequence 29696, A
c 309	11	73.3	15843	10	US-09-764-869-2396	Sequence 2396, Ap	382	10	66.7	128	10	US-09-294-093B-1263	Sequence 1263, Ap
c 310	11	73.3	16774	10	US-09-764-869-2396	Sequence 2396, Ap	383	10	66.7	128	10	US-09-923-876-1504	Sequence 1504, Ap
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386	10	66.7	148	10	US-09-866-108-15665	Sequence 15665, A	c 459	10	66.7	291	10	US-09-867-550-1437	Sequence 1437, Ap
387	10	66.7	160	10	US-09-864-761-17796	Sequence 17796, A	c 460	10	66.7	291	10	US-09-880-107-1982	Sequence 1982, Ap
c 388	10	66.7	168	10	US-09-563-817-496	Sequence 496, App	c 461	10	66.7	292	9	US-10-040-739-441	Sequence 441, App
389	10	66.7	175	10	US-09-923-876-6221	Sequence 6221, A	c 462	10	66.7	293	9	US-09-736-457-1684	Sequence 1684, Ap
c 390	10	66.7	178	10	US-09-878-574-14466	Sequence 14466, A	c 463	10	66.7	293	9	US-09-902-941-1684	Sequence 1684, Ap
391	10	66.7	180	10	US-09-855-722-10	Sequence 10, Appl	c 464	10	66.7	294	10	US-09-783-590-9255	Sequence 9255, Ap
c 392	10	66.7	187	10	US-09-983-965-2925	Sequence 2925, Ap	c 465	10	66.7	294	10	US-09-974-300-6621	Sequence 6621, Ap
c 393	10	66.7	187	10	US-09-783-590-2317	Sequence 2317, Ap	c 466	10	66.7	295	10	US-09-294-093B-1118	Sequence 1118, Ap
c 394	10	66.7	195	10	US-09-563-817-14	Sequence 14, Appl	c 467	10	66.7	295	10	US-09-294-093B-4189	Sequence 4189, Ap
c 395	10	66.7	197	10	US-09-998-598-205	Sequence 205, App	c 468	10	66.7	296	10	US-09-294-093B-859	Sequence 859, App
396	10	66.7	197	10	US-09-988-598-2327	Sequence 2327, Ap	c 469	10	66.7	297	10	US-09-923-876-3903	Sequence 3903, Ap
397	10	66.7	200	10	US-09-867-701-8772	Sequence 8772, Ap	c 470	10	66.7	300	10	US-09-294-093B-5901	Sequence 5901, Ap
c 398	10	66.7	223	10	US-09-983-965-5109	Sequence 5109, Ap	c 471	10	66.7	300	10	US-09-767-870-7	Sequence 7, Appl
c 399	10	66.7	224	10	US-09-960-352-446	Sequence 446, App	c 472	10	66.7	304	10	US-09-922-217-726	Sequence 726, App
c 400	10	66.7	225	10	US-09-974-300-5821	Sequence 5821, Ap	c 473	10	66.7	305	10	US-09-833-263-726	Sequence 726, App
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c 402	10	66.7	234	10	US-09-923-876-903	Sequence 903, App	c 475	10	66.7	306	9	US-10-079-623-73	Sequence 73, Appl
c 403	10	66.7	234	10	US-09-864-761-20819	Sequence 20819, A	c 476	10	66.7	309	10	US-09-294-093B-1630	Sequence 1630, Ap
c 404	10	66.7	236	10	US-09-983-965-5108	Sequence 5108, Ap	c 477	10	66.7	310	10	US-09-294-093B-1620	Sequence 1620, Ap
c 405	10	66.7	237	10	US-09-783-590-8300	Sequence 8300, Ap	c 478	10	66.7	311	10	US-09-867-701-9720	Sequence 9720, Ap
406	10	66.7	243	10	US-09-960-352-3063	Sequence 3063, Ap	c 479	10	66.7	311	10	US-09-960-352-14967	Sequence 14967, A
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c 409	10	66.7	244	10	US-09-878-574-10577	Sequence 10577, A	c 482	10	66.7	322	10	US-09-964-824A-525	Sequence 525, App
c 410	10	66.7	246	10	US-09-983-965-2298	Sequence 2298, Ap	c 483	10	66.7	322	10	US-09-967-768A-129	Sequence 129, App
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c 412	10	66.7	248	10	US-09-960-352-3802	Sequence 3802, Ap	c 485	10	66.7	325	10	US-09-960-352-5391	Sequence 5391, Ap
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414	10	66.7	249	10	US-09-867-701-4203	Sequence 4203, Ap	c 487	10	66.7	325	10	US-09-960-352-6698	Sequence 14887, A
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c 417	10	66.7	251	10	US-09-923-876-3041	Sequence 3041, Ap	c 490	10	66.7	334	9	US-09-954-531-394	Sequence 394, App
418	10	66.7	251	10	US-09-878-574-5722	Sequence 5722, Ap	c 491	10	66.7	334	9	US-09-736-457-394	Sequence 389, App
c 419	10	66.7	256	10	US-09-878-574-181	Sequence 181, App	c 492	10	66.7	336	10	US-09-902-941-394	Sequence 2440, Ap
c 420	10	66.7	257	10	US-09-878-574-6977	Sequence 6977, Ap	c 493	10	66.7	337	10	US-09-983-965-2440	Sequence 2232, Ap
c 421	10	66.7	257	10	US-09-764-877-2995	Sequence 2995, Ap	c 494	10	66.7	340	10	US-09-878-574-2232	Sequence 2232, Ap
c 422	10	66.7	258	10	US-09-878-574-7576	Sequence 7576, Ap	c 495	10	66.7	345	10	US-09-815-343-1122	Sequence 1211, Ap
c 423	10	66.7	258	10	US-09-974-300-5995	Sequence 5995, Ap	c 496	10	66.7	345	10	US-09-815-343-1211	Sequence 437, App
424	10	66.7	259	10	US-09-923-876-5822	Sequence 5822, Ap	c 497	10	66.7	345	10	US-09-920-300A-437	Sequence 1053, Ap
c 425	10	66.7	259	10	US-09-864-761-18646	Sequence 18646, A	c 498	10	66.7	345	10	US-09-920-300A-1053	Sequence 437, App
c 426	10	66.7	259	10	US-09-864-761-20166	Sequence 20166, A	c 499	10	66.7	345	12	US-10-033-528-437	Sequence 1053, Ap
c 427	10	66.7	259	10	US-09-960-352-4925	Sequence 4925, Ap	c 500	10	66.7	345	12	US-10-033-528-1053	Sequence 1053, Ap
c 428	10	66.7	261	10	US-09-923-876-5650	Sequence 5650, Ap	c 501	10	66.7	346	10	US-09-983-965-3296	Sequence 3296, Ap
c 429	10	66.7	261	10	US-09-864-761-26238	Sequence 26238, A	c 502	10	66.7	347	10	US-09-960-352-756	Sequence 756, App
c 430	10	66.7	262	10	US-09-764-864-593	Sequence 593, App	c 503	10	66.7	348	10	US-09-864-761-24324	Sequence 24324, A
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c 432	10	66.7	265	10	US-09-960-352-9338	Sequence 9338, Ap	c 505	10	66.7	351	10	US-09-974-300-7989	Sequence 7989, Ap
c 433	10	66.7	265	10	US-09-878-574-6564	Sequence 6564, Ap	c 506	10	66.7	354	10	US-09-815-343-1307	Sequence 1307, Ap
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c 435	10	66.7	268	10	US-09-878-574-12242	Sequence 12242, A	c 508	10	66.7	354	10	US-09-960-352-8198	Sequence 8198, Ap
c 436	10	66.7	269	10	US-09-878-574-6213	Sequence 6213, Ap	c 509	10	66.7	355	10	US-09-919-580-752	Sequence 752, App
c 437	10	66.7	269	10	US-09-878-574-8785	Sequence 8785, Ap	c 510	10	66.7	355	10	US-09-878-574-2983	Sequence 2983, Ap
c 438	10	66.7	272	10	US-09-294-093B-4109	Sequence 4109, Ap	c 511	10	66.7	361	10	US-09-878-574-2975	Sequence 2975, Ap
c 439	10	66.7	272	10	US-09-878-574-12222	Sequence 12222, A	c 512	10	66.7	362	10	US-09-960-352-9441	Sequence 9441, Ap
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c 442	10	66.7	278	10	US-09-923-876-4044	Sequence 4044, Ap	c 515	10	66.7	366	12	US-10-033-528-1457	Sequence 1457, Ap
c 443	10	66.7	278	10	US-09-878-574-6718	Sequence 6718, Ap	c 516	10	66.7	366	10	US-09-864-761-20764	Sequence 20764, A
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c 446	10	66.7	282	10	US-09-294-093B-2123	Sequence 2123, Ap	c 519	10	66.7	367	10	US-09-960-352-9316	Sequence 9316, Ap
c 447	10	66.7	285	10	US-09-878-574-5407	Sequence 5407, Ap	c 520	10	66.7	368	10	US-09-878-574-810	Sequence 810, App
c 448	10	66.7	286	9	US-10-040-739-75	Sequence 75, Appl	c 521	10	66.7	369	10	US-09-867-701-5181	Sequence 5181, Ap
c 449	10	66.7	287	10	US-09-969-708-227	Sequence 227, App	c 522	10	66.7	374	10	US-09-878-574-3508	Sequence 3508, Ap
c 450	10	66.7	287	10	US-09-878-574-12671	Sequence 12671, A	c 523	10	66.7	374	10	US-09-878-574-1663	Sequence 1663, Ap
c 451	10	66.7	287	10	US-09-783-590-11346	Sequence 11346, A	c 524	10	66.7	380	10	US-09-878-574-321	Sequence 321, App
c 452	10	66.7	287	10	US-09-960-352-478	Sequence 478, App	c 525	10	66.7	380	10	US-09-960-352-10593	Sequence 10593, A
c 453	10	66.7	288	10	US-09-294-093B-285	Sequence 285, App	c 526	10	66.7	383	10	US-09-960-352-5227	Sequence 5227, Ap
c 454	10	66.7	288	10	US-09-294-093B-1489	Sequence 1489, Ap	c 527	10	66.7	383	10	US-09-960-352-37	Sequence 37, Appl
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c 457	10	66.7	289	10	US-09-294-093B-2606	Sequence 2606, Ap	c 530	10	66.7	385	9		



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c 532	10	66.7	386	10	US-09-881-752A-1115	Sequence 115, App	c 605	10	66.7	480	10	US-09-878-574-4688	Sequence 4688, Ap
c 533	10	66.7	387	10	US-09-216-393-61	Sequence 61, Appl	c 606	10	66.7	480	10	US-09-974-300-4502	Sequence 4502, Ap
c 534	10	66.7	389	10	US-09-960-352-220	Sequence 220, App	c 607	10	66.7	486	10	US-09-878-574-4269	Sequence 4269, Ap
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c 536	10	66.7	390	10	US-09-783-590-10785	Sequence 10785, A	c 609	10	66.7	487	10	US-09-747-155-159	Sequence 159, App
c 537	10	66.7	392	10	US-09-878-574-106	Sequence 106, App	c 610	10	66.7	487	10	US-09-747-155-228	Sequence 228, App
c 538	10	66.7	392	10	US-09-960-352-9126	Sequence 9126, App	c 611	10	66.7	487	10	US-09-747-155-287	Sequence 287, App
c 539	10	66.7	394	10	US-09-960-352-6266	Sequence 6266, Ap	c 612	10	66.7	488	10	US-09-867-701-3971	Sequence 3971, Ap
c 540	10	66.7	396	10	US-09-974-300-2211	Sequence 2211, Ap	c 613	10	66.7	491	10	US-09-833-381-24	Sequence 24, Appl
c 541	10	66.7	398	10	US-09-878-574-2550	Sequence 2550, Ap	c 614	10	66.7	493	10	US-09-833-381-24	Sequence 24, Appl
c 542	10	66.7	398	10	US-09-783-590-4352	Sequence 4352, Ap	c 615	10	66.7	495	9	US-09-783-295A-191	Sequence 8994, Ap
c 543	10	66.7	399	10	US-09-974-300-3251	Sequence 3251, Ap	c 616	10	66.7	495	9	US-09-978-697-191	Sequence 191, App
c 544	10	66.7	403	10	US-09-878-574-3926	Sequence 3926, Ap	c 617	10	66.7	495	9	US-09-978-697-191	Sequence 191, App
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c 546	10	66.7	406	10	US-09-974-300-1971	Sequence 1971, Ap	c 619	10	66.7	499	10	US-09-880-107-3569	Sequence 3569, Ap
c 547	10	66.7	407	10	US-09-925-302-390	Sequence 390, App	c 620	10	66.7	500	9	US-10-047-542-33	Sequence 33, Appl
c 548	10	66.7	407	10	US-09-922-217-175	Sequence 175, App	c 621	10	66.7	500	10	US-09-866-108-15709	Sequence 15709, A
c 549	10	66.7	407	10	US-09-833-263-175	Sequence 175, App	c 622	10	66.7	505	10	US-09-864-761-7619	Sequence 7619, Ap
c 550	10	66.7	407	10	US-09-960-352-10916	Sequence 10916, A	c 623	10	66.7	511	10	US-09-814-122-18	Sequence 18, Appl
c 551	10	66.7	408	10	US-09-764-877-3715	Sequence 3715, Ap	c 624	10	66.7	511	10	US-09-917-800A-220	Sequence 220, App
c 552	10	66.7	408	10	US-09-764-877-3716	Sequence 3716, Ap	c 625	10	66.7	512	10	US-09-828-313-2	Sequence 2, Appl
c 553	10	66.7	409	10	US-09-864-761-1024	Sequence 1024, Ap	c 626	10	66.7	513	9	US-09-991-496-136	Sequence 136, App
c 554	10	66.7	409	10	US-09-960-352-8974	Sequence 8974, Ap	c 627	10	66.7	514	9	US-09-736-457-1656	Sequence 1656, Ap
c 555	10	66.7	413	10	US-09-960-352-7928	Sequence 7288, Ap	c 628	10	66.7	514	9	US-09-902-941-1656	Sequence 1656, Ap
c 556	10	66.7	414	10	US-09-974-300-5024	Sequence 5024, Ap	c 629	10	66.7	515	10	US-09-917-800A-73	Sequence 73, Appl
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c 559	10	66.7	417	10	US-09-864-761-13856	Sequence 13856, A	c 632	10	66.7	519	9	US-10-040-733-939	Sequence 939, App
c 560	10	66.7	421	10	US-09-960-352-9855	Sequence 9855, Ap	c 633	10	66.7	519	10	US-09-887-576-780	Sequence 780, App
c 561	10	66.7	422	10	US-09-960-352-9158	Sequence 9158, Ap	c 634	10	66.7	519	12	US-10-095-492-12	Sequence 12, Appl
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c 564	10	66.7	425	10	US-09-960-352-7427	Sequence 7427, Ap	c 637	10	66.7	527	10	US-09-925-299-684	Sequence 684, App
c 565	10	66.7	425	10	US-09-960-352-8301	Sequence 8301, Ap	c 638	10	66.7	527	10	US-09-443-704-1	Sequence 1, Appl
c 566	10	66.7	426	9	US-10-125-815-6	Sequence 6, Appl	c 639	10	66.7	534	10	US-09-801-115-1	Sequence 1, Appl
c 567	10	66.7	427	10	US-09-864-761-4063	Sequence 4063, Ap	c 640	10	66.7	536	10	US-09-764-855-30	Sequence 30, Appl
c 568	10	66.7	427	10	US-09-764-847-266	Sequence 266, App	c 641	10	66.7	537	10	US-09-765-111A-36	Sequence 36, Appl
c 569	10	66.7	427	10	US-09-960-352-11827	Sequence 11827, A	c 642	10	66.7	538	10	US-09-922-217-928	Sequence 928, App
c 570	10	66.7	428	10	US-09-864-761-18340	Sequence 18340, A	c 643	10	66.7	538	10	US-09-833-263-928	Sequence 928, App
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c 572	10	66.7	431	10	US-09-867-550-23	Sequence 23, Appl	c 645	10	66.7	540	10	US-09-922-217-964	Sequence 964, App
c 573	10	66.7	431	10	US-09-924-035A-333	Sequence 333, App	c 646	10	66.7	540	10	US-09-833-263-964	Sequence 964, App
c 574	10	66.7	433	10	US-09-956-004-116	Sequence 116, App	c 647	10	66.7	540	10	US-09-887-576-796	Sequence 796, App
c 575	10	66.7	433	10	US-09-960-352-818	Sequence 818, App	c 648	10	66.7	543	10	US-09-864-761-14939	Sequence 14939, A
c 576	10	66.7	434	9	US-10-079-623-245	Sequence 245, App	c 649	10	66.7	543	10	US-09-970-532-3	Sequence 3, Appl
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c 578	10	66.7	438	9	US-09-938-842A-899	Sequence 899, App	c 651	10	66.7	549	10	US-09-867-701-4856	Sequence 4856, Ap
c 579	10	66.7	440	10	US-09-960-352-12870	Sequence 12870, A	c 652	10	66.7	549	10	US-09-734-017A-45	Sequence 45, Appl
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c 581	10	66.7	442	10	US-09-867-701-5221	Sequence 5221, Ap	c 654	10	66.7	551	10	US-09-969-708-592	Sequence 592, App
c 582	10	66.7	445	10	US-09-783-590-3731	Sequence 3731, Ap	c 655	10	66.7	552	10	US-09-917-800A-1272	Sequence 1272, Ap
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c 584	10	66.7	447	10	US-09-998-598-884	Sequence 884, App	c 657	10	66.7	555	10	US-09-919-580-327	Sequence 95, Appl
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c 586	10	66.7	450	10	US-09-974-300-3110	Sequence 3110, Ap	c 659	10	66.7	567	10	US-09-864-761-25808	Sequence 25808, A
c 587	10	66.7	451	9	US-09-954-531-460	Sequence 460, App	c 660	10	66.7	567	10	US-09-864-761-31880	Sequence 31880, A
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c 589	10	66.7	453	10	US-09-960-352-6118	Sequence 6118, Ap	c 662	10	66.7	569	10	US-09-864-761-13135	Sequence 13135, A
c 590	10	66.7	456	10	US-09-974-300-6234	Sequence 6234, Ap	c 663	10	66.7	571	10	US-09-833-790-344	Sequence 344, App
c 591	10	66.7	460	10	US-09-864-761-15176	Sequence 15176, A	c 664	10	66.7	572	10	US-09-974-300-1878	Sequence 1878, Ap
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c 593	10	66.7	462	10	US-09-735-705-289	Sequence 289, App	c 666	10	66.7	573	10	US-09-764-869-1484	Sequence 1484, Ap
c 594	10	66.7	462	10	US-09-850-716A-289	Sequence 289, App	c 667	10	66.7	574	10	US-09-864-761-18330	Sequence 18330, Ap
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c 597	10	66.7	467	10	US-09-864-761-2463	Sequence 2463, Ap	c 670	10	66.7	578	10	US-09-833-263-840	Sequence 840, App
c 598	10	66.7	468	10	US-09-864-761-672	Sequence 672, App	c 671	10	66.7	578	10	US-09-764-853-411	Sequence 411, App
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c 680	10	66.7	597	10	US-09-974-300-4977	Sequence 4977, Ap	c 753	10	66.7	818	10	US-09-878-574-4624	Sequence 4624, Ap
c 681	10	66.7	598	10	US-09-770-149-992	Sequence 992, App	c 754	10	66.7	818	10	US-09-983-580-3	Sequence 3, Appli
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c 683	10	66.7	599	10	US-09-925-300-100	Sequence 100, App	c 756	10	66.7	831	9	US-10-001-887-58	Sequence 58, Appl
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c 687	10	66.7	607	10	US-09-833-263-951	Sequence 951, App	c 760	10	66.7	858	10	US-09-815-242-4013	Sequence 4013, Ap
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c 691	10	66.7	619	10	US-09-879-536-815	Sequence 815, App	c 764	10	66.7	871	10	US-09-956-999-7	Sequence 7, Appli
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c 694	10	66.7	630	10	US-09-925-299-293	Sequence 293, App	c 767	10	66.7	873	10	US-09-815-242-7800	Sequence 7800, Ap
c 695	10	66.7	633	10	US-09-867-550-777	Sequence 777, App	c 768	10	66.7	882	10	US-09-974-300-2352	Sequence 2352, Ap
c 696	10	66.7	633	10	US-09-974-300-6076	Sequence 6076, Ap	c 769	10	66.7	882	10	US-09-764-864-642	Sequence 642, App
c 697	10	66.7	633	10	US-09-833-381-1326	Sequence 1326, App	c 770	10	66.7	885	10	US-09-815-242-9236	Sequence 9236, Ap
c 698	10	66.7	641	10	US-09-770-149-604	Sequence 604, App	c 771	10	66.7	885	10	US-09-884-441-22	Sequence 22, Appl
c 699	10	66.7	642	10	US-09-974-300-1333	Sequence 1333, Ap	c 772	10	66.7	900	10	US-09-764-864-211	Sequence 211, App
c 700	10	66.7	644	10	US-09-886-404-1	Sequence 1, Appli	c 773	10	66.7	903	10	US-09-764-877-2956	Sequence 2956, Ap
c 701	10	66.7	648	12	US-10-001-843-114	Sequence 114, App	c 774	10	66.7	905	10	US-09-748-033-5	Sequence 5, Appli
c 702	10	66.7	657	10	US-09-974-300-5602	Sequence 5602, Ap	c 775	10	66.7	905	10	US-09-969-708-88	Sequence 88, Appl
c 703	10	66.7	663	9	US-09-978-298A-189	Sequence 189, App	c 776	10	66.7	905	10	US-09-969-708-88	Sequence 88, Appl
c 704	10	66.7	663	9	US-09-978-697-189	Sequence 189, App	c 777	10	66.7	912	8	US-08-902-572-13	Sequence 13, Appl
c 705	10	66.7	663	9	US-09-978-192A-189	Sequence 189, App	c 778	10	66.7	912	10	US-09-862-179A-40	Sequence 40, Appl
c 706	10	66.7	675	10	US-09-764-864-678	Sequence 678, App	c 779	10	66.7	918	10	US-09-815-242-7705	Sequence 7705, Ap
c 707	10	66.7	678	10	US-09-815-242-7612	Sequence 7612, Ap	c 780	10	66.7	918	10	US-09-886-055-300	Sequence 300, App
c 708	10	66.7	680	10	US-09-974-300-5462	Sequence 5462, Ap	c 781	10	66.7	928	12	US-10-001-843-115	Sequence 115, App
c 709	10	66.7	683	10	US-09-867-701-6261	Sequence 6261, Ap	c 782	10	66.7	930	10	US-09-771-161A-49	Sequence 49, Appl
c 710	10	66.7	686	10	US-09-910-943-313	Sequence 313, App	c 783	10	66.7	938	10	US-09-770-445-367	Sequence 367, App
c 711	10	66.7	693	10	US-09-974-300-1576	Sequence 1576, Ap	c 784	10	66.7	938	10	US-09-833-381-1064	Sequence 1064, Ap
c 712	10	66.7	714	12	US-10-078-929-85	Sequence 85, Appl	c 785	10	66.7	949	10	US-09-791-171-11	Sequence 11, Appl
c 713	10	66.7	717	10	US-09-815-242-7765	Sequence 7765, Ap	c 786	10	66.7	951	10	US-09-974-300-5212	Sequence 5212, Ap
c 714	10	66.7	717	12	US-10-024-579-15	Sequence 15, Appl	c 787	10	66.7	954	9	US-09-877-650-12	Sequence 12, Appl
c 715	10	66.7	718	10	US-09-759-143-313	Sequence 313, App	c 788	10	66.7	954	10	US-09-871-856-12	Sequence 12, Appl
c 716	10	66.7	718	10	US-09-780-669-313	Sequence 313, App	c 789	10	66.7	957	10	US-09-974-300-7292	Sequence 7292, Ap
c 717	10	66.7	718	10	US-09-822-827-313	Sequence 313, App	c 790	10	66.7	958	10	US-09-864-761-15366	Sequence 15366, A
c 718	10	66.7	719	10	US-09-920-345-28	Sequence 28, Appl	c 791	10	66.7	960	10	US-09-741-669-186	Sequence 186, App
c 719	10	66.7	722	10	US-09-764-870-230	Sequence 230, App	c 792	10	66.7	961	10	US-09-815-242-6301	Sequence 6301, Ap
c 720	10	66.7	723	10	US-09-791-578-5	Sequence 5, Appli	c 793	10	66.7	961	10	US-09-974-300-2788	Sequence 2788, Ap
c 721	10	66.7	723	10	US-09-791-540-5	Sequence 5, Appli	c 794	10	66.7	961	10	US-09-974-300-4233	Sequence 4233, Ap
c 722	10	66.7	724	10	US-09-070-927A-931	Sequence 931, App	c 795	10	66.7	964	10	US-09-974-300-1894	Sequence 1894, Ap
c 723	10	66.7	726	10	US-09-143-127-3	Sequence 3, Appli	c 796	10	66.7	968	10	US-09-864-761-1572	Sequence 1572, Ap
c 724	10	66.7	726	10	US-09-143-127-4	Sequence 4, Appli	c 797	10	66.7	968	10	US-09-864-761-2761	Sequence 2761, Ap
c 725	10	66.7	726	10	US-09-815-242-6075	Sequence 6075, Ap	c 798	10	66.7	969	10	US-09-886-055-254	Sequence 254, App
c 726	10	66.7	747	10	US-09-791-578-1	Sequence 1, Appli	c 799	10	66.7	978	9	US-09-938-842A-1549	Sequence 1549, Ap
c 727	10	66.7	749	10	US-09-791-540-1	Sequence 1, Appli	c 800	10	66.7	980	10	US-09-752-514-2	Sequence 2, Appli
c 728	10	66.7	753	10	US-09-887-576-822	Sequence 822, App	c 801	10	66.7	984	10	US-09-770-445-266	Sequence 266, App
c 729	10	66.7	756	10	US-09-915-580-806	Sequence 806, App	c 802	10	66.7	987	10	US-09-738-396-41	Sequence 41, Appl
c 730	10	66.7	758	9	US-09-956-086-1	Sequence 1, Appli	c 803	10	66.7	987	10	US-09-974-300-1183	Sequence 1183, Ap
c 731	10	66.7	758	9	US-09-956-087-1	Sequence 1, Appli	c 804	10	66.7	990	10	US-09-919-344-25	Sequence 25, Appl
c 732	10	66.7	762	9	US-09-826-025-21	Sequence 21, Appl	c 805	10	66.7	993	10	US-09-974-300-4796	Sequence 4796, Ap
c 733	10	66.7	763	10	US-09-919-580-862	Sequence 862, App	c 806	10	66.7	995	12	US-10-021-509-4	Sequence 4, Appli
c 734	10	66.7	763	10	US-09-764-877-3667	Sequence 3667, Ap	c 807	10	66.7	995	12	US-10-021-509-12	Sequence 12, Appl
c 735	10	66.7	772	10	US-09-764-870-95	Sequence 95, Appl	c 808	10	66.7	1011	10	US-09-742-732-3	Sequence 3, Appli
c 736	10	66.7	772	10	US-09-764-887-60	Sequence 60, Appl	c 809	10	66.7	1017	10	US-09-961-527A-14	Sequence 14, Appl
c 737	10	66.7	782	9	US-10-024-579-13	Sequence 13, Appl	c 810	10	66.7	1030	9	US-09-925-301-334	Sequence 334, App
c 738	10	66.7	782	9	US-09-985-442-1	Sequence 1, Appli	c 811	10	66.7	1035	9	US-09-938-842A-5334	Sequence 5334, Ap
c 739	10	66.7	782	10	US-09-791-578-3	Sequence 3, Appli	c 812	10	66.7	1035	10	US-09-815-242-7269	Sequence 7269, Ap
c 740	10	66.7	782	10	US-09-791-540-3	Sequence 3, Appli	c 813	10	66.7	1048	10	US-09-815-242-7269	Sequence 7269, Ap
c 741	10	66.7	787	10	US-09-983-580-1	Sequence 1, Appli	c 814	10	66.7	1054	9	US-09-822-849A-117	Sequence 117, App
c 742	10	66.7	788	10	US-09-764-887-60	Sequence 60, Appl	c 815	10	66.7	1054	9	US-09-966-546-27	Sequence 27, Appl
c 743	10	66.7	792	10	US-09-974-300-5996	Sequence 5996, Ap	c 816	10	66.7	1077	9	US-09-966-545-27	Sequence 27, Appl
c 744	10	66.7	795	12	US-09-974-300-2830	Sequence 2830, Ap	c 817	10	66.7	1077	9	US-09-815-242-7426	Sequence 7426, Ap
c 745	10	66.7	799	10	US-10-024-579-11	Sequence 11, Appl	c 818	10	66.7	1077	10	US-09-938-842A-700	Sequence 700, App
c 746	10	66.7	800	10	US-09-864-761-19477	Sequence 19477, A	c 819	10	66.7	1077	10	US-09-841-132-283	Sequence 283, App
c 747	10	66.7	800	10	US-09-791-171-51	Sequence 51, Appl	c 820	10	66.7	1088	10	US-09-974-300-3031	Sequence 3031, Ap
c 748	10	66.7	810	10	US-09-974-300-1331	Sequence 1331, Ap	c 821	10	66.7	1088	10	US-09-828-313-15	Sequence 15, Appl
c 749	10	66.7	812	10	US-09-759-143-471	Sequence 471, App	c 822	10	66.7	1093	10	US-09-969-708-214	Sequence 214, App
c 749	10	66.7	812	10	US-09-780-669-471	Sequence 471, App	c 822	10	66.7	1093	10	US-09-880-107-2302	Sequence 2302, Ap

c 823	10	66.7	1099	9	US-09-966-546-25	Sequence 25, Appl	c 896	10	66.7	1366	10	US-09-917-800A-1527	Sequence 1527, Ap
c 824	10	66.7	1099	9	US-09-966-545-25	Sequence 25, Appl	c 897	10	66.7	1368	10	US-09-815-242-9922	Sequence 9922, Ap
c 825	10	66.7	1111	10	US-09-833-381-1175	Sequence 1175, Ap	c 898	10	66.7	1369	10	US-09-822-830A-589	Sequence 589, App
c 826	10	66.7	1122	10	US-09-887-576-802	Sequence 802, App	c 899	10	66.7	1372	10	US-09-765-111A-13	Sequence 13, Appl
c 827	10	66.7	1128	10	US-09-815-242-5968	Sequence 5968, Ap	c 900	10	66.7	1376	10	US-09-756-283A-19	Sequence 19, Appl
c 828	10	66.7	1131	10	US-09-815-242-9836	Sequence 9836, Ap	c 901	10	66.7	1379	10	US-09-873-880-27	Sequence 27, Appl
c 829	10	66.7	1131	10	US-09-934-778-1	Sequence 1, Appl	c 902	10	66.7	1380	9	US-09-981-353-137	Sequence 137, App
c 830	10	66.7	1137	10	US-09-815-242-9304	Sequence 9304, Ap	c 903	10	66.7	1383	10	US-09-974-300-916	Sequence 916, App
c 831	10	66.7	1142	9	US-09-935-390A-11	Sequence 11, Appl	c 904	10	66.7	1395	10	US-09-815-242-7769	Sequence 7769, Ap
c 832	10	66.7	1146	9	US-09-924-400-9	Sequence 9, Appl	c 905	10	66.7	1395	10	US-09-924-703-5	Sequence 5, Appl
c 833	10	66.7	1146	10	US-09-810-936-9	Sequence 9, Appl	c 906	10	66.7	1398	9	US-09-981-353-134	Sequence 134, App
c 834	10	66.7	1146	10	US-09-429-755-9	Sequence 9, Appl	c 907	10	66.7	1398	10	US-09-815-242-7777	Sequence 7777, Ap
c 835	10	66.7	1152	10	US-09-745-763-149	Sequence 149, App	c 908	10	66.7	1414	9	US-09-996-634-127	Sequence 127, App
c 836	10	66.7	1172	9	US-09-895-913A-55	Sequence 55, Appl	c 909	10	66.7	1418	9	US-09-862-802-7	Sequence 7, Appl
c 837	10	66.7	1173	10	US-09-815-242-7383	Sequence 7383, Ap	c 910	10	66.7	1420	10	US-09-872-153-9	Sequence 9, Appl
c 838	10	66.7	1175	10	US-09-851-194-3	Sequence 3, Appl	c 911	10	66.7	1422	10	US-09-962-055-13	Sequence 13, Appl
c 839	10	66.7	1188	10	US-09-815-242-7518	Sequence 7518, Ap	c 912	10	66.7	1422	12	US-10-023-529-13	Sequence 13, Appl
c 840	10	66.7	1191	10	US-09-822-830A-414	Sequence 414, App	c 913	10	66.7	1422	12	US-10-023-523-13	Sequence 13, Appl
c 841	10	66.7	1192	10	US-09-961-527A-18	Sequence 18, Appl	c 914	10	66.7	1426	12	US-10-002-600-49	Sequence 49, Appl
c 842	10	66.7	1194	10	US-09-778-927A-22	Sequence 22, Appl	c 915	10	66.7	1427	12	US-10-044-090-278	Sequence 278, App
c 843	10	66.7	1197	10	US-09-729-835-26	Sequence 26, Appl	c 916	10	66.7	1430	10	US-09-864-864-250	Sequence 250, App
c 844	10	66.7	1200	10	US-09-815-242-4132	Sequence 4132, Ap	c 917	10	66.7	1430	10	US-09-864-864-328	Sequence 328, App
c 845	10	66.7	1204	10	US-09-924-256A-87	Sequence 87, Appl	c 918	10	66.7	1449	10	US-09-974-300-6077	Sequence 6077, Ap
c 846	10	66.7	1209	10	US-09-143-127-9	Sequence 9, Appl	c 919	10	66.7	1452	10	US-09-790-264-41	Sequence 41, Appl
c 847	10	66.7	1217	10	US-09-925-301-137	Sequence 9, Appl	c 920	10	66.7	1461	9	US-09-712-363-79	Sequence 79, Appl
c 848	10	66.7	1219	12	US-10-044-090-236	Sequence 127, App	c 921	10	66.7	1474	10	US-09-840-795-7	Sequence 7, Appl
c 849	10	66.7	1221	10	US-09-974-300-2319	Sequence 2319, Ap	c 922	10	66.7	1476	10	US-09-815-242-7177	Sequence 7177, Ap
c 850	10	66.7	1224	10	US-09-974-300-8308	Sequence 8308, Ap	c 923	10	66.7	1479	10	US-09-741-669-213	Sequence 213, App
c 851	10	66.7	1231	10	US-09-974-300-909	Sequence 909, App	c 924	10	66.7	1479	10	US-09-974-300-1149	Sequence 1149, Ap
c 852	10	66.7	1236	10	US-09-764-877-2565	Sequence 2565, Ap	c 925	10	66.7	1482	10	US-09-974-300-2645	Sequence 2645, Ap
c 853	10	66.7	1244	10	US-09-764-864-101	Sequence 101, App	c 926	10	66.7	1482	10	US-09-547-267-6	Sequence 6, Appl
c 854	10	66.7	1245	10	US-09-765-205-17	Sequence 17, Appl	c 927	10	66.7	1485	9	US-09-712-363-76	Sequence 76, Appl
c 855	10	66.7	1246	10	US-09-974-300-38	Sequence 38, Appl	c 928	10	66.7	1494	10	US-09-974-300-663	Sequence 663, App
c 856	10	66.7	1250	10	US-09-925-301-538	Sequence 538, App	c 929	10	66.7	1497	9	US-09-870-759-79	Sequence 79, Appl
c 857	10	66.7	1250	10	US-09-764-864-551	Sequence 551, App	c 930	10	66.7	1498	9	US-09-981-353-99	Sequence 99, Appl
c 858	10	66.7	1251	10	US-09-801-368-79	Sequence 79, Appl	c 931	10	66.7	1498	10	US-09-919-172-100	Sequence 100, App
c 859	10	66.7	1257	9	US-09-971-536-29	Sequence 29, Appl	c 932	10	66.7	1502	12	US-10-024-579-17	Sequence 17, Appl
c 860	10	66.7	1257	10	US-09-815-242-7780	Sequence 7780, Ap	c 933	10	66.7	1502	12	US-09-895-652-14	Sequence 14, Appl
c 861	10	66.7	1257	10	US-09-974-300-1172	Sequence 1172, Ap	c 934	10	66.7	1555	10	US-09-964-824A-241	Sequence 241, App
c 862	10	66.7	1266	9	US-09-938-842A-1752	Sequence 1752, Ap	c 935	10	66.7	1555	10	US-09-815-242-7449	Sequence 7449, Ap
c 863	10	66.7	1269	10	US-09-815-242-4153	Sequence 4153, Ap	c 936	10	66.7	1560	10	US-10-112-645-1	Sequence 1, Appl
c 864	10	66.7	1270	12	US-10-052-545-1	Sequence 1, Appl	c 937	10	66.7	1564	10	US-09-823-356-33	Sequence 33, Appl
c 865	10	66.7	1274	10	US-09-887-054-1	Sequence 1, Appl	c 938	10	66.7	1573	10	US-09-917-800A-1540	Sequence 1540, Ap
c 866	10	66.7	1278	10	US-09-815-242-7186	Sequence 7186, Ap	c 939	10	66.7	1575	10	US-09-841-132-188	Sequence 188, App
c 867	10	66.7	1278	10	US-09-943-671-18	Sequence 18, Appl	c 940	10	66.7	1578	10	US-09-880-107-3440	Sequence 3440, Ap
c 868	10	66.7	1278	12	US-10-044-090-177	Sequence 177, Appl	c 941	10	66.7	1578	10	US-09-956-004-67	Sequence 67, Appl
c 869	10	66.7	1281	12	US-10-027-559-11	Sequence 11, Appl	c 942	10	66.7	1580	10	US-09-815-242-9901	Sequence 9901, Ap
c 870	10	66.7	1289	9	US-09-764-868-416	Sequence 416, App	c 943	10	66.7	1596	10	US-09-815-242-9901	Sequence 286, App
c 871	10	66.7	1290	9	US-09-938-842A-2090	Sequence 2090, Ap	c 944	10	66.7	1601	10	US-09-938-842A-2304	Sequence 2304, Ap
c 872	10	66.7	1290	12	US-10-052-545-1	Sequence 3, Appl	c 945	10	66.7	1602	9	US-09-938-842A-2304	Sequence 55, Appl
c 873	10	66.7	1290	12	US-10-105-150-3	Sequence 3, Appl	c 946	10	66.7	1606	10	US-09-815-242-7760	Sequence 7760, Ap
c 874	10	66.7	1294	10	US-09-748-033-2	Sequence 2, Appl	c 947	10	66.7	1611	10	US-09-815-242-7831	Sequence 7831, Ap
c 875	10	66.7	1295	10	US-09-867-550-1319	Sequence 1319, Ap	c 948	10	66.7	1611	10	US-09-962-055-11	Sequence 11, Appl
c 876	10	66.7	1299	10	US-09-815-242-9140	Sequence 9140, Ap	c 949	10	66.7	1617	12	US-10-023-529-11	Sequence 11, Appl
c 877	10	66.7	1302	10	US-09-887-576-783	Sequence 783, App	c 950	10	66.7	1617	12	US-10-023-523-11	Sequence 11, Appl
c 878	10	66.7	1306	10	US-09-974-300-6231	Sequence 6231, Ap	c 951	10	66.7	1636	10	US-09-925-301-104	Sequence 104, App
c 879	10	66.7	1320	9	US-09-874-503-5	Sequence 5, Appl	c 952	10	66.7	1637	10	US-09-827-937A-3	Sequence 3, Appl
c 880	10	66.7	1320	10	US-09-727-238-1	Sequence 1, Appl	c 953	10	66.7	1650	10	US-09-974-300-42	Sequence 42, Appl
c 881	10	66.7	1320	12	US-10-006-867-155	Sequence 155, App	c 954	10	66.7	1650	10	US-09-974-300-42	Sequence 13, Appl
c 882	10	66.7	1322	10	US-09-864-761-16987	Sequence 16987, A	c 955	10	66.7	1660	10	US-09-143-127-13	Sequence 13, Appl
c 883	10	66.7	1332	10	US-09-954-456-1141	Sequence 1141, Ap	c 956	10	66.7	1665	10	US-09-771-161A-56	Sequence 56, Appl
c 884	10	66.7	1333	10	US-09-829-482-1	Sequence 1, Appl	c 957	10	66.7	1668	10	US-09-993-811-13	Sequence 13, Appl
c 885	10	66.7	1340	10	US-09-809-545A-1	Sequence 1, Appl	c 958	10	66.7	1675	10	US-09-938-641-1	Sequence 1, Appl
c 886	10	66.7	1344	10	US-09-741-669-212	Sequence 212, App	c 959	10	66.7	1680	9	US-09-364-847-20	Sequence 20, Appl
c 887	10	66.7	1350	10	US-09-790-264-35	Sequence 35, Appl	c 959	10	66.7	1680	10	US-09-820-721A-2	Sequence 2, Appl
c 888	10	66.7	1350	10	US-09-793-693-12	Sequence 12, Appl	c 960	10	66.7	1686	10	US-09-925-301-157	Sequence 157, App
c 889	10	66.7	1350	10	US-09-801-368-129	Sequence 129, App	c 961	10	66.7	1686	10	US-09-815-242-6114	Sequence 6114, Ap
c 890	10	66.7	1352	10	US-09-756-283A-21	Sequence 21, Appl	c 962	10	66.7	1697	10	US-09-862-027-7	Sequence 7, Appl
c 891	10	66.7	1353	10	US-09-741-669-192	Sequence 192, App	c 963	10	66.7	1704	10	US-09-866-562-51	Sequence 51, Appl
c 892	10	66.7	1356	10	US-09-815-242-6624	Sequence 6624, Ap	c 964	10	66.7	1709	10	US-09-864-864-285	Sequence 285, App
c 893	10	66.7	1362	10	US-09-962-055-12	Sequence 12, Appl	c 965	10	66.7	1711	9	US-10-093-619-1	Sequence 1, Appl
c 894	10	66.7	1362	12	US-10-023-529-12	Sequence 12, Appl	c 966	10	66.7	1711	10	US-09-935-390A-17	Sequence 17, Appl
c 895	10	66.7	1362	12	US-10-023-523-12	Sequence 12, Appl	c 967	10	66.7	1716	10	US-09-801-852A-1	Sequence 1, Appl
c 896	10	66.7	1362	12	US-10-023-523-12	Sequence 12, Appl	c 968	10	66.7	1716	10	US-09-919-781-3	Sequence 3, Appl

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c 969      10 66.7 1739 10 US-09-864-711-4
c 970      10 66.7 1755 10 US-09-954-456-1166
c 971      10 66.7 1756 9  US-09-895-913A-267
c 972      10 66.7 1758 10 US-09-815-242-7656
c 973      10 66.7 1767 10 US-09-801-368-45
c 974      10 66.7 1773 9  US-09-894-844-1
c 975      10 66.7 1794 10 US-09-943-671-36
c 976      10 66.7 1812 10 US-09-815-242-4147
c 977      10 66.7 1818 10 US-09-758-269-15
c 978      10 66.7 1831 10 US-09-853-386-75
c 979      10 66.7 1838 10 US-09-764-887-620
c 980      10 66.7 1869 10 US-09-864-761-3765
c 981      10 66.7 1889 10 US-09-779-307-10
c 982      10 66.7 1890 10 US-09-791-171-71
c 983      10 66.7 1890 10 US-09-880-107-3390
c 984      10 66.7 1891 10 US-09-779-307-9
c 985      10 66.7 1902 10 US-09-815-242-7979
c 986      10 66.7 1902 10 US-09-779-307-1
c 987      10 66.7 1904 10 US-09-840-787-95
c 988      10 66.7 1911 10 US-09-815-242-7963
c 989      10 66.7 1917 10 US-09-919-781-1
c 990      10 66.7 1918 9  US-09-860-670-77
c 991      10 66.7 1926 10 US-09-764-853-238
c 992      10 66.7 1945 10 US-09-925-301-588
c 993      10 66.7 1949 10 US-09-740-027-1
c 994      10 66.7 1961 10 US-09-864-761-9239
c 995      10 66.7 1967 10 US-09-880-107-2417
c 996      10 66.7 1969 9  US-09-981-876-107
c 997      10 66.7 1977 10 US-09-954-456-804
c 998      10 66.7 1977 10 US-09-880-107-3407
c 999      10 66.7 1977 10 US-09-967-768A-190
1000      10 66.7 1984 10 US-09-887-576-38
```

ALIGNMENTS

```
RESULT 1
US-09-944-807-9
; Sequence 9, Application US/09944807
; Patent No. US2002011949A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim Pharma KG
; TITLE OF INVENTION: Method for identifying substances which positively
; TITLE OF INVENTION: influence inflammatory conditions of chronic
; TITLE OF INVENTION: inflammatory airway diseases
; FILE REFERENCE: 082.00n
; CURRENT APPLICATION NUMBER: US/09/944,807
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: UK 0021484.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 3992
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-944-807-9

Query Match      86.7%; Score 13; DB 10; Length 3992;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCTCTCGCCCTG 13
Db      764 CCTCTCGCCCTG 776

RESULT 2
US-09-764-878-258/c
; Sequence 258, Application US/09764878
; Patent No. US20020090615A1
; GENERAL INFORMATION:
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```
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA121
; CURRENT APPLICATION NUMBER: US/09/764,878
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 258
; LENGTH: 4558
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-878-258

Query Match      86.7%; Score 13; DB 10; Length 4558;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CTCTCGCCCTGT 14
Db      3383 CTCTCGCCCTGT 3371

RESULT 3
US-09-764-860-937/c
; Sequence 937, Application US/09764860
; Patent No. US20020094953A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC008
; CURRENT APPLICATION NUMBER: US/09/764,860
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1198
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 937
; LENGTH: 4558
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-860-937

Query Match      86.7%; Score 13; DB 10; Length 4558;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CTCTCGCCCTGT 14
Db      3383 CTCTCGCCCTGT 3371

RESULT 4
US-09-430-029-1/c
; Sequence 1, Application US/09430029
; Patent No. US20020168738A1
; GENERAL INFORMATION:
; APPLICANT: Yano, Tetsuya; No. US20020168738A1ot, tsuyoshi; Imamura, Takeshi; Canc
; TITLE OF INVENTION: DNA Fragment Carrying Toluene Monooxygenase Gene,
; TITLE OF INVENTION: Recombinant Plasmid, Transformed Microorganism,
; TITLE OF INVENTION: Method for Degrading Chlorinated Aliphatic Hydrocarbon
; TITLE OF INVENTION: Compounds and Aromatic Compounds, and
; TITLE OF INVENTION: Method for Environmental Remediation
; FILE REFERENCE: CPO13982US
; CURRENT APPLICATION NUMBER: US/09/430,029
; CURRENT FILING DATE: 1999-10-29
; EARLIER APPLICATION NUMBER: JP P1998-310801
; EARLIER FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 5828
; TYPE: DNA
; ORGANISM: Burkholderia cepacia
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FEATURE:  
NAME/KEY: CDS  
LOCATION: (234)..(443)  
OTHER INFORMATION: tomk  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (463)..(1455)  
OTHER INFORMATION: tomL  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1495)..(1761)  
OTHER INFORMATION: tomM  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1803)..(3350)  
OTHER INFORMATION: tomN  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (3428)..(3781)  
OTHER INFORMATION: tomO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (3810)..(4871)  
OTHER INFORMATION: tomP  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (4876)..(5229)  
OTHER INFORMATION: tomQ  
US-09-430-029-1

Query Match 86.7%; Score 13; DB 9; Length 5828;  
Best Local Similarity 100.0%; Pred. No. 9.9;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTG 13  
|||||  
Db 2013 CCTTCTCGCCCTG 2001

RESULT 5  
US-09-761-534A-17  
; Sequence 17, Application US/09761534A  
; Patent No. US20020146426A1  
; GENERAL INFORMATION:  
; APPLICANT: Huang, Qian  
; APPLICANT: Richmond, Joan F.L.  
; APPLICANT: Cho, Bryan K.  
; APPLICANT: Palliser, Deborah  
; APPLICANT: Chen, Jianzhu  
; APPLICANT: Eisen, Herman N.  
; APPLICANT: Young, Richard A.  
; TITLE OF INVENTION: In Vivo CTL Elicitation By Heat Shock  
; TITLE OF INVENTION: Protein Fusion Proteins Maps To A Discrete Domain and is  
; FILE REFERENCE: CD4+T Cell-Independent  
; CURRENT APPLICATION NUMBER: US/09/761,534A  
; CURRENT FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: PCT/US00/32831  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: US 60/176,143  
; PRIOR FILING DATE: 2000-01-14  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 49  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: PCR Primer OQH011  
US-09-761-534A-17

Query Match 80.0%; Score 12; DB 10; Length 49;  
Best Local Similarity 100.0%; Pred. No. 47;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CCTTCTCGCCCT 12  
|||||  
Db 31 CCTTCTCGCCCT 42  
RESULT 6  
US-09-864-761-17150  
; Sequence 17150, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL  
; FILE REFERENCE: Aecmica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/006666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/006667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/006664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/006669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/006665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/006668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/006663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/006662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/006661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/006670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 17150  
; LENGTH: 152  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AF000341.1  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.8  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5  
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.4  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.1  
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.8

; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2  
; OTHER INFORMATION: NT HIT: AL163303.2, EVALUE 1.00e-80  
; OTHER INFORMATION: SWISSPROT HIT: O60241, EVALUE 4.00e+00  
US-09-864-761-17150

Query Match 80.0%; Score 12; DB 10; Length 152;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTCTCGCCCTG 13  
|||||  
Db 56 CTCTCGCCCTG 67

RESULT 7  
US-09-974-300-7193/c  
; Sequence 7193, Application US/09974300  
; Patent No. US20020146721A1  
; GENERAL INFORMATION:  
; APPLICANT: Berka, Randy M.  
; APPLICANT: Clausen, Ib Groth  
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene  
; TITLE OF INVENTION: Expression  
; FILE REFERENCE: 10085.500-US  
; CURRENT APPLICATION NUMBER: US/09/974,300  
; CURRENT FILING DATE: 2001-10-05  
; PRIOR APPLICATION NUMBER: 09/680,598  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/279,526  
; PRIOR FILING DATE: 2001-03-27  
; NUMBER OF SEQ ID NOS: 8481  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7193  
; LENGTH: 173  
; TYPE: DNA  
; ORGANISM: Bacillus clausii  
US-09-974-300-7193

Query Match 80.0%; Score 12; DB 10; Length 173;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTCTCGCCCTG 13  
|||||  
Db 99 CTCTCGCCCTG 88

RESULT 8  
US-09-923-876-97/c  
; Sequence 97, Application US/09923876  
; Patent No. US2002013958A1  
; GENERAL INFORMATION:  
; APPLICANT: Lalgudi, Raghunath V.  
; APPLICANT: Kamigaki, Laura Y. (Ito)  
; APPLICANT: Sherman, Bradley K.  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING  
; FILE REFERENCE: PL-0012-1 CON  
; CURRENT APPLICATION NUMBER: US/09/923,876  
; CURRENT FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: 09/298,329  
; PRIOR FILING DATE: 1999-04-21  
; PRIOR APPLICATION NUMBER: 60/085,331  
; PRIOR FILING DATE: 1998-05-05  
; NUMBER OF SEQ ID NOS: 6332  
; SOFTWARE: PERL Program  
; SEQ ID NO 97  
; LENGTH: 235  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: misc-feature  
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700142552H1

US-09-923-876-97

Query Match 80.0%; Score 12; DB 10; Length 235;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTCTCGCCCTG 13  
|||||  
Db 50 CTCTCGCCCTG 39

RESULT 9  
US-09-983-965-5128/c  
; Sequence 5128, Application US/09983965  
; Patent No. US20020137160A1  
; GENERAL INFORMATION:  
; APPLICANT: Warren, Wesley C.  
; APPLICANT: Tao, Nengbing  
; APPLICANT: Byatt, John C.  
; APPLICANT: Mathialagan, Nagappan  
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND  
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION  
; FILE REFERENCE: 37-21(10297)C  
; CURRENT APPLICATION NUMBER: US/09/983,965  
; CURRENT FILING DATE: 2001-10-26  
; PRIOR APPLICATION NUMBER: US 09/465,231  
; PRIOR FILING DATE: 1999-12-15  
; PRIOR APPLICATION NUMBER: US 60/113,678  
; PRIOR FILING DATE: 1998-12-17  
; NUMBER OF SEQ ID NOS: 5912  
; SEQ ID NO 5128  
; LENGTH: 356  
; TYPE: DNA  
; ORGANISM: Bos taurus  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 33-LIB34-055-Q1-E1-A2  
US-09-983-965-5128

Query Match 80.0%; Score 12; DB 10; Length 356;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTCTCGCCCTG 13  
|||||  
Db 216 CTCTCGCCCTG 205

RESULT 10  
US-09-867-701-5624  
; Sequence 5624, Application US/09867701  
; Patent No. US2002013237A1  
; GENERAL INFORMATION:  
; APPLICANT: Aglate, Paul A.  
; APPLICANT: Jones, Robert  
; APPLICANT: Harlocker, Susan L.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.497  
; CURRENT APPLICATION NUMBER: US/09/867,701  
; CURRENT FILING DATE: 2001-05-29  
; NUMBER OF SEQ ID NOS: 10912  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5624  
; LENGTH: 380  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-867-701-5624

Query Match 80.0%; Score 12; DB 10; Length 380;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCTCGCCCTGTT 15

Db 19 TCTCGCCCTGTT 30  
|||||

## RESULT 11

US-09-864-761-3392/c  
; Sequence 3392, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aeonica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 3392  
; LENGTH: 396  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AL109748.2  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.4  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3  
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.4  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.2  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.7  
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.5  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.9  
US-09-864-761-3392

Query Match 80.0%; Score 12; DB 10; Length 396;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTTCTCGCCCTG 13  
|||||  
Db 283 CTTCTCGCCCTG 272

## RESULT 12

US-09-954-531-880/c  
; Sequence 880, Application US/09954531  
; Patent No. US20020165180A1  
; GENERAL INFORMATION:  
; APPLICANT: Weaver, Zoe  
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using  
; FILE REFERENCE: Gene Sets  
; FILE REFERENCE: 689290-77  
; CURRENT APPLICATION NUMBER: US/09/954,531  
; CURRENT FILING DATE: 2002-05-02  
; PRIOR APPLICATION NUMBER: US/60/233,133  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: US/60/234,009  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: US/60/234,034  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: US/60/234,509  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: US/60/234,567  
; PRIOR FILING DATE: 2000-09-22  
; NUMBER OF SEQ ID NOS: 1392  
; SOFTWARE: PatentIn version 3.0.  
; SEQ ID NO 880  
; LENGTH: 414  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-954-531-880

Query Match 80.0%; Score 12; DB 9; Length 414;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CTTCTCGCCCTG 13  
|||||  
Db 300 CTTCTCGCCCTG 289

## RESULT 13

US-09-864-761-337  
; Sequence 337, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL  
; FILE REFERENCE: Aeonica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666

;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00667  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00664  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00669  
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;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00662  
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;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00670  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: US 60/234,687  
;; PRIOR FILING DATE: 2000-09-21  
;; PRIOR APPLICATION NUMBER: US 09/608,408  
;; PRIOR FILING DATE: 2000-06-30  
;; PRIOR APPLICATION NUMBER: US 09/774,203  
;; PRIOR FILING DATE: 2001-01-29  
;; NUMBER OF SEQ ID NOS: 49117  
;; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
;; SEQ ID NO 337  
;; LENGTH: 445  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; OTHER INFORMATION: MAP TO AP000341.1  
;; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4  
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7  
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3  
;; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.8  
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5  
;; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.4  
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.1  
;; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.8  
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4  
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2  
US-09-864-761-337

Query Match 80.0%; Score 12; DB 10; Length 445;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 353 CTTCTCGCCCTG 364  
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RESULT 14  
US-09-784-423-17  
; Sequence 17, Application US/09784423  
; Patent No. US20020012924A1  
; GENERAL INFORMATION:  
; APPLICANT: Schumm, James W.  
; Bacher, Jeffery W.

; TITLE OF INVENTION: MATERIALS AND METHODS FOR  
IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM  
REPEAT DNA MARKERS

NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Promega Corporation  
STREET: 2800 Woods Hollow Road  
CITY: Madison  
STATE: Wisconsin  
COUNTRY: U.S.A.  
ZIP: 53711-5399  
COMPUTER READABLE FORM:

;; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb  
;; COMPUTER: IBM compatible PC  
;; OPERATING SYSTEM: Windows 95  
;; SOFTWARE: Word 97 (DOS text format)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/784,423  
;; FILING DATE: 15-Feb-2001  
;; CLASSIFICATION: <Unknown>  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 09/018,584  
;; FILING DATE: 04-Feb-1998  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Grady J. Frenchick  
;; REGISTRATION NUMBER: 29,018  
;; REFERENCE/DOCKET NUMBER: 16026.9180  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (608) 257-3501  
;; TELEFAX: (608) 257-2275  
;; INFORMATION FOR SEQ ID NO: 17  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 447 bp  
;; TYPE: Nucleic Acid  
;; STRANDEDNESS: Double  
;; TOPOLOGY: Circular  
;; MOLECULE TYPE: Genomic DNA  
;; HYPOTHETICAL: no  
;; IMMEDIATE SOURCE:  
;; LIBRARY: plasmid, pGem3Zf(+)  
;; CLONE: G158  
;; POSITION IN GENOME:  
;; CHROMOSOME/SEGMENT: 5q  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
US-09-784-423-17

Query Match 80.0%; Score 12; DB 10; Length 447;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 85 CCTTCTCGCCCT 96  
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RESULT 15

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; Sequence 813, Application US/09954531  
; Patent No. US20020165180A1  
; GENERAL INFORMATION:

; APPLICANT: Weaver, Zoe  
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C  
; FILE OF INVENTION: Gene Sets  
; FILE REFERENCE: 689290-77  
; CURRENT APPLICATION NUMBER: US/09/954,531  
; CURRENT FILING DATE: 2002-05-02  
; PRIOR APPLICATION NUMBER: US/60/233,133  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: US/60/234,009  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: US/60/234,034  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: US/60/234,509  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: US/60/234,567  
; PRIOR FILING DATE: 2000-09-22  
; NUMBER OF SEQ ID NOS: 1392  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 813  
; LENGTH: 461  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(461)



; OTHER INFORMATION: n=a,t,g or c  
US-09-954-531-813

Query Match 80.0%; Score 12; DB 9; Length 461;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGGCCT 12  
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Db 342 CCTTCTCGGCCT 331

Search completed: December 11, 2002, 20:32:12  
Job time : 72.5 secs

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model  
Run on: December 11, 2002, 16:56:23 ; Search time 1655.5 Seconds  
(without alignments)  
146.743 Million cell updates/sec

Title: US-09-750-609-9  
Perfect score: 15  
Sequence: 1 cttctgcgcctgtt 15

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues  
Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

EST:\*

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- 2: em\_esthum:\*
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- 4: em\_estmu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_htc:\*
- 9: gb\_esti:\*
- 10: gb\_est2:\*
- 11: gb\_htc:\*
- 12: gb\_est3:\*
- 13: gb\_est4:\*
- 14: gb\_est5:\*
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- 16: em\_estom:\*
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- 21: em\_gss\_vrt:\*
- 22: em\_gss\_fun:\*
- 23: em\_gss\_mam:\*
- 24: em\_gss\_mus:\*
- 25: em\_gss\_other:\*
- 26: em\_gss\_pro:\*
- 27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 4	15	100.0	513	17	BH019101
C 5	15	100.0	543	10	AV434035
C 6	15	100.0	551	13	BM142008

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C 81	14	93.3	561	13	BI483276	BI483276	RE56147.5	C 154	13	86.7	293	10	BB091489	BB091489	BB091489
C 82	14	93.3	564	13	BI371565	BI371565	RE58483.5	C 155	13	86.7	296	12	BF665526	BF665526	BF665526
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C 86	14	93.3	593	13	BI964495	BI964495	ID38909.Y	C 159	13	86.7	319	10	BB464836	BB464836	BB464836
C 87	14	93.3	598	12	BF492172	BF492172	AT29061.5	C 160	13	86.7	322	9	AV149524	AV149524	AV149524
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C 89	14	93.3	620	10	AV752075	AV752075	AV752075	C 162	13	86.7	339	17	AQ570264	AQ570264	AQ570264
C 90	14	93.3	624	17	B02517	B02517	CSRL-155A7-	C 163	13	86.7	344	9	AL132817	AL132817	AL132817
C 91	14	93.3	633	12	BB619005	BB619005	BB619005	C 164	13	86.7	348	9	AU041899	AU041899	AU041899
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C 93	14	93.3	641	13	BI612566	BI612566	RH41483.5	C 166	13	86.7	351	13	BM089644	BM089644	BM089644
C 94	14	93.3	650	17	AQ952273	AQ952273	Sheared.D	C 167	13	86.7	357	17	AZ708915	AZ708915	AZ708915
C 95	14	93.3	675	12	BG821198	BG821198	GO2724668	C 168	13	86.7	358	9	AA523160	AA523160	AA523160
C 96	14	93.3	678	12	BG600136	BG600136	ESF505031	C 169	13	86.7	361	9	AA131959	AA131959	AA131959
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C 98	14	93.3	765	12	BG696837	BG696837	GO2659892	C 171	13	86.7	364	12	BG072218	BG072218	BG072218
C 99	14	93.3	765	13	BI655867	BI655867	GO3284885	C 172	13	86.7	365	10	AW910077	AW910077	AW910077
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C 101	14	93.3	789	12	BG474591	BG474591	GO2517381	C 174	13	86.7	367	13	BM639696	BM639696	BM639696
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C 105	14	93.3	820	9	AA736192	AA736192	HL08145.5	C 178	13	86.7	374	17	AQ772705	AQ772705	AQ772705
C 106	14	93.3	821	17	CNS01ZBM	AL174091	Tetraodon	C 179	13	86.7	378	10	AW711363	AW711363	AW711363
C 107	14	93.3	831	17	CNS01YK1	AL173098	Tetraodon	C 180	13	86.7	379	10	AW98307	AW98307	AW98307
C 108	14	93.3	839	12	BG780574	BG780574	SEADMC000	C 181	13	86.7	380	14	H00632	H00632	H00632
C 109	14	93.3	875	12	BF978039	BF978039	GO3147938	C 182	13	86.7	381	13	BJ191222	BJ191222	BJ191222
C 110	14	93.3	877	12	BF141948	BF141948	GO1790438	C 183	13	86.7	383	12	BG085052	BG085052	BG085052
C 111	14	93.3	879	17	CNS03M2K	AL251417	Tetraodon	C 184	13	86.7	384	10	AW670067	AW670067	AW670067
C 112	14	93.3	894	12	BF182664	BF182664	GO1809444	C 185	13	86.7	387	10	AW287074	AW287074	AW287074
C 113	14	93.3	895	12	BG864418	BG864418	GO2798623	C 186	13	86.7	387	14	T56696	T56696	T56696
C 114	14	93.3	913	12	BG425118	BG425118	GO2446607	C 187	13	86.7	387	13	BM291738	BM291738	BM291738
C 115	14	93.3	936	12	BF699731	BF699731	GO2127158	C 188	13	86.7	392	9	AA636988	AA636988	AA636988
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C 120	14	93.3	1039	17	CNS03F6G	AL241297	Tetraodon	C 193	13	86.7	399	10	AW479086	AW479086	AW479086
C 121	14	93.3	1065	14	BM06011	BM06011	AGENCOURT	C 194	13	86.7	400	10	BE036904	BE036904	BE036904
C 122	14	93.3	1075	12	BG026887	BG026887	GO2294186	C 195	13	86.7	403	10	AW240878	AW240878	AW240878
C 123	14	93.3	1300	17	AG064777	AG064777	Pan trogl	C 196	13	86.7	403	13	BI517072	BI517072	BI517072
C 124	14	93.3	1553	12	BF164622	BF164622	GO1772403	C 197	13	86.7	404	9	AJ312766	AJ312766	AJ312766
C 125	14	93.3	1686	12	BG256672	BG256672	GO2370859	C 198	13	86.7	404	13	BI900964	BI900964	BI900964
C 126	14	93.3	3776	11	BC021653	BC021653	Mus muscu	C 199	13	86.7	404	14	BQ910504	BQ910504	BQ910504
C 127	13	86.7	106	10	AW818491	AW818491	RC1-ST027	C 200	13	86.7	405	9	AA664487	AA664487	AA664487
C 128	13	86.7	166	12	BF431844	BF431844	nab51b09.	C 201	13	86.7	413	12	BF386784	BF386784	BF386784
C 129	13	86.7	178	10	BB201173	BB201173	BB201173	C 202	13	86.7	415	9	AI135691	AI135691	AI135691
C 130	13	86.7	182	9	AV122504	AV122504	AV122504	C 203	13	86.7	416	10	AV646225	AV646225	AV646225
C 131	13	86.7	192	9	AV287339	AV287339	AV287339	C 204	13	86.7	420	10	AW784309	AW784309	AW784309
C 132	13	86.7	193	14	BQ041219	BQ041219	9D35C04.Y	C 205	13	86.7	420	14	T71501	T71501	T71501
C 133	13	86.7	196	9	AA254435	AA254435	val6603.r	C 206	13	86.7	422	9	AI018097	AI018097	AI018097
C 134	13	86.7	199	13	BI187373	BI187373	a2912fs.r	C 207	13	86.7	423	9	AA290403	AA290403	AA290403
C 135	13	86.7	201	10	BB425208	BB425208	BB425208	C 208	13	86.7	426	12	BG050015	BG050015	BG050015
C 136	13	86.7	215	13	BJ194203	BJ194203	BJ194203	C 209	13	86.7	427	13	BM536448	BM536448	BM536448
C 137	13	86.7	216	10	BB583079	BB583079	BB583079	C 210	13	86.7	428	10	BE593521	BE593521	BE593521
C 138	13	86.7	216	13	BI97929	BI97929	BI97929	C 211	13	86.7	428	12	BF737928	BF737928	BF737928
C 139	13	86.7	220	17	BB583033	BB583033	BOHMH11TR	C 212	13	86.7	430	17	BH225420	BH225420	BH225420
C 140	13	86.7	227	10	BB451401	BB451401	BB451401	C 213	13	86.7	431	13	BI215727	BI215727	BI215727
C 141	13	86.7	227	10	BB469156	BB469156	BB469156	C 214	13	86.7	431	10	BE109473	BE109473	BE109473
C 142	13	86.7	228	10	BB394206	BB394206	BB394206	C 215	13	86.7	436	13	BI615436	BI615436	BI615436
C 143	13	86.7	233	10	BB578929	BB578929	BB578929	C 216	13	86.7	436	10	AV934403	AV934403	AV934403
C 144	13	86.7	269	10	BB298225	BB298225	BB298225	C 217	13	86.7	437	10	BF046660	BF046660	BF046660
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C 148	13	86.7	274	10	BB414286	BB414286	BB414286	C 221	13	86.7	445	14	N6866975	N6866975	N6866975
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C 150	13	86.7	277	10	BB164207	BB164207	BB164207	C 223	13	86.7	445	14	R75714	R75714	R75714
C 151	13	86.7	283	10	BB694772	BB694772	BB694772	C 224	13	86.7	447	10	AV940105	AV940105	AV940105
C 152	13	86.7	287	10	BB159014	BB159014	BB159014	C 225	13	86.7	452	9	AA696511	AA696511	AA696511

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c 231	13	86.7	456	9	AA710755	AA710755 vt44a10.r	304	13	86.7	521	9	AU030909	AU030909 AU030909
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233	13	86.7	457	13	BJ200466	BJ200466 BJ200466	306	13	86.7	521	13	BI365549	BI365549 RE50905.5
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237	13	86.7	464	13	BI619411	BI619411 RH50443.5	310	13	86.7	525	17	AQ466318	AQ466318 HS.5130.A
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c 247	13	86.7	477	17	AQ811825	AQ811825 HS.5528.B	320	13	86.7	533	13	BI577793	BI577793 RE71538.5
248	13	86.7	478	9	AI106622	AI106622 GH06680.5	321	13	86.7	536	14	BQ798685	BQ798685 EST.854.G
249	13	86.7	480	13	BI623787	BI623787 RH56130.5	322	13	86.7	537	13	BI610256	BI610256 RH15345.5
c 250	13	86.7	480	12	BF651974	BF651974 RH75400.MA	323	13	86.7	538	9	AI296743	AI296743 LP10808.5
c 251	13	86.7	481	10	AV783662	AV783662 AV783662	324	13	86.7	538	13	BI614737	BI614737 RH44194.5
252	13	86.7	481	12	BF489488	BF489488 AT25444.5	325	13	86.7	539	13	BI241339	BI241339 RE38377.5
253	13	86.7	482	9	AU239566	AU239566 AU239566	326	13	86.7	539	13	BI579102	BI579102 RE73078.5
254	13	86.7	482	13	BM279151	BM279151 ND.ad1.03	327	13	86.7	540	13	BI169418	BI169418 RE10586.5
255	13	86.7	484	9	AI110083	AI110083 GH09542.5	328	13	86.7	540	13	BI171609	BI171609 RE13422.5
256	13	86.7	484	13	BI581272	BI581272 RH18642.5	329	13	86.7	540	13	BI236916	BI236916 RE33046.5
257	13	86.7	485	9	AI047269	AI047269 uh63e04.r	330	13	86.7	540	13	BI630205	BI630205 RH50194.5
258	13	86.7	485	9	AI134755	AI134755 GH12301.5	331	13	86.7	540	13	BI191484	BI191484 BJ191484
c 259	13	86.7	485	10	BE147095	BE147095 PM0-HT02	332	13	86.7	541	13	BI161509	BI161509 RE01015.5
260	13	86.7	485	13	BI610405	BI610405 RH15868.5	333	13	86.7	541	13	BI216627	BI216627 RE23829.5
261	13	86.7	486	13	BI623054	BI623054 RH55122.5	334	13	86.7	541	13	BI370587	BI370587 RE57271.5
262	13	86.7	487	13	BI626701	BI626701 RH67720.5	335	13	86.7	541	13	BI609439	BI609439 RH14223.5
263	13	86.7	487	13	BJ484529	BJ484529 BJ484529	c 336	13	86.7	542	12	BF041710	BF041710 BP250024B
264	13	86.7	488	13	BI365627	BI365627 RE50990.5	337	13	86.7	542	13	BI566640	BI566640 RH36343.5
265	13	86.7	488	13	BI201503	BI201503 BJ201503	338	13	86.7	542	13	BI607400	BI607400 RH74463.5
c 266	13	86.7	489	9	AI518882	AI518882 LD35707.5	339	13	86.7	542	13	BI617234	BI617234 RH47505.5
c 267	13	86.7	490	9	AJ447458	AJ447458 AJ447458	340	13	86.7	543	9	AT002733	AT002733 AT002733
268	13	86.7	490	13	BM309327	BM309327 sak57c11.	341	13	86.7	543	13	BI629035	BI629035 RH57830.5
269	13	86.7	495	13	BI165053	BI165053 RE04858.5	342	13	86.7	543	13	BI634996	BI634996 RH39989.5
c 270	13	86.7	495	13	BI173536	BI173536 RE16472.5	343	13	86.7	544	13	BI231198	BI231198 RE20428.5
271	13	86.7	495	13	BI374597	BI374597 RE52232.5	344	13	86.7	544	13	BI231291	BI231291 RE20739.5
c 272	13	86.7	496	10	AV602894	AV602894 AV602894	345	13	86.7	544	13	BI371124	BI371124 RE57949.5
c 273	13	86.7	497	13	BI128944	BI128944 G083P83Y	346	13	86.7	544	13	BI613562	BI613562 RH42739.5
274	13	86.7	498	13	BI213621	BI213621 RE19058.5	347	13	86.7	546	9	AI517081	AI517081 GH27714.5
275	13	86.7	499	9	AA940917	AA940917 LD23250.5	348	13	86.7	546	10	AV945840	AV945840 AV945840
276	13	86.7	501	9	AI542802	AI542802 SD09267.5	349	13	86.7	546	13	BI581633	BI581633 RH19160.5
277	13	86.7	502	9	AA698182	AA698182 HL03902.5	350	13	86.7	547	13	BI243132	BI243132 RE40689.5
c 278	13	86.7	502	12	BG659553	BG659553 ygeSTzy4	351	13	86.7	547	13	BI608146	BI608146 RH12321.5
c 279	13	86.7	503	9	AU081722	AU081722 AU081722	352	13	86.7	547	13	BJ206395	BJ206395 BJ206395
280	13	86.7	504	10	AW287123	AW287123 LG1.265	353	13	86.7	547	17	AZ015890	AZ015890 RPCT-23-3
281	13	86.7	505	14	BQ799248	BQ799248 EST.147	354	13	86.7	548	9	AI517287	AI517287 GH27981.5
c 282	13	86.7	506	12	BF490629	BF490629 AT27162.5	355	13	86.7	548	13	BJ482922	BJ482922 BJ482922
c 283	13	86.7	507	10	AA264300	AA264300 LD07994.5	356	13	86.7	548	13	BJ483825	BJ483825 BJ483825
c 284	13	86.7	511	9	AA288248	AA288248 vb32h12.r	357	13	86.7	548	13	BJ486538	BJ486538 BJ486538
285	13	86.7	511	13	BI214056	BI214056 RE19755.5	358	13	86.7	549	9	AI256946	AI256946 LP04028.5
c 286	13	86.7	511	13	BM115115	BM115115 LO815G11	c 359	13	86.7	549	13	BI355859	BI355859 GM32619.5
287	13	86.7	512	13	BI235492	BI235492 RE31342.5	c 360	13	86.7	549	13	BM328657	BM328657 PIC1.24.H
288	13	86.7	513	9	AI534378	AI534378 SD07181.5	361	13	86.7	550	14	BQ041241	BQ041241 qd35e07.y
c 289	13	86.7	513	10	AV601487	AV601487 AV601487	362	13	86.7	551	12	BF491989	BF491989 AT28848.5
290	13	86.7	513	13	BI366667	BI366667 RE52254.5	363	13	86.7	551	13	BI624809	BI624809 RH64508.5
291	13	86.7	513	13	BI618056	BI618056 RH48577.5	c 364	13	86.7	552	10	BE518496	BE518496 EST00072
292	13	86.7	514	9	AI135681	AI135681 GH13519.5	365	13	86.7	552	13	BI366118	BI366118 RE51573.5
293	13	86.7	514	13	BI486624	BI486624 RE70074.5	366	13	86.7	553	9	AI258807	AI258807 LP02090.5
294	13	86.7	514	13	BI615513	BI615513 RH45180.5	367	13	86.7	553	12	BG906909	BG906909 TALr1155B
c 295	13	86.7	514	14	BQ038360	BQ038360 p9nic.pk0	368	13	86.7	553	13	BI622940	BI622940 RH34983.5
296	13	86.7	518	9	AI388875	AI388875 GH19918.5	369	13	86.7	554	13	BM495747	BM495747 IPCGB3-2
297	13	86.7	518	13	BI587001	BI587001 RH27249.5	c 370	13	86.7	555	9	AI770230	AI770230 SAL2.C10
298	13	86.7	518	13	BI620636	BI620636 RH51825.5	371	13	86.7	556	13	BI339487	BI339487 364471.MA

[illegible]

518	13	86.7	563	9	AA567886	AA567886	HL01944.5	591	13	86.7	806	12	BG843178	BG843178	1024001G0
519	13	86.7	563	17	AG158219	AG158219	Pan trogl	592	13	86.7	806	12	BG923173	BG923173	602824014
520	13	86.7	564	13	BI577896	BI577896	RE71660.5	593	13	86.7	807	13	BF233687	BF233687	602024723
c 521	13	86.7	564	13	BM328060	BM328060	PICL-20.F	c 594	13	86.7	809	12	BE889765	BE889765	601512005
c 522	13	86.7	565	13	BI356971	BI356971	RE43289.5	c 595	13	86.7	811	14	BQ443985	BQ443985	UI-M-EWO-
c 523	13	86.7	568	12	BF504646	BF504646	AT06245.5	c 596	13	86.7	811	12	BF382784	BF382784	601816561
524	13	86.7	568	14	BQ412744	BQ412744	GA_E0006	597	13	86.7	824	13	BI683605	BI683605	603306326
525	13	86.7	569	9	AI238336	AI238336	GH14363.5	c 598	13	86.7	824	13	BI161136	BI161136	602865179
526	13	86.7	569	10	BB641769	BB641769	BB641769	c 599	13	86.7	828	12	BF302804	BF302804	602032685
527	13	86.7	569	13	BI369054	BI369054	RE55136.5	c 600	13	86.7	846	17	BE525267	BE525267	BOHOE04TR
528	13	86.7	569	13	BJ523319	BJ523319	BJ523319	c 601	13	86.7	851	10	BE546565	BE546565	601076577
529	13	86.7	569	10	AV646123	AV646123	AV646123	c 602	13	86.7	856	12	BG497157	BG497157	602537658
530	13	86.7	570	13	BI237634	BI237634	RE33888.5	603	13	86.7	859	13	BI248784	BI248784	602992758
c 531	13	86.7	572	12	BF008340	BF008340	I606544.A	c 604	13	86.7	860	17	CNS012BN	CNS012BN	Tetraodon
c 532	13	86.7	574	13	BI586463	BI586463	RH26415.5	c 605	13	86.7	866	12	BF303388	BF303388	602030114
533	13	86.7	576	12	BF499121	BF499121	AV13616.5	c 606	13	86.7	871	17	AZ127971	AZ127971	OSJNB0006
534	13	86.7	576	17	AZ574428	AZ574428	328PVF01	c 607	13	86.7	876	13	BI101360	BI101360	602887114
c 535	13	86.7	577	13	BJ482072	BJ482072	BJ482072	c 608	13	86.7	879	12	BF974098	BF974098	602243701
c 536	13	86.7	577	13	BM654425	BM654425	170006873	c 609	13	86.7	890	12	BF241496	BF241496	601876555
537	13	86.7	578	9	AI134184	AI134184	GH11565.5	c 610	13	86.7	890	17	CNS04AUK	CNS04AUK	601876555
538	13	86.7	578	17	AZ574323	AZ574323	327PVDO3	c 611	13	86.7	891	12	BF673085	BF673085	602152993
539	13	86.7	580	13	BI214309	BI214309	RE20078.5	c 612	13	86.7	895	12	BG251001	BG251001	602363862
c 540	13	86.7	582	12	BG633804	BG633804	AT29733.5	c 613	13	86.7	905	13	BI460555	BI460555	603201178
541	13	86.7	583	14	BQ990424	BQ990424	QGF20C06.	614	13	86.7	910	12	BF141152	BF141152	601789149
542	13	86.7	584	9	AI405800	AI405800	GH25932.5	c 615	13	86.7	911	12	BE959822	BE959822	601654738
c 543	13	86.7	585	13	BI557061	BI557061	603238633	c 616	13	86.7	916	17	AQ743736	AQ743736	HS_5501.A
c 544	13	86.7	586	17	AZ566829	AZ566829	227PVA08	617	13	86.7	919	9	AL548995	AL548995	AL548995
c 545	13	86.7	587	13	BM591656	BM591656	170006873	c 618	13	86.7	920	13	BI948315	BI948315	HVSME1000
546	13	86.7	587	13	BM591656	BM591656	170006873	c 619	13	86.7	923	12	BF974200	BF974200	602243830
c 547	13	86.7	592	10	BJ523320	BJ523320	BU523320	c 620	13	86.7	928	10	AW661684	AW661684	ESTPMC16
c 548	13	86.7	594	12	BE988154	BE988154	601440284	c 621	13	86.7	936	12	BF790002	BF790002	602249973
c 549	13	86.7	595	14	BQ907162	BQ907162	N004C07.O	622	13	86.7	939	12	BF971128	BF971128	602270706
550	13	86.7	598	12	BG074658	BG074658	H3137G04.	623	13	86.7	944	10	BE039851	BE039851	OC09A11.O
551	13	86.7	700	12	BG635476	BG635476	SD12889.5	624	13	86.7	945	17	AG145841	AG145841	Pan trogl
552	13	86.7	700	14	BU007527	BU007527	QGH3509.Y	c 625	13	86.7	946	10	BE213911	BE213911	HV_Ceb000
c 553	13	86.7	701	9	AI405028	AI405028	GH24935.5	c 626	13	86.7	954	17	CNS05LRN	CNS05LRN	Tetraodon
554	13	86.7	701	17	AG080306	AG080306	Pan trogl	c 627	13	86.7	959	12	BF797734	BF797734	602257679
555	13	86.7	705	9	AU119272	AU119272	AU119272	c 628	13	86.7	970	12	BG105691	BG105691	602312290
556	13	86.7	705	14	BQ241102	BQ241102	TaeO5009B	c 629	13	86.7	974	17	CNS02BMG	CNS02BMG	Tetraodon
c 557	13	86.7	708	10	BE455119	BE455119	HVSMEH009	c 630	13	86.7	975	14	BQ890286	BQ890286	AGENCOURT
c 558	13	86.7	708	13	BM627874	BM627874	170006874	c 631	13	86.7	979	14	BQ679820	BQ679820	AGENCOURT
559	13	86.7	710	12	BG844543	BG844543	1024006H0	c 632	13	86.7	985	14	BQ226384	BQ226384	AGENCOURT
c 560	13	86.7	711	12	BF505970	BF505970	AT0R8311.5	c 633	13	86.7	991	12	BF164265	BF164265	601773022
c 561	13	86.7	711	14	BQ780720	BQ780720	UI-R-FFO-	c 634	13	86.7	991	13	BM063000	BM063000	603614980
562	13	86.7	712	9	AI517055	AI517055	GH27682.5	c 635	13	86.7	994	12	BF125562	BF125562	601763316
563	13	86.7	712	13	BI231265	BI231265	RE20711.5	c 636	13	86.7	994	17	CNS02KPI	CNS02KPI	Tetraodon
c 564	13	86.7	714	13	BM620991	BM620991	170006874	c 637	13	86.7	1001	12	BF032661	BF032661	601453191
c 565	13	86.7	716	14	BQ869659	BQ869659	QGD6N05.Y	c 638	13	86.7	1003	12	BF237568	BF237568	601842082
566	13	86.7	721	13	BI544387	BI544387	603241788	c 639	13	86.7	1003	14	BQ884024	BQ884024	AGENCOURT
567	13	86.7	721	14	BU007443	BU007443	QGH2912.Y	c 640	13	86.7	1010	10	BE620575	BE620575	601483079
568	13	86.7	724	9	AI534898	AI534898	SD01167.5	c 641	13	86.7	1012	12	BG614407	BG614407	602642535
c 569	13	86.7	728	17	BH838311	BH838311	LMCR10001	c 642	13	86.7	1016	14	BQ707142	BQ707142	AGENCOURT
c 570	13	86.7	729	12	BF863315	BF863315	963042G03	c 643	13	86.7	1028	14	BM904873	BM904873	AGENCOURT
571	13	86.7	732	13	BM200229	BM200229	C0207E11-	c 644	13	86.7	1034	12	BF531935	BF531935	602072878
c 572	13	86.7	738	17	AQ751483	AQ751483	HS_5576.B	c 645	13	86.7	1042	14	BQ963025	BQ963025	AGENCOURT
573	13	86.7	744	10	AV712791	AV712791	AV712791	c 646	13	86.7	1058	12	BG026430	BG026430	602291812
c 574	13	86.7	745	17	BH386968	BH386968	AG-ND-102	647	13	86.7	1062	17	CNS04NNC	CNS04NNC	Tetraodon
575	13	86.7	750	9	AI406247	AI406247	GH26477.5	c 648	13	86.7	1070	12	BF120134	BF120134	601756436
576	13	86.7	756	9	AA697370	AA697370	HL02339.5	c 649	13	86.7	1086	12	BF300932	BF300932	602028939
c 577	13	86.7	758	13	BI080925	BI080925	602878836	c 650	13	86.7	1087	12	BG249508	BG249508	602319571
c 578	13	86.7	769	12	BG854557	BG854557	1024040C0	c 651	13	86.7	1088	13	BM562441	BM562441	AGENCOURT
c 579	13	86.7	769	12	BF127518	BF127518	601810149	c 652	13	86.7	1090	13	BI655365	BI655365	603285006
c 580	13	86.7	770	9	AJ444359	AJ444359	AJ444359	c 653	13	86.7	1091	17	CNS00EAC	CNS00EAC	Drosophil
581	13	86.7	771	9	AA698039	AA698039	HL03667.5	c 654	13	86.7	1101	17	CNS00E79	CNS00E79	AL069032
582	13	86.7	772	13	BI217290	BI217290	602933372	c 655	13	86.7	1109	12	BF244595	BF244595	601862612
c 583	13	86.7	778	14	BQ042264	BQ042264	UI-M-EQO-	c 656	13	86.7	1115	17	AG082764	AG082764	Pan trogl
584	13	86.7	783	12	BG810248	BG810248	mgc0003x1	c 657	13	86.7	1122	14	BQ717951	BQ717951	AGENCOURT
c 585	13	86.7	785	17	AQ361717	AQ361717	mgxb0004D	c 658	13	86.7	1128	12	BG776928	BG776928	602664121
586	13	86.7	787	17	BI9062	BI9062	T5L21-Sp6.T	c 659	13	86.7	1129	13	BM467209	BM467209	AGENCOURT
587	13	86.7	795	13	BI520313	BI520313	603071178	c 660	13	86.7	1132	12	BG257183	BG257183	602370785
c 588	13	86.7	798	12	BF569236	BF569236	602185601	c 661	13	86.7	1134	10	BE572592	BE572592	601329548
589	13	86.7	803	10	BE397525	BE397525	601290163	c 662	13	86.7	1137	12	BG473760	BG473760	602515752
590	13	86.7	805	17	AQ364242	AQ364242	nbxb0060P	c 663	13	86.7	1158	12	BF688714	BF688714	602185366

c 664	13	86.7	1163	12	BG258338	BG258338	602379785	c 737	12	80.0	172	17	AZ101784	AZ101784	RP01-23-2
c 665	13	86.7	1167	12	BG536614	BG536614	602566244	738	12	80.0	173	17	AZ504600	AZ504600	IM0344B05
c 666	13	86.7	1183	13	BI410243	BI410243	602963694	739	12	80.0	175	9	AA257919	AA257919	EST 376 B
c 667	13	86.7	1210	13	BI256946	BI256946	602975555	c 740	12	80.0	179	13	BI239287	BI239287	RE35740.5
c 668	13	86.7	1211	12	BG479463	BG479463	602525957	741	12	80.0	180	9	A1538252	A1538252	tp55b05.x
c 669	13	86.7	1212	12	BG033864	BG033864	602301148	c 742	12	80.0	180	9	AU110801	AU110801	AU110801
c 670	13	86.7	1236	17	AG080176	AG080176	Pan trogl	743	12	80.0	182	13	BG953195	BG953195	CM4-CT063
c 671	13	86.7	1272	13	BI161234	BI161234	602865696	744	12	80.0	185	9	AA719003	AA719003	zh22h11.s
c 672	13	86.7	1363	13	BM542097	BM542097	AGENCOURT	745	12	80.0	188	10	BE003350	BE003350	QV4-BN009
c 673	13	86.7	1367	14	BO886911	BO886911	AGENCOURT	746	12	80.0	188	13	BJ163151	BJ163151	BU163151
c 674	13	86.7	1367	14	BO886911	BO886911	AGENCOURT	747	12	80.0	189	12	BF497730	BF497730	AU11996.5
c 675	13	86.7	1384	12	BF300658	BF300658	602031833	748	12	80.0	191	9	AA113295	AA113295	zm28d05.s
c 676	13	86.7	1411	12	BE962808	BE962808	601656518	749	12	80.0	196	9	A1186279	A1186279	qd28c04.x
c 677	13	86.7	1443	12	BG433848	BG433848	602497372	c 750	12	80.0	197	9	AA381873	AA381873	ES711197
c 678	13	86.7	1463	12	BG866747	BG866747	602786566	c 751	12	80.0	197	10	BE660913	BE660913	6-A7 Gmax
c 679	13	86.7	1493	12	BG298764	BG298764	603385589	c 752	12	80.0	198	9	AA112518	AA112518	zm28d05.r
c 680	13	86.7	1507	14	BQ068097	BQ068097	AGENCOURT	c 753	12	80.0	200	14	C74297	C74297	C74297 Rice
c 681	13	86.7	1534	14	BM904434	BM904434	AGENCOURT	c 754	12	80.0	200	17	AO629360	AO629360	RP01-11-4
c 682	13	86.7	1581	12	BG118402	BG118402	602348017	755	12	80.0	202	17	BF718618	BF718618	KEST89 no
c 683	13	86.7	1612	12	BF690854	BF690854	602246853	756	12	80.0	202	17	AO091456	AO091456	HS-3016_B
c 684	13	86.7	1642	12	BF570926	BF570926	602076123	757	12	80.0	203	12	BF718270	BF718270	EST40 mic
c 685	13	86.7	1698	12	BG822684	BG822684	602725814	c 758	12	80.0	203	12	BF930644	BF930644	IL5-NT022
c 686	13	86.7	1701	13	BM452308	BM452308	AGENCOURT	759	12	80.0	206	10	AW139000	AW139000	UT-H-B11
c 687	13	86.7	1717	12	BG284363	BG284363	602408469	760	12	80.0	206	10	BF806393	BF806393	RC2-CI008
c 688	13	86.7	3015	11	AK014519	AK014519	Mus muscu	761	12	80.0	206	10	BB419535	BB419535	BB419535
c 689	13	86.7	5054	11	AK004773	AK004773	Mus muscu	762	12	80.0	207	10	BB596021	BB596021	BB596021
c 690	12	80.0	52	12	BG694448	BG694448	NISC_lv02	c 763	12	80.0	209	10	BB298438	BB298438	BB298438
c 691	12	80.0	53	17	BH633045	BH633045	1007058F1	764	12	80.0	210	9	AV080134	AV080134	AV080134
c 692	12	80.0	55	9	AA970079	AA970079	op65c11.s	765	12	80.0	214	14	T18393	T18393	AF092807
c 693	12	80.0	63	13	BI820770	BI820770	603034371	766	12	80.0	216	9	AI318940	AI318940	a5a09nm.f
c 694	12	80.0	68	17	AZ577398	AZ577398	09409 Sho	c 772	12	80.0	216	10	BB287391	BB287391	BB287391
c 695	12	80.0	72	13	BI488965	BI488965	603021690	773	12	80.0	216	12	BE697675	BE697675	RC0-CT047
c 696	12	80.0	83	9	AA708193	AA708193	zg04g01.s	c 774	12	80.0	217	9	AI701380	AI701380	wb91f11.x
c 697	12	80.0	85	12	BF024197	BF024197	Pvp 545 L	775	12	80.0	217	10	BB414692	BB414692	BB414692
c 698	12	80.0	88	9	AA9889206	AA9889206	or9bh02.s	776	12	80.0	217	17	BH228878	BH228878	1006149B0
c 699	12	80.0	91	9	AI018792	AI018792	ot9f9f08.s	c 777	12	80.0	219	14	F02757	F02757	HSC19E072 n
c 700	12	80.0	91	9	AI185398	AI185398	qe52e06.x	778	12	80.0	221	10	AW327140	AW327140	20733 MAR
c 701	12	80.0	93	10	AW722741	AW722741	c6c03nm.f	c 779	12	80.0	221	10	AW718324	AW718324	14g10nm.f
c 702	12	80.0	99	17	AZ477457	AZ477457	LM0296019	779	12	80.0	221	14	F02836	F02836	HSC19G052 n
c 703	12	80.0	109	12	BF900273	BF900273	PM2-MT020	c 780	12	80.0	223	10	BB589564	BB589564	BB589564
c 704	12	80.0	110	13	BI756148	BI756148	603030051	c 781	12	80.0	225	10	BB587480	BB587480	BB587480
c 705	12	80.0	116	12	BG085551	BG085551	H3114F06-	c 782	12	80.0	226	9	AI669515	AI669515	w88f11.x
c 706	12	80.0	116	12	BF349563	BF349563	UI-R-CA0-	c 783	12	80.0	226	10	BB009372	BB009372	BB009372
c 707	12	80.0	117	12	BF145536	BF145536	WHE1841-1	c 784	12	80.0	226	12	BG044841	BG044841	saa33b10.
c 708	12	80.0	120	13	BI818802	BI818802	603037654	c 785	12	80.0	226	17	AO527440	AO527440	RP01-11-3
c 709	12	80.0	121	10	AW303248	AW303248	xr90e02.x	c 786	12	80.0	227	12	BF760815	BF760815	RC4-CT062
c 710	12	80.0	123	17	B82206	B82206	RPC111-13C4	c 787	12	80.0	229	12	BF811752	BF811752	QV1-CI017
c 711	12	80.0	126	17	AZ100181	AZ100181	RP01-23-4	c 788	12	80.0	230	9	AA982299	AA982299	ua53a06.x
c 712	12	80.0	128	17	AZ500419	AZ500419	LM0338H16	c 789	12	80.0	230	12	BF379273	BF379273	RC6-UT001
c 713	12	80.0	130	17	AZ451984	AZ451984	LM0251A11	c 790	12	80.0	232	10	AV346323	AV346323	RC6-UT001
c 714	12	80.0	135	10	AW327142	AW327142	20739 MAR	c 791	12	80.0	232	12	BG044841	BG044841	saa33b10.
c 715	12	80.0	137	10	AW832984	AW832984	RC3-TT000	c 792	12	80.0	233	12	BE938080	BE938080	MRI-TN004
c 716	12	80.0	139	17	BH629679	BH629679	1007075B0	c 793	12	80.0	233	17	BH222866	BH222866	1006109F0
c 717	12	80.0	140	9	AA471103	AA471103	PMY2037 K	c 794	12	80.0	234	12	BF918950	BF918950	QV0-NT014
c 718	12	80.0	141	13	BI724512	BI724512	1031072D0	c 795	12	80.0	234	17	BH403207	BH403207	AG-ND-126
c 719	12	80.0	142	9	AA441863	AA441863	zw62d04.r	c 796	12	80.0	235	14	T166233	T166233	NIB1570 Nor
c 720	12	80.0	146	17	BH230907	BH230907	1006160A0	c 797	12	80.0	237	9	AI799967	AI799967	wc46e05.x
c 721	12	80.0	146	14	BQ097199	BQ097199	IFHdk0098	c 798	12	80.0	237	10	AV322152	AV322152	AV322152
c 722	12	80.0	146	17	AO897850	AO897850	HS_3144_A	c 799	12	80.0	238	10	BB426394	BB426394	BB426394
c 723	12	80.0	147	13	BM200713	BM200713	C0215B01-	c 800	12	80.0	239	9	AT006295	AT006295	AT006295
c 724	12	80.0	148	9	AA774504	AA774504	zg76c06.s	c 801	12	80.0	239	12	BF870843	BF870843	CM3-ET009
c 725	12	80.0	148	17	B41513	B41513	HS-1053-B2-	c 802	12	80.0	240	14	BI014554	BI014554	CM3-ET009
c 726	12	80.0	155	9	AV173703	AV173703	AV173703	c 803	12	80.0	241	9	AI048764	AI048764	CM3-ET009
c 727	12	80.0	155	14	BG659681	BG659681	TGESTeva4	c 804	12	80.0	241	10	AW482781	AW482781	47074 MAR
c 728	12	80.0	155	14	F03378	F03378	HSC1VC072 n	c 805	12	80.0	242	9	AV223269	AV223269	AV223269
c 729	12	80.0	156	12	BG016125	BG016125	SrlHW24-8	c 806	12	80.0	242	13	BI014001	BI014001	PM1-ET020
c 730	12	80.0	158	9	AL363444	AL363444	AL363444	c 807	12	80.0	242	17	AZ756867	AZ756867	ew02f10.x
c 731	12	80.0	162	12	BF552165	BF552165	UI-R-C2p-	c 808	12	80.0	243	9	AI707571	AI707571	as30H02.x
c 732	12	80.0	163	14	D29185	D29185	HUMNK222 Hu	c 809	12	80.0	243	14	BQ342615	BQ342615	RC4-NN108
c 733	12	80.0	166	10	BB512941	BB512941	BB512941								
c 734	12	80.0	166	14	BM857729	BM857729	i167e09.y								
c 735	12	80.0	167	17	AO643429	AO643429	RFC193-DP								
c 736	12	80.0	168	10	AV389853	AV389853	AV389853								



c 810	12	80.0	244	9	AI524790	AI524790	ti77e01.x	c 883	12	80.0	278	9	AA352372	AA352372	EST60380
c 811	12	80.0	245	12	BE827268	BE827268	QV1-ET000	c 884	12	80.0	278	10	AA355231	AA355231	pnf-b.pk0
c 812	12	80.0	246	10	AW545321	AW545321	Q1-ET007-	c 885	12	80.0	278	10	BE528288	BE528288	M79011STM
c 813	12	80.0	247	9	AV233291	AV233291	AV233291	c 886	12	80.0	280	10	BE562662	BE562662	BS562662
c 814	12	80.0	247	10	AV374705	AV374705	AV374705	c 887	12	80.0	280	14	F29584	F29584	HSPD19526 H
c 815	12	80.0	248	9	AI327998	AI327998	Ogallal.f	c 888	12	80.0	282	9	AI724190	AI724190	RHI21-B.C
c 816	12	80.0	248	14	H26197	H26197	y15a05.r1	c 889	12	80.0	282	10	BB580920	BB580920	BS580920
c 817	12	80.0	249	9	AI213865	AI213865	z6e0a1.f	c 890	12	80.0	282	17	AZ755592	AZ755592	ev01g10.x
c 818	12	80.0	249	9	AV026183	AV026183	AV026183	c 891	12	80.0	282	17	AZ755698	AZ755698	ev05b05.r
c 819	12	80.0	249	10	AW671423	AW671423	LGL1344.F	c 892	12	80.0	282	17	AQ365061	AQ365061	nrbx00620
c 820	12	80.0	249	14	F02756	F02756	HSC19E062.n	c 893	12	80.0	283	9	AI969833	AI969833	wq75e05.x
c 821	12	80.0	250	10	AW074892	AW074892	xa62e06.x	c 894	12	80.0	283	9	AA285163	AA285163	zs48e07.s
c 822	12	80.0	250	14	W40764	W40764	mc38c11.r1	c 895	12	80.0	283	9	AA555778	AA555778	vk50d04.r
c 823	12	80.0	251	9	AI307017	AI307017	qw76b12.x	c 896	12	80.0	283	12	BF837262	BF837262	RC4-HT004
c 824	12	80.0	251	10	AW072899	AW072899	xa60h08.x	c 897	12	80.0	283	14	BM821892	BM821892	K4-EST0091
c 825	12	80.0	252	14	N61346	N61346	TgESTy31c0	c 898	12	80.0	284	9	AI945100	AI945100	bs03a01.y
c 826	12	80.0	253	10	BE662087	BE662087	bs20e09.y	c 899	12	80.0	284	14	C01170	C01170	HUMG5000785
c 827	12	80.0	254	10	AW074765	AW074765	xa70a07.x	c 900	12	80.0	285	9	AA775410	AA775410	ad13c01.s
c 828	12	80.0	254	10	BB599087	BB599087	BB599087	c 901	12	80.0	285	13	BM481391	BM481391	533476 MA
c 829	12	80.0	254	14	BQ372396	BQ372396	QVO-FN018	c 902	12	80.0	286	10	BB585849	BB585849	BS585849
c 830	12	80.0	255	9	AI349796	AI349796	ta96g05.x	c 903	12	80.0	287	9	AI698396	AI698396	tx64e03.x
c 831	12	80.0	255	10	AV525807	AV525807	AV525807	c 904	12	80.0	287	10	AW229783	AW229783	uo42h09.y
c 832	12	80.0	255	10	AW718495	AW718495	15f08nm.f	c 905	12	80.0	287	10	BB381078	BB381078	BB381078
c 833	12	80.0	255	10	BE526865	BE526865	M67C05STM	c 906	12	80.0	287	13	BI848981	BI848981	471596 MA
c 834	12	80.0	255	17	AQ275511	AQ275511	RPCI-4-59	c 907	12	80.0	288	9	AI790097	AI790097	ue64e01.r
c 835	12	80.0	256	10	AW187336	AW187336	17b07nm.f	c 908	12	80.0	289	9	AA726913	AA726913	vu37b08.r
c 836	12	80.0	256	10	AW18737	AW18737	17b07nm.f	c 909	12	80.0	289	9	AI453226	AI453226	tj21g03.x
c 837	12	80.0	256	12	BF942278	BF942278	nae90e11.	c 910	12	80.0	289	10	BB500838	BB500838	BB500838
c 838	12	80.0	258	9	AI224664	AI224664	qw97h09.x	c 911	12	80.0	289	13	BJ163858	BJ163858	BJ163858
c 839	12	80.0	258	9	AI345069	AI345069	tb62b03.x	c 912	12	80.0	291	10	BB567423	BB567423	BB567423
c 840	12	80.0	258	9	AI345296	AI345296	tb68c10.x	c 913	12	80.0	292	9	AI370188	AI370188	qu44c09.x
c 841	12	80.0	258	9	AA455998	AA455998	aa02d12.s	c 914	12	80.0	292	9	AL041776	AL041776	DKF2p434A
c 842	12	80.0	258	10	AW722739	AW722739	c6c01nm.f	c 915	12	80.0	292	10	BB721709	BB721709	BB721709
c 843	12	80.0	258	10	BE043381	BE043381	hk37e06.y	c 916	12	80.0	293	10	AV998199	AV998199	AV998199
c 844	12	80.0	258	10	BE151300	BE151300	CM1-HT028	c 917	12	80.0	293	10	AW718686	AW718686	16q09nm.f
c 845	12	80.0	258	14	BE153590	BE153590	WHE3094.A	c 918	12	80.0	293	10	BB110385	BB110385	BB110385
c 846	12	80.0	259	9	AA307429	AA307429	o102e11.s	c 919	12	80.0	293	10	BB607761	BB607761	BB607761
c 847	12	80.0	259	10	BB523646	BB523646	BB523646	c 920	12	80.0	294	9	AA077197	AA077197	7B14G04.C
c 848	12	80.0	260	9	AI308902	AI308902	tb50401.x	c 921	12	80.0	295	10	BB599479	BB599479	BB599479
c 849	12	80.0	260	9	AI310785	AI310785	ta42h02.x	c 922	12	80.0	296	9	AI321829	AI321829	ef12nm.f
c 850	12	80.0	260	14	W17791	W17791	mb73d03.r1	c 923	12	80.0	296	10	AW051003	AW051003	wz06b10.x
c 851	12	80.0	261	13	BI035917	BI035917	IL5-NT022	c 924	12	80.0	297	10	AI209755	AI209755	c9b01a1.r
c 852	12	80.0	262	10	AW072708	AW072708	xa59b05.x	c 925	12	80.0	297	9	AI321753	AI321753	e2q08nm.f
c 853	12	80.0	262	17	BH696197	BH696197	BOMCH07TR	c 926	12	80.0	297	10	AW718367	AW718367	15a07nm.f
c 854	12	80.0	263	17	AZ701528	AZ701528	RPCI-23-2	c 927	12	80.0	297	10	AW859239	AW859239	MRI-CT035
c 855	12	80.0	264	13	BI430868	BI430868	94963E04	c 928	12	80.0	297	13	BI013706	BI013706	RC4-ET013
c 856	12	80.0	264	14	H95220	H95220	yw59e12.s1	c 929	12	80.0	297	14	C27000	C27000	C27000 Rice
c 857	12	80.0	264	14	N89576	N89576	zb08c04.s1	c 930	12	80.0	298	9	AA768025	AA768025	oa60e05.s
c 858	12	80.0	264	17	BH195904	BH195904	TC3-59F15	c 931	12	80.0	298	10	BE001826	BE001826	PM1-BN008
c 859	12	80.0	267	10	BB597613	BB597613	BB597613	c 932	12	80.0	298	13	BM448717	BM448717	DSA027C08
c 860	12	80.0	268	9	AA066316	AA066316	mm08g04.r	c 933	12	80.0	299	9	AA823015	AA823015	vw33f07.r
c 861	12	80.0	268	9	AI556001	AI556001	UI-R-C2p-	c 934	12	80.0	299	10	AV644619	AV644619	AV644619
c 862	12	80.0	269	10	BB598976	BB598976	BB598976	c 935	12	80.0	299	10	BB548971	BB548971	BB548971
c 863	12	80.0	269	17	AQ663198	AQ663198	HS_5463.B	c 936	12	80.0	299	14	H93816	H93816	yy06h10.r1
c 864	12	80.0	271	9	AI111563	AI111563	UI-R-C2-n	c 937	12	80.0	300	9	AJ466877	AJ466877	AJ466877
c 865	12	80.0	271	10	AW427877	AW427877	64454.MAR	c 938	12	80.0	300	10	AV628960	AV628960	AV628960
c 866	12	80.0	271	12	BE760110	BE760110	an_0212.A	c 939	12	80.0	300	10	AW859095	AW859095	MRI-CT035
c 867	12	80.0	271	14	L38101	L38101	BNAP0557E.M	c 940	12	80.0	300	12	BF728678	BF728678	1000065F0
c 868	12	80.0	272	9	AA934898	AA934898	op47e07.s	c 941	12	80.0	300	12	BE775574	BE775574	MY-04-A-1
c 869	12	80.0	273	9	AA786415	AA786415	15f07a1.f	c 942	12	80.0	301	9	AA928410	AA928410	on49f10.s
c 870	12	80.0	273	10	BB566740	BB566740	BB566740	c 943	12	80.0	301	9	AI453796	AI453796	tj29a11.x
c 871	12	80.0	274	12	BF764615	BF764615	CM3-CS004	c 944	12	80.0	301	10	BB044485	BB044485	BB044485
c 872	12	80.0	274	14	BQ693931	BQ693931	NXRV127_C	c 945	12	80.0	301	17	AQ115405	AQ115405	RPC111-56
c 873	12	80.0	275	14	BQ464819	BQ464819	HU01K18T	c 946	12	80.0	302	9	AI023671	AI023671	ow67h01.x
c 874	12	80.0	276	9	AI328103	AI328103	t2e10a1.f	c 947	12	80.0	303	9	AA010523	AA010523	z109h05.r
c 875	12	80.0	276	10	AV389613	AV389613	AV389613	c 948	12	80.0	304	9	AA414328	AA414328	vc60f07.s
c 876	12	80.0	276	12	BF478123	BF478123	7q21e07.x	c 949	12	80.0	304	13	BM425320	BM425320	IPSPn0158
c 877	12	80.0	276	12	BF357264	BF357264	CM2-HT093	c 950	12	80.0	304	14	D25082	D25082	RICR3129A.R
c 878	12	80.0	276	13	BI023427	BI023427	FW4-TM024	c 951	12	80.0	305	9	AA834380	AA834380	of67e08.s
c 879	12	80.0	276	14	BM770032	BM770032	K-EST0053	c 952	12	80.0	305	10	BB517965	BB517965	BB517965
c 880	12	80.0	276	17	TA65C12P	TA65C12P	T.brucel	c 953	12	80.0	305	10	BB601268	BB601268	BB601268
c 881	12	80.0	277	10	BB468508	BB468508	BB468508	c 954	12	80.0	305	10	AW974222	AW974222	EST386325
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c 956 12 80.0 306 13 B1530279 10241040H0
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c 991 12 80.0 318 10 BB600156 BB600156
c 992 12 80.0 318 14 D47132 D47132
c 993 12 80.0 318 14 F02835 F02835
c 994 12 80.0 320 10 BB143612 BB143612
c 995 12 80.0 321 9 AI652650 AI652650
c 996 12 80.0 321 14 C97210 C97210
c 997 12 80.0 322 14 H45960 H45960
c 998 12 80.0 323 14 D49193 D49193
c 999 12 80.0 324 9 AI932842 AI932842
c 1000 12 80.0 324 10 BE119265 BE119265

```

## ALIGNMENTS

```

RESULT 1
T48892/c 309 bp mRNA linear EST 06-FEB-1995
LOCUS yb07a09.r1 Stratagene placenta (#937225) Homo sapiens cDNA clone
DEFINITION IMAGE:70456 5' similar to similar to SP:S28778 S28778 COLLAGEN
ALPHA 1(XV) CHAIN - HUMAN, mRNA sequence.

```

```

T48892
T48892.1 GI:650752
EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 309)
AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins
, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore
, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,
Underwood, K., Wohlmann, P., Waterston, R., Wilson, R., and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478

```

## COMMENT

Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

High quality sequence stops: 239

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

Seq primer: M13RPI

High quality sequence stop: 239.

## FEATURES

## source

```

1..309
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="GB:491353"
/db_xref="taxon:9606"
/clone="IMAGE:70456"
/clone_lib="Stratagene placenta (#937225)"
/sex="male"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: placenta; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dr. Caucasian. Average insert size: 1.2 kb; Uni-ZAP
XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3'
adaptor sequence: 5' CTCGAGTTTTTTTTTTT 3'"
BASE COUNT 82 a 70 c 101 g 51 t
ORIGIN

```

```

Query Match 100.0%; Score 15; DB 14; Length 309;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
QY 1 CCTTCTCGCCCTGTT 15
|||||

```

```
Db 107 CCTTCTCGCCCTGTT 93
|||||

```

## RESULT 2

## BH019102

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## FEATURES

## source

```

1..313
Location/Qualifiers
/organism="Leishmania major"
/strain="Friedlin"
/db_xref="taxon:5664"
/clone="L2358k"
/clone_lib="Leishmania major Friedlin Cosmid Genomic
Library"
/lab_host="E. coli ED8767"

```

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 239

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

Seq primer: M13RPI

High quality sequence stop: 239.

Location/Qualifiers

1..309

/organism="Homo sapiens"

/db\_xref="GB:491353"

/db\_xref="taxon:9606"

/clone="IMAGE:70456"

/clone\_lib="Stratagene placenta (#937225)"

/sex="male"

/lab\_host="SOLR cells (kanamycin resistant)"

/note="Organ: placenta; Vector: pBluescript SK-; Site\_1:

EcoRI; Site\_2: XhoI; Cloned unidirectionally. Primer:

Oligo dr. Caucasian. Average insert size: 1.2 kb; Uni-ZAP

XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3'

adaptor sequence: 5' CTCGAGTTTTTTTTTTT 3'"

BASE COUNT 82 a 70 c 101 g 51 t

ORIGIN

Query Match 100.0%; Score 15; DB 14; Length 309;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15

|||||

Db 107 CCTTCTCGCCCTGTT 93

|||||

RESULT 2

BH019102

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..313

Location/Qualifiers

/organism="Leishmania major"

/strain="Friedlin"

/db\_xref="taxon:5664"

/clone="L2358k"

/clone\_lib="Leishmania major Friedlin Cosmid Genomic

Library"

/lab\_host="E. coli ED8767"

```

/note="Vector: cLHYG; Site_1: BamHI; Genomic DNA from
Leishmania major Friedlin was partially digested with
Sau3AI, size selected, and ligated with BamHI-digested
cLHYG cosmid vector DNA. 9216 clones were picked and
arrayed. Library construction is described in Ivens et
al., Genomics Research, 8:135-145 (1998). The cLHYG
vector (Acc. No. CVU59231) is described in Ryan et al.,
Gene, 131:145-150 (1993)"
BASE COUNT      90 a      86 c      67 t      2 others
ORIGIN
Query Match      100.0%; Score 15; DB 17; Length 313;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
    |||||
Db 57 CCTTCTCGCCCTGTT 71

RESULT 3
BM273267/c
LOCUS      BM273267      505 bp      mRNA      linear      EST 12-MAR-2002
DEFINITION cDNA clone IMAGE:5677896 5' similar to SW:CAIE_HUMAN P39059
COLLAGEN ALPHA 1(XV) CHAIN PRECURSOR. [1] ; mRNA sequence.
ACCESSION  BM273267
VERSION     BM273267.1 GI:17966560
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 505)
AUTHORS    Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blustain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.,
Jackson,Y. and Bowers,Y.
JOURNAL     Endocrine Pancreas Consortium
COMMENT     Unpublished (2000)
Other_ESTs: if28e01.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu) This sequence now available from the IMAGE
consortium, for clone orders contact: info@image.llnl.gov
Seq primer: -40RP from Gibco
High quality sequence stop: 432.
FEATURES
    source
        1..505
            Location/Qualifiers
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:5677896"
                /clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
                /sex="Both"
                /tissue_type="Islets of Langerhans"
                /dev_stage="Adult"
                /lab_host="DH10B"
/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
Site_2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was

```

```

amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an EcoT of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."
BASE COUNT      133 a      138 c      148 g      86 t
ORIGIN
Query Match      100.0%; Score 15; DB 13; Length 505;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
    |||||
Db 50 CCTTCTCGCCCTGTT 36

RESULT 4
BH019101
LOCUS      BH019101      513 bp      DNA      linear      GSS 25-MAY-2001
DEFINITION L2357K.d.Hygt3.1 Leishmania major Friedlin Cosmid Genomic Library
Leishmania major genomic clone L2357K, DNA sequence.
ACCESSION  BH019101
VERSION     BH019101.1 GI:14197807
KEYWORDS    GSS.
SOURCE      Leishmania major.
ORGANISM    Leishmania major
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Leishmania.
REFERENCE   1 (bases 1 to 513)
AUTHORS    Myler,P.J., Vogt,C., Cawthra,J., Klacking,M., Marty,A., Mack,J.,
Munden,H., Nguyen,D., Robertson,L., Sisk,E., Fazelinia,G., Aggarwal
,G., Nelson,S., Seyler,A., Worthey,E. and Stuart,K.
Leishmania major Friedlin Cosmid End Sequences
Unpublished (2000)
JOURNAL     Contact: Myler PJ
COMMENT     Seattle Biomedical Research Institute
4 Nickerson Street, Seattle, WA 98109-1651, USA
Tel: 206 284-8846
Fax: 206 284-0313
Email: mylerpj@sbri.org
Seq primer: Hygt3
Class: cosmid ends.
FEATURES
    source
        1..513
            Location/Qualifiers
                /organism="Leishmania major"
                /strain="Friedlin"
                /db_xref="taxon:5664"
                /clone="L2357K"
                /clone_lib="Leishmania major Friedlin Cosmid Genomic
                Library"
                /lab_host="E. coli ED8767"
                /note="vector: cLHYG; Site_1: BamHI; Genomic DNA from
                Leishmania major Friedlin was partially digested with
                Sau3AI, size selected, and ligated with BamHI-digested
                cLHYG cosmid vector DNA. 9216 clones were picked and
                arrayed. Library construction is described in Ivens et
                al., Genomics Research, 8:135-145 (1998). The cLHYG
                vector (Acc. No. CVU59231) is described in Ryan et al.,
                Gene, 131:145-150 (1993)"
                Gene, 131:145-150 (1993)"
BASE COUNT      141 a      154 c      100 g      118 t
ORIGIN
Query Match      100.0%; Score 15; DB 17; Length 513;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
    |||||

```

Db 52 CCTTCTCGCCCTGTT 66

# RESULT 5

AV434035  
LOCUS AV434035 Porphyra yezoensis TU-1 Porphyra yezoensis cDNA clone  
DEFINITION PM037d06\_r 5', mRNA sequence.

AV434035  
ACCESSION AV434035.1 GI:8589260

# KEYWORDS

EST.

# SOURCE

ORGANISM Porphyra yezoensis.  
Porphyra yezoensis.  
Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae;  
Porphyra.

# REFERENCE

AUTHORS 1 (bases 1 to 543)  
Nikaido, I., Asamizu, E., Nakajima, M., Nakamura, Y., Saga, N. and  
Tabata, S.

TITLE Generation of 10,154 expressed sequence tags from a leafy

JOURNAL gametophyte of a marine red alga, Porphyra yezoensis

MEDLINE DNA Res. 7, 223-227 (2000)

# COMMENT

20363100  
Contact: Erika Asamizu  
The First Laboratory for Plant Gene Research  
Kazusa DNA Research Institute  
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan  
Email: asamizuekazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

# FEATURES

source

1..543  
/organism="Porphyra yezoensis"  
/strain="TU-1"  
/db\_xref="taxon:2788"  
/clone="PM037d06\_r"  
/clone\_lib="Porphyra yezoensis TU-1"  
/note="vector: pBluescriptII SK-; Site\_1: EcoRI; Site\_2:  
XhoI"

BASE COUNT 55 a 163 c 190 g 135 t

# ORIGIN

Query Match 100.0%; Score 15; DB 10; Length 543;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15

|||||

Db 423 CCTTCTCGCCCTGTT 437

# RESULT 6

BM142008/c

# LOCUS

BM142008 551 bp mRNA linear EST 12-MAR-2002  
if25d08.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens  
cDNA clone IMAGE:5677479 5' similar to SW:CAIE\_HUMAN P39059  
COLLAGEN ALPHA 1(XV) CHAIN PRECURSOR. [1]; mRNA sequence.

# ACCESSION

BM142008

# VERSION

BM142008.1 GI:17152075

# KEYWORDS

EST.

# SOURCE

human.

# ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 551)

# REFERENCE

# AUTHORS

Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,  
Lemishka, I., Secear, M., Brestelli, J., Gradwohl, G., Clifton, S.,  
Hillier, L., Marra, M., Pape, D., Wyllie, T., Martin, J., Blistain, A.,  
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas  
M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T.,  
Jackson, Y. and Bowers, Y.

# TITLE

Endocrine Pancreas Consortium

# JOURNAL

Other ESTs: if25d08.x1

# COMMENT

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute  
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
MA 02138  
Tel: 617-495-1812  
Fax: 617-495-8557  
Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Douglas Melton DNA sequencing by:  
Washington University Genome Sequencing Center for information on  
obtaining a clone please contact: Juliana Brown  
(brown@fas.harvard.edu) This sequence now available from the IMAGE  
consortium, for clone orders contact: info@image.llnl.gov  
Seq primer: -40RP from Gibco  
High quality sequence stop: 414.

Location/Qualifiers

1..551

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:5677479"

/clone\_lib="Melton Normalized Human Islet 4 N4-HIS 1"

/sex="Both"

/tissue\_type="Islets of Langerhans"

/dev\_stage="Adult"

/lab\_host="DH10B"

/note="Organ: Pancreas; Vector: pSPORT1; Site\_1: Not 1;  
Site\_2: Sal 1; Starting library constructed using  
SuperScript plasmid library kit (Life Technologies). cDNA  
made by oligo-dT priming. Size-selected by column  
fractionation; average insert size 1.08 kb. Library was  
amplified once on solid support and plasmid DNA from  
library was prepared. The library DNA was normalized by  
method #4 from Bonaldo, Lennon, and Soares 1996 Genome  
Research 6:791-806; 0.5 microgram single-stranded library  
plasmid DNA was mixed with 5 micrograms PCR product  
representing library inserts and hybridized to an EcoT of  
20. Single-stranded (unhybridized) plasmids were isolated  
by hydroxyapatite chromatography and used to make this  
library."

BASE COUNT 145 a 148 c 159 g 99 t

# ORIGIN

Query Match 100.0%; Score 15; DB 13; Length 551;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15

|||||

Db 50 CCTTCTCGCCCTGTT 36

# RESULT 7

BF971415/c

# LOCUS

BF971415 617 bp mRNA linear EST 22-JAN-2001

DEFINITION 602272934F1 NIH\_MGC\_84 Homo sapiens cDNA clone IMAGE:4361024 5',  
mRNA sequence.

BF971415

BF971415.1 GI:12338630

EST.

human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 617)

NIH-MGC http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:



```

BASE COUNT      154 a      158 c      189 g      122 t      5 others
ORIGIN

Query Match      100.0%; Score 15; DB 9; Length 628;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
|||||
Db 252 CCTTCTCGCCCTGTT 238

RESULT 10
LOCUS      BI997613/c
DEFINITION      653 bp mRNA linear EST 25-OCT-2001
LAMBDA Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION      BI997613
VERSION
KEYWORDS
SOURCE
ORGANISM      Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
REFERENCE
AUTHORS      Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C., Lefebvre
,P., McDermott,J.P., Shrager,J., Silflow,C. and Stern,D.
TITLE      Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants. Project: 1031
JOURNAL
COMMENT      Unpublished (2001)
Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.

FEATURES
source
1..653
/organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 2lgr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, Stress II (normalized
), Lambda Zap II"
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
XhoI; Stress condition II library, constructed by John
Davies and Jeffrey McDermott, combines cDNAs from CC-1690
cells grown to mid-log phase in TAP (NH4+ - containing)
and shifted to TAP - NO3- (24hrs); H2 production
conditions (0, 12hr, 24hr) see Mellis et al.,(2000) Plant
Phys. 122: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP +
sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr).
PolyA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
Zap II (Stratagene) in the EcoRI (5') and XhoI (3')
sites. pBluescript II SK- plasmids were excised from the
lambda Zap clones by superinfection with ExAssist
(Stratagene) phage. The library was normalized using
method 4 described in Bonaldo et al., (1996) Genome
Research 6: 791-806."
BASE COUNT      141 a      174 c      252 g      86 t
ORIGIN

Query Match      100.0%; Score 15; DB 13; Length 653;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
|||||
Db 644 CCTTCTCGCCCTGTT 630

RESULT 11
LOCUS      BE313934
DEFINITION      659 bp mRNA linear EST 26-OCT-2000
601147310F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3162555 5',
mRNA sequence.
ACCESSION      BE313934
VERSION
KEYWORDS
SOURCE
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
COMMENT      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-femail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. consortium/LLNL at: image.llnl.gov
Plate: LLCM122 row: c column: 04
High quality sequence stop: 618.

FEATURES
source
1..659
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3162555"
/clone_lib="NIH_MGC_19"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: Brain; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using Zap-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
Note: this is a NIH_MGC Library."
BASE COUNT      125 a      203 c      166 g      165 t
ORIGIN

Query Match      100.0%; Score 15; DB 10; Length 659;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
|||||
Db 42 CCTTCTCGCCCTGTT 56

RESULT 12
LOCUS      BE776197/c
DEFINITION      MY-12-B-02 PinfeestansMY Phytophthora infestans cDNA, mRNA sequence.
ACCESSION      BE776197
VERSION
KEYWORDS
SOURCE
ORGANISM      Phytophthora infestans
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.
REFERENCE
AUTHORS      1 (bases 1 to 676)
Kamoun,S., Hraber,P.T., Sobral,B.W.S., Nuss,D. and Govers,F.
TITLE      Initial assessment of gene diversity for the oomycete pathogen
Phytophthora infestans based on expressed sequences
JOURNAL      Fungal Genet. Biol. 28 (2), 94-106 (1999)
MEDLINE
COMMENT      20056376
Contact: Govers F
Laboratory of Phytopathology

```

Wageningen University  
 Binnenhaven 9, P.O.Box 8025, 6700 EE, Wageningen, The Netherlands  
 Tel: 31 317 483 138  
 Fax: 31 317 483 412  
 Email: Francine.Govers@medew.fyto.wau.nl.

#### FEATURES

source  
 1. .676  
 /organism="Phytophthora infestans"  
 /strain="DDR7602, Al mating type"  
 /db\_xref="taxon:4787"  
 /clone\_lib="PinfestansMY"  
 /dev\_stage="4-week old vegetative, non-sporulating  
 mycelium in synthetic medium"  
 /lab\_host="E. coli, strain DH5-alpha"  
 /note="Vector: pSPORT1; Site.1: Sali; Site.2: NotI; Total  
 RNA was isolated from mycelium of P. infestans DDR7602  
 cultured for 4 weeks in synthetic medium. EST clones were  
 named by their position in the microtiter plate, preceded  
 by the prefix MY (for mycelial) and the successive number  
 of the microtiter plate (e.g. MY-06-A-04)."  
 BASE COUNT 144 a 180 c 198 g 151 t 3 others  
 ORIGIN

Query Match 100.0%; Score 15; DB 12; Length 676;  
 Best Local Similarity: 100.0%; Pred. No. 1.9e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15  
 |||||

Db 110 CCTTCTCGCCCTGTT 96

#### RESULT 13

BF315344/c  
 LOCUS 601902627F1 NTH\_MGC\_19 Homo sapiens cDNA clone IMAGE:4135278 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BF315344  
 VERSION BF315344.1 GI:11263579  
 KEYWORDS EST.  
 SOURCE human.

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 713)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at: image.llnl.gov  
 Plate: LLC1039 row: e column: 07  
 High quality sequence stop: 644.  
 Location/Qualifiers  
 1. .713

#### FEATURES

source  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4135278"  
 /clone\_lib="NTH\_MGC\_19"  
 /tissue\_type="neuroblastoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: brain; Vector: pORF7; Site.1: XhoI; Site.2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGACGAG(G). Library constructed by Ling Hong  
 in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 189 a 169 c 203 g 152 t  
 ORIGIN

Query Match 100.0%; Score 15; DB 12; Length 713;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15  
 |||||

Db 274 CCTTCTCGCCCTGTT 260

#### RESULT 14

BG444893/c  
 LOCUS BG444893  
 DEFINITION GA\_Ea0025P19f Gossypium arboreum 7-10 dpa fiber library Gossypium  
 ACCESSION BG444893  
 VERSION BG444893.1 GI:13354545  
 KEYWORDS EST.  
 SOURCE Gossypium arboreum.

ORGANISM Gossypium arboreum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.

REFERENCE 1 (bases 1 to 830)  
 AUTHORS Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry  
 ,D., Wood,T.C., Leslie,A. and Wilkins,T.A.  
 TITLE An integrated analysis of the genetics, development, and evolution  
 of the cotton fiber  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Wing RA  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Tel: 864 656 7288  
 Fax: 864 656 4293  
 Email: rwing@clemson.edu

Seq primer: TAATACGACTCATATAGG  
 High quality sequence stop: 182.  
 Location/Qualifiers  
 1. .830  
 /organism="Gossypium arboreum"  
 /strain="AKA"  
 /cultivar="8400"  
 /db\_xref="taxon:29729"  
 /clone="GA\_Ea0025P19f"  
 /clone\_lib="Gossypium arboreum 7-10 dpa fiber library"  
 /tissue\_type="Fibers isolated from bolls harvested 7-10  
 dpa"  
 /lab\_host="E. coli"  
 /note="Vector: pBK-CMV; Site.1: EcoRI; Site.2: XhoI"

#### FEATURES

source  
 BASE COUNT 218 a 111 c 385 g 116 t  
 ORIGIN

Query Match 100.0%; Score 15; DB 12; Length 830;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15  
 |||||

Db 752 CCTTCTCGCCCTGTT 738

#### RESULT 15

BQ609181  
 LOCUS BQ609181  
 DEFINITION BRY-5105 wheat EST endosperm library Triticum aestivum cDNA 5',  
 mRNA sequence.  
 ACCESSION BQ609181  
 VERSION BQ609181.1 GI:21558520  
 KEYWORDS EST.

SOURCE bread wheat.  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae  
; Triticeae; Triticum.  
REFERENCE 1 (bases 1 to 839)  
AUTHORS Clarke,B., Lambrecht,M. and Rhee,S.  
TITLE Assessing the utility of Arabidopsis genomic information for  
interpreting wheat EST sequences  
JOURNAL Unpublished (2002)  
COMMENT Contact: Lambrecht M  
The Arabidopsis Information Resource  
Carnegie Institution of Washington, Dept. of Plant Biology  
260 Panama Street, Stanford, CA 94305, USA  
Tel: 1 650 325 1521 x 251  
Fax: 1 650 325 3748  
Email: rheee@coma.stanford.edu.  
FEATURES  
source  
1..839  
Location/Qualifiers  
/organism="Triticum aestivum"  
/cultivar="Wyuna"  
/db\_xref="taxon:4565"  
/clone\_lib="wheat EST endosperm library"  
/tissue\_type="endosperm"  
/dev\_stage="developing endosperm tissue 8, 10 and 12 DPA  
(days post anthesis)"  
/note="Vector: Bluescript II SK(-)"  
BASE COUNT 36 a 409 C 68 g 326 t  
ORIGIN  
Query Match 100.0%; Score 15; DB 14; Length 839;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CCTTCTCGCCCTGTT 15  
Db 399 CCTTCTCGCCCTGTT 413  
Search completed: December 11, 2002, 19:00:29  
Job time : 1722.5 secs



GenCore version 5.1.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 12:26:07 ; Search time 1657 Seconds  
(without alignments)  
263.453 Million cell updates/sec

Title: US-09-750-609-9  
Perfect score: 15  
Sequence: 1 cctctgcgcctgtt 15

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 2054640 seqs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb.ba:\*  
2: gb.htg:\*  
3: gb.in:\*  
4: gb.om:\*  
5: gb.ov:\*  
6: gb.pat:\*  
7: gb.ph:\*  
8: gb.pl:\*  
9: gb.pr:\*  
10: gb.ro:\*  
11: gb.sts:\*  
12: gb.sy:\*  
13: gb.un:\*  
14: gb.vi:\*  
15: em.ba:\*  
16: em.fun:\*  
17: em.hum:\*  
18: em.in:\*  
19: em.mu:\*  
20: em.om:\*  
21: em.or:\*  
22: em.ov:\*  
23: em.pat:\*  
24: em.ph:\*  
25: em.pl:\*  
26: em.ro:\*  
27: em.sts:\*  
28: em.un:\*  
29: em.vi:\*  
30: em.htg\_hum:\*  
31: em.htg\_inv:\*  
32: em.htg\_other:\*  
33: em.htg\_mus:\*  
34: em.htg\_pln:\*  
35: em.htg\_rod:\*  
36: em.htg\_mam:\*  
37: em.htg\_vrt:\*  
38: em.sy:\*  
39: em.htgo\_hum:\*  
40: em.htgo\_mus:\*  
41: em.htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	15	100.0	920	6	AX194629	AX194629 Sequence
2	15	100.0	920	6	AX194634	AX194634 Sequence
3	15	100.0	980	9	HSNETEX9	X91127 Homo sapien
4	15	100.0	1411	9	BC000563	BC000563 Homo sapi
5	15	100.0	1983	9	HUMNORTR	M65105 Human norad
c 6	15	100.0	2127	9	HUMCOLA1XV	L01697 Homo sapien
c 7	15	100.0	5161	9	HUMCOLXVAL	L25286 Homo sapien
8	15	100.0	14621	2	AC020425	AC020425 Drosophill
9	15	100.0	61956	2	AC101376	AC101376 Mus muscu
10	15	100.0	65851	2	AC124280	AC124280 Homo sapi
11	15	100.0	80669	2	AC130797	AC130797 Chlamydom
c 12	15	100.0	90280	2	AC009031	AC009031 Homo sapi
13	15	100.0	110000	2	LMFLCHR12_1	Continuation (2 of
14	15	100.0	150765	2	AC094766	AC094766 Rattus no
15	15	100.0	160755	6	AX195074	AX195074 Sequence
16	15	100.0	167094	9	AC007602	AC007602 Homo sapi
c 17	15	100.0	169763	2	AC120748	AC120748 Rattus no
c 18	15	100.0	178965	2	AC096167	AC096167 Rattus no
19	15	100.0	181066	2	AC099635	AC099635 Mus muscu
c 20	15	100.0	181650	2	AC097825	AC097825 Rattus no
21	15	100.0	183105	3	AC104606	AC104606 Drosophill
c 22	15	100.0	187359	8	OSJN00259	AL731609 Oryza sat
c 23	15	100.0	188913	9	AC026802	AC026802 Homo sapi
24	15	100.0	224592	2	AC074209	AC074209 Mus muscu
c 25	15	100.0	285272	3	AE003441	AE003441 Drosophill
c 26	14	93.3	708	6	AX120618	AX120618 Sequence
27	14	93.3	1773	9	AB057774	AB057774 Homo sapi
28	14	93.3	1987	10	MUSCAT2A	AF158025 Rattus no
29	14	93.3	1989	10	MUSCAT2A	L03290 Mus musculu
30	14	93.3	1989	10	MUSCAAT2X	L11600 Mouse catio
c 31	14	93.3	2072	3	AF145606	AF145606 Drosophill
c 32	14	93.3	2306	9	AK054811	AK054811 Homo sapi
c 33	14	93.3	2324	8	SCYGR002C	Z72787 S.cerevisia
c 34	14	93.3	2393	8	AF435646	AF435646 Oryza sat
c 35	14	93.3	2397	6	AR054116	AR054116 Sequence
36	14	93.3	2397	6	IL13751	IL13751 Sequence 5
37	14	93.3	2723	10	MUSTEAB	M62838 Mouse T cel
c 38	14	93.3	3507	10	AF301152	AF301152 Mus muscu
39	14	93.3	3698	10	MUSMEMPROT	L29006 Mouse membr
c 40	14	93.3	4420	1	CGL300822	AJ300822 Corynebac
c 41	14	93.3	5245	1	AF130462	AF130462 Corynebac
c 42	14	93.3	12563	1	AE000769	AE000769 Aquifex a
c 43	14	93.3	13782	1	AE009777	AE009777 Pyrobacul
44	14	93.3	16387	5	AF002935	AF002935 Poromitra
45	14	93.3	18518	1	AE001068	AE001068 Archaeogl

ALIGNMENTS

RESULT 1	AX194629	Sequence 99 from Patent WO0151659.	920 bp	DNA	linear	PAT 28-AUG-2001
LOCUS	AX194629	Sequence 99 from Patent WO0151659.				
DEFINITION	AX194629					
ACCESSION	AX194629.1	GI:15385276				
VERSION						
KEYWORDS						
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
TITLE	1 (bases 1 to 920)					
	Chu,T., Blumenfeld,M. and Cohen,D.					
	Blallelic markers derived from genomic regions carrying genes					
	involved in central nervous system disorders					

JOURNAL Patent: WO 0151659-A 99 19-JUL-2001;  
GENSET (FR)

FEATURES  
Source Location/Qualifiers  
1. .920  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
20. .39  
primer\_bind /note="upstream amplification primer"  
misc\_feature 76. .94  
misc\_feature /note="16-2-76.misl"  
83. .107  
variation /note="16-2-76 potential probe"  
95  
misc\_feature /note="16-2-76 : polymorphic base A or G"  
96. .114  
primer\_bind /note="16-2-76.mis2, complement"  
240. .260  
/note="downstream amplification primer, complement"  
204 a 260 c 225 g 227 t 4 others

BASE COUNT 204 a 260 c 225 g 227 t 4 others

ORIGIN  
Query Match 100.0%; Score 15; DB 6; Length 920;  
Best Local Similarity 100.0%; Pred. No. 6.6e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15  
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Db 170 CCTTCTCGCCCTGTT 184

RESULT 2  
AX194634  
LOCUS AX194634 920 bp DNA linear PAT 28-AUG-2001  
DEFINITION Sequence 104 from Patent WO0151659.  
ACCESSION AX194634  
VERSION AX194634.1 GI:15385281  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 920)  
AUTHORS Chu,T., Blumenfeld,M. and Cohen,D.  
TITLE Biallelic markers derived from genomic regions carrying genes involved in central nervous system disorders  
JOURNAL Patent: WO 0151659-A 104 19-JUL-2001;  
GENSET (FR)

FEATURES  
Source Location/Qualifiers  
1. .920  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
20. .39  
primer\_bind /note="upstream amplification primer"  
misc\_feature 183. .205  
misc\_feature /note="16-2-187.misl"  
194. .218  
variation /note="16-2-187 potential probe"  
206  
misc\_feature /note="16-2-187 : polymorphic base A or G"  
207. .225  
primer\_bind /note="16-2-187.mis2, complement"  
240. .260  
/note="downstream amplification primer, complement"  
204 a 260 c 225 g 227 t 4 others

BASE COUNT 204 a 260 c 225 g 227 t 4 others

ORIGIN  
Query Match 100.0%; Score 15; DB 6; Length 920;  
Best Local Similarity 100.0%; Pred. No. 6.6e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15  
|||||

Db 170 CCTTCTCGCCCTGTT 184

RESULT 3  
HSNETEX9  
LOCUS HSNETEX9 980 bp DNA linear PRI 06-JUL-2001  
DEFINITION Homo sapiens partial SLC6A2 gene for norepinephrine transporter, exons 9-10.  
X91127  
ACCESSION X91127.1 GI:1143488  
VERSION X91127  
KEYWORDS norepinephrine transporter; SLC6A2 gene.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 980)  
AUTHORS Porzgen,P., Bonisch,H. and Bruss,M.  
TITLE Molecular cloning and organization of the coding region of the human norepinephrine transporter gene  
JOURNAL Biochem. Biophys. Res. Commun. 215 (3), 1145-1150 (1995)  
MEDLINE 96028030  
PUBMED 748042  
REFERENCE 2 (bases 1 to 980)  
AUTHORS Porzgen,P., Bonisch,H., Hammermann,R. and Bruss,M.  
TITLE The human noradrenaline transporter gene contains multiple polyadenylation sites and two alternatively spliced C-terminal exons  
JOURNAL Biochim. Biophys. Acta 1398 (3), 365-370 (1998)  
MEDLINE 98322125  
PUBMED 9655936  
REFERENCE 3 (bases 1 to 980)  
AUTHORS Bonisch,H.  
TITLE Direct Submission  
JOURNAL Submitted (30-AUG-1995) H. Bonisch, Institut fuer Pharmacologie und Toxikologie, Universitaet Bonn, Reuterstr 2b, 53113 Bonn, FRG  
COMMENT Related sequences: M65105 and X57700.  
FEATURES  
Location/Qualifiers  
1. .980  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="16"  
/map="16q12.2"  
/cell\_line="W138"  
/cell\_type="fibroblast"  
/tissue\_type="lung"  
/clone\_lib="lambda FIX (Stratagene)"  
129. .800  
/gene="SLC6A2"  
129. .257  
/gene="SLC6A2"  
/number=9  
/usedin=X91117:SLC6A2\_CDSA  
/usedin=X91117:SLC6A2\_mRNAa  
/usedin=X91117:SLC6A2\_mRNAB  
701. .800  
/gene="SLC6A2"  
/number=10  
/usedin=X91117:SLC6A2\_CDSA  
/usedin=X91117:SLC6A2\_mRNAa  
/usedin=X91117:SLC6A2\_mRNAB  
218 a 275 c 246 g 238 t 3 others

BASE COUNT 218 a 275 c 246 g 238 t 3 others

ORIGIN  
Query Match 100.0%; Score 15; DB 9; Length 980;  
Best Local Similarity 100.0%; Pred. No. 6.6e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15  
|||||

Db 230 CCTTCTCGCCCTGTT 244

RESULT 4  
BC000563

LOCUS BC000563 1411 bp mRNA linear PRI 12-JUL-2001  
 DEFINITION Homo sapiens, clone IMAGE:3162672, mRNA, partial cds.  
 ACCESSION BC000563  
 VERSION BC000563.1 GI:12653576  
 KEYWORDS  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 1411)  
 Strausberg,R.  
 Direct Submission  
 Submitted (15-NOV-2000) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: National Institutes of Health Intramural  
 Sequencing Center (NISC),  
 Gaithersburg, Maryland;  
 Web site: <http://www.nisc.nih.gov/>  
 Contact: [nisc.mgc@nih.gov](mailto:nisc.mgc@nih.gov)  
 Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,  
 Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,  
 Dietrich,N.L., Guan,J., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,  
 Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,  
 McDowell,J., Pearson,R., Snyder,B., Stantripoop,S., Thomas,P.J.,  
 Tionson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,  
 Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAL Plate: 5 Row: 1 Column: 7  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: Hexamer frequency ORF  
 analysis.

FEATURES Location/Qualifiers  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3162672"  
 /tissue\_type="Brain, neuroblastoma"  
 /clone\_lib="NIH\_MGC\_19"  
 /lab\_host="DH10B-R"  
 /note="Vector: pOTB7"  
 <1..988  
 /codon\_start=2  
 /product="Unknown (protein for IMAGE:3162672)"  
 /protein\_id="AAH00563.1"  
 /db\_xref="GI:12653577"  
 /translation="ARGLFSLWKGKVTSGKVIDAATQIFSLGAGFGVLIAFASVY  
 KFDNCRDALLTSINCITFSVSGFAIFSLCYMAHEHVNIEDVATEGAGLVILY  
 PRAITSLSGTWAVFFVLLALGLDSSMGMEAVITGLADDFQVLRKRKLFTFGV  
 TPTSLALFCITKGGIYVLLDITFAAGTSILFAVLEAIGVSWFYGVDVRFSDIOQ  
 MNGFRGLWRCLWKFVSPAFLLFVVVSIINFKPLTYDDYIFPPANWYGVGIALSS  
 MVLPIYIVIKFLSTQGSLEWRLAYGTTPEHHLVAQRDIRQFQLQHLAI"  
 BASE COUNT 304 a 378 c 356 g 373 t  
 ORIGIN

Query Match 100.0%; Score 15; DB 9; Length 1411;  
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CCTTCTCGCCCTGTT 15  
 |||||||||||||||  
 Db 496 CCTTCTCGCCCTGTT 510

RESULT 5  
 HUMNORTR 1983 bp mRNA linear PRI 07-JAN-1995  
 LOCUS Human noradrenaline transporter mRNA, complete cds.  
 DEFINITION M65105  
 ACCESSION M65105.1 GI:189257  
 VERSION noradrenaline transporter.  
 KEYWORDS Human, CDNA to mRNA.  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 1983)  
 Pacholczyk,T., Blakely,R.D. and Amara,S.G.  
 Expression cloning of a cocaine- and antidepressant-sensitive human  
 noradrenaline transporter  
 JOURNAL Nature 350 (6316), 350-354 (1991)  
 MEDLINE 91179515  
 PUBMED 2008212  
 FEATURES

Source  
 1..1983  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /map="Unassigned"  
 /cell\_type="neuroblastoma"  
 1..1983  
 /gene="NAT1"  
 61..1914  
 /gene="NAT1"  
 /codon\_start=1  
 /product="noradrenaline transporter"  
 /protein\_id="AAA59943.1"  
 /db\_xref="GI:189258"  
 /db\_xref="GDB:600-127-367"  
 /translation="MLLARNPQVQENNGADTGPQPLRKATBELLVVYKERNGVQC  
 LLAPRDGDAQPRETWGKKIDFLSVVGFADLANWRFYLCYKNGGAFILPYTLFL  
 ITAGPLFYMETALQYINREGAATVWIKCPFFKGVGYAVILIALYGVFYNYIAMS  
 YVLFSSFTNLPTWDCGHTWSPNCTDKLLNGSVLGNHTKYSKYFTPAAEYERGV  
 LHLHSSGIDHIGLPQWLLCLMVVIVLYFLSKGVKTSKVWVITATLPYVLFV  
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 DEFINITION L01697  
 ACCESSION L01697  
 VERSION alpha-1 type XV collagen.  
 KEYWORDS Homo sapiens (library: gtl1 from Clonotech Laboratories) placenta  
 SOURCE CDNA to mRNA.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 2127)  
 Myers,J.C., Kivirikko,S., Gordon,M.K., Dion,A.S. and  
 Pihlajaniemi,T.  
 Identification of a previously unknown human collagen chain, alpha  
 1(XV), characterized by extensive interruptions in the

triple-helical region  
Proc. Natl. Acad. Sci. U.S.A. 89 (21), 10144-10148 (1992)  
93066196  
PUBMED  
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LOCUS HUMCOLXVA1 5161 bp mRNA linear PRI 31-DEC-1994  
DEFINITION Homo sapiens alpha-1 type XV collagen mRNA, complete cds.  
ACCESSION L25286  
VERSION L25286.1 GI:461396  
KEYWORDS alpha-1 type XV collagen.  
SOURCE Homo sapiens (tissue library: Clontech bases 955-5167) umbilical cord (bases 1-954) cDNA to mRNA.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 5161)  
AUTHORS Myers, J.C., Kivirikko, S., Gordon, M.K., Dion, A.S. and Pihlajaniemi, T.  
TITLE Identification of a previously unknown human collagen chain, alpha 1(XV), characterized by extensive interruptions in the triple-helical region  
Proc. Natl. Acad. Sci. U.S.A. 89 (21), 10144-10148 (1992)  
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PUBMED  
1279671  
REFERENCE 2 (bases 1 to 5161)  
AUTHORS Kivirikko, S., Heinamaki, P., Rehn, M., Honkanen, N., Myers, J.C. and Pihlajaniemi, T.  
TITLE Primary structure of the alpha 1 chain of human type XV collagen and exon-intron organization in the 3' region of the corresponding gene  
J. Biol. Chem. 269 (7), 4773-4779 (1994)  
JOURNAL J. Biol. Chem. 269 (7), 4773-4779 (1994)  
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AC020425
ACCESSION
AC020425.1 GI:6664472
VERSION
HTG: HTGS_PHASE2.
KEYWORDS
Drosophila melanogaster.
SOURCE
Drosophila melanogaster.
ORGANISM
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 14621)
Adams,M. and Venter,J.C.
Direct Submission
Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
This sequence was identified as CDM:10213135 by the submitter.
For more information on this record e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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ACCESSION
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VERSION
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ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
1 (bases 1 to 61956)
Mus musculus, clone RP23-117121
Unpublished
REFERENCE
2 (bases 1 to 61956)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepe,I., Colangelo,M., Collins,S., Collumore,A., Cook,A.,
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McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,
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Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L16579
Center clone name: L17_I_21
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* NOTE: This record contains 79 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
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* 731 1391: contig of 661 bp in length
* 1392 1491: gap of 100 bp
* 1492 2138: contig of 647 bp in length
* 2139 2238: gap of 100 bp
* 2239 3005: contig of 767 bp in length
* 3006 3105: gap of 100 bp
* 3106 3860: contig of 755 bp in length
* 3861 3960: gap of 100 bp
* 3961 4639: contig of 679 bp in length
* 4640 4739: gap of 100 bp
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* 5415 5514: gap of 100 bp
* 5515 6290: contig of 776 bp in length
* 6291 6390: gap of 100 bp
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* 7172 7853: contig of 682 bp in length
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* 8628 8727: gap of 100 bp
* 8728 9409: contig of 682 bp in length
* 9410 9509: gap of 100 bp
* 9510 10180: contig of 671 bp in length
* 10181 10280: gap of 100 bp
* 10281 10969: contig of 689 bp in length
* 10970 11069: gap of 100 bp
* 11070 11740: contig of 671 bp in length
* 11741 11840: gap of 100 bp
* 11841 12509: contig of 669 bp in length
* 12510 12609: gap of 100 bp
* 12610 13254: contig of 645 bp in length
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* 13355 14028: contig of 674 bp in length
* 14029 14128: gap of 100 bp

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TITLE  
JOURNAL

COMMENT

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DEFINITION

AC124280

VERSION

AC124280.3 GI:22004380

KEYWORDS

HTG; HTGS\_PHASE0.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 65851)

Authors

Birren, B., Nusbaum, C. and Lander, E.

Unpublished

JOURNAL

REFERENCE

2 (bases 1 to 65851)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,

Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,

Boukhalter, B., Brown, A., Camarata, J., Campotiano, A., Chang, J.,

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SEQUENCE SAMPLING.

AC124280

AC124280.3 GI:22004380

HTG; HTGS\_PHASE0.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 65851)

Birren, B., Nusbaum, C. and Lander, E.

Unpublished

JOURNAL

REFERENCE

2 (bases 1 to 65851)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,

Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,

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Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

Submitted (14-JUN-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 65851)

Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,  
Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B.,  
Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,  
Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S.,  
Far, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,  
Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,  
Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,  
Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,  
Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C.,  
McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,  
Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H.,  
O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,  
Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,  
Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P.,  
Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,  
Testfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,  
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,  
Zembek, L., Zimmer, A. and Zody, M.

## Direct Submission

## TITLE

## JOURNAL

## COMMENT

Submitted (30-JUL-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA

On Jul 30, 2002 this sequence version replaced gi:2169374.

All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: [sequence.submissions@genome.wi.mit.edu](mailto:sequence.submissions@genome.wi.mit.edu)

----- Project Information

Center project name: I27356

Center clone name: 519\_O\_19

-----

\* NOTE: This record contains 80 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1 707: contig of 707 bp in length  
\* 708 807: gap of 100 bp  
\* 808 1542: contig of 735 bp in length  
\* 1543 1642: gap of 100 bp  
\* 1643 2336: contig of 694 bp in length  
\* 2337 2436: gap of 100 bp  
\* 2437 3166: contig of 730 bp in length  
\* 3167 3266: gap of 100 bp  
\* 3267 3987: contig of 721 bp in length  
\* 3988 4087: gap of 100 bp  
\* 4088 4813: contig of 726 bp in length  
\* 4814 4913: gap of 100 bp  
\* 4914 5651: contig of 738 bp in length  
\* 5652 5751: gap of 100 bp  
\* 5752 6473: contig of 722 bp in length  
\* 6474 6573: gap of 100 bp  
\* 6574 7300: contig of 727 bp in length  
\* 7301 7400: gap of 100 bp  
\* 7401 8134: contig of 734 bp in length

8135 8234: gap of 100 bp  
\* 8235 8966: contig of 732 bp in length  
\* 8967 9066: gap of 100 bp  
\* 9067 9714: contig of 648 bp in length  
\* 9715 9814: gap of 100 bp  
\* 9815 10534: contig of 720 bp in length  
\* 10535 10634: gap of 100 bp  
\* 10635 11348: contig of 714 bp in length  
\* 11349 11448: gap of 100 bp  
\* 11449 12160: contig of 712 bp in length  
\* 12161 12260: gap of 100 bp  
\* 12261 12986: contig of 726 bp in length  
\* 12987 13086: gap of 100 bp  
\* 13087 13816: contig of 730 bp in length  
\* 13817 13916: gap of 100 bp  
\* 13917 14633: contig of 717 bp in length  
\* 14634 14733: gap of 100 bp  
\* 14734 15446: contig of 713 bp in length  
\* 15447 15546: gap of 100 bp  
\* 15547 16272: contig of 726 bp in length  
\* 16273 16372: gap of 100 bp  
\* 16373 17115: contig of 743 bp in length  
\* 17116 17215: gap of 100 bp  
\* 17216 17930: contig of 715 bp in length  
\* 17931 18030: gap of 100 bp  
\* 18031 18748: contig of 718 bp in length  
\* 18749 18848: gap of 100 bp  
\* 18849 19574: contig of 726 bp in length  
\* 19575 19674: gap of 100 bp  
\* 19675 20393: contig of 719 bp in length  
\* 20394 20493: gap of 100 bp  
\* 20494 21206: contig of 713 bp in length  
\* 21207 21306: gap of 100 bp  
\* 21307 22020: contig of 714 bp in length  
\* 22021 22120: gap of 100 bp  
\* 22121 22852: contig of 732 bp in length  
\* 22853 22952: gap of 100 bp  
\* 22953 23692: contig of 740 bp in length  
\* 23693 23792: gap of 100 bp  
\* 23793 24520: contig of 728 bp in length  
\* 24521 24620: gap of 100 bp  
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\* 25369 25468: gap of 100 bp  
\* 25469 26186: contig of 718 bp in length  
\* 26187 26286: gap of 100 bp  
\* 26287 27015: contig of 729 bp in length  
\* 27016 27115: gap of 100 bp  
\* 27116 27837: contig of 722 bp in length  
\* 27838 27937: gap of 100 bp  
\* 27938 28649: contig of 712 bp in length  
\* 28650 28749: gap of 100 bp  
\* 28750 29479: contig of 730 bp in length  
\* 29480 29579: gap of 100 bp  
\* 29580 30264: contig of 685 bp in length  
\* 30265 30364: gap of 100 bp  
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\* 31204 31943: contig of 740 bp in length  
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\* 36125 36224: gap of 100 bp  
\* 36225 36946: contig of 722 bp in length  
\* 36947 37046: gap of 100 bp  
\* 37047 37776: contig of 730 bp in length  
\* 37777 37876: gap of 100 bp

FEATURES  
source



\* 6274 6962: contig of 689 bp in length  
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\* 9240 9982: contig of 743 bp in length  
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\* 12990 13644: contig of 655 bp in length  
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\* 18136 18738: contig of 603 bp in length  
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\* 18739 19363: contig of 625 bp in length  
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\* 19364 20076: contig of 713 bp in length  
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\* 20850 22064: contig of 1215 bp in length  
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\* 22065 23060: contig of 996 bp in length  
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\* 28326 29243: contig of 918 bp in length  
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\* 29244 30009: contig of 766 bp in length  
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\* 30010 30770: contig of 761 bp in length  
\* gap of unknown length  
\* 30771 31472: contig of 702 bp in length  
\* gap of unknown length  
\* 31473 32518: contig of 1046 bp in length  
\* gap of unknown length  
\* 32519 33729: contig of 1211 bp in length

\* 33730 gap of unknown length  
\* 33804: contig of 75 bp in length  
\* gap of unknown length  
\* 34775: contig of 971 bp in length  
\* gap of unknown length  
\* 35568: contig of 793 bp in length  
\* gap of unknown length  
\* 36526: contig of 958 bp in length  
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\* 37178: contig of 652 bp in length  
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\* 38597: contig of 1419 bp in length  
\* gap of unknown length  
\* 39399: contig of 802 bp in length  
\* gap of unknown length  
\* 40532: contig of 1133 bp in length  
\* gap of unknown length  
\* 41611: contig of 1079 bp in length  
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\* 43644: contig of 987 bp in length  
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\* 55711: contig of 1248 bp in length  
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\* 56683: contig of 972 bp in length  
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\* 61209: contig of 1446 bp in length  
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\* 62915: contig of 1706 bp in length  
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\* 64134: contig of 1219 bp in length  
\* gap of unknown length  
\* 65998: contig of 1864 bp in length  
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\* 67325: contig of 1327 bp in length  
\* gap of unknown length  
\* 68610: contig of 1285 bp in length  
\* gap of unknown length  
\* 70086: contig of 1476 bp in length  
\* gap of unknown length  
\* 71288: contig of 1202 bp in length  
\* gap of unknown length  
\* 73310: contig of 2022 bp in length  
\* gap of unknown length  
\* 74258: contig of 948 bp in length  
\* gap of unknown length  
\* 75836: contig of 1578 bp in length  
\* gap of unknown length

100.08; Score 15; DB 2; Length 90280;

Query Match

Best Local Similarity 100.0%; Pred. No. 6.5e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15

Db 63309 CCTTCTCGCCCTGTT 63295

RESULT 13

LMFLCHR12\_1

WPCOMMENT

Sequence split into 8 fragments LOCUS LMFLCHR12 Accession AL390114

Fragment Name	Begin	End
LMFLCHR12_0	1	110000
LMFLCHR12_1	100001	210000
LMFLCHR12_2	200001	310000
LMFLCHR12_3	300001	410000
LMFLCHR12_4	400001	510000
LMFLCHR12_5	500001	610000
LMFLCHR12_6	600001	710000
LMFLCHR12_7	700001	757191

Continuation (2 of 8) of LMFLCHR12 from base 100001 (AL390114 Leishmania major chromosome)

Query Match

Best Local Similarity 100.0%; Score 15; DB 2; Length 110000;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15

Db 46567 CCTTCTCGCCCTGTT 46581

RESULT 14

AC094766

LOCUS

DEFINITION Rattus norvegicus clone CH230-5L5, \*\*\* SEQUENCING IN PROGRESS \*\*\*

ACCESSION AC094766

VERSION AC094766.2 GI:17941546

KEYWORDS HTG; HTGS-PHASE1

SOURCE Rattus norvegicus

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus

1 (bases 1 to 150765)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C.,

Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,

Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.,

Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,

Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,

Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,

Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,

Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,

Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,C.,

Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,

Duggan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,

Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,

Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,

Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,

Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A.,

Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,

Hollins,B., Honsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,

Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jollivet,S.,

Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,

Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,

Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,

Louisege,H., Lozada,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,

Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,

Martinez,E., Massey,E., Mawhney,E., McLeod,M.P., Meador,M.,

Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,

Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,

Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenwo,S.,

Oguh,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,  
Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,  
Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Roife,M.,  
Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shoohtari,N.,  
Sisson,I., Sodergren,E., Sonaie,T., Sparks,A., Stanley,H.,  
Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K.,  
Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N.,  
Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R.,  
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,  
Watlington,S., Williams,G., Williamson,A., Wleczek,R., Wooden,S.,  
Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,  
Weinstock,G. and Gibbs,R.  
Direct Submission  
Unpublished  
2 (bases 1 to 150765)  
Worley,K.C.  
Direct Submission  
Submitted (15-SEP-2001) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
On Dec 20, 2001 this sequence version replaced gi:15624602.

COMMENT

Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: GBID  
Center clone name: CH230-5L5  
----- Summary Statistics  
Assembly program: Phrap; version 0.990329First call to  
findPhrapList  
Consensus quality: 115371 bases at least Q40  
Consensus quality: 123148 bases at least Q30  
Consensus quality: 129020 bases at least Q20  
Estimated insert size: 114258; sum-of-contigs estimation  
Quality coverage: 0x in Q20 bases; agarose-fp estimation  
Quality coverage: 1.6x in Q20 bases; sum-of-contigs estimation

\* NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 65 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

Contig	Length
1	7731: contig of 7731 bp in length
7732	7831: gap of unknown length
7832	12932: contig of 5101 bp in length
12933	13032: gap of unknown length
13033	13264: contig of 6232 bp in length
19265	19364: gap of unknown length
19365	24766: contig of 5402 bp in length
24767	24866: gap of unknown length
24867	29281: contig of 4415 bp in length
29282	35253: contig of 5872 bp in length
35254	35353: gap of unknown length
35354	38906: contig of 3553 bp in length
38907	39006: gap of unknown length
39007	43062: contig of 4056 bp in length
43063	43162: gap of unknown length
43163	46845: contig of 3683 bp in length
46846	46945: gap of unknown length
46946	50669: contig of 3724 bp in length
50670	50769: gap of unknown length
50770	52753: contig of 1984 bp in length
52754	52853: gap of unknown length
52854	56708: contig of 3855 bp in length
56709	56808: gap of unknown length

\* 56809 60130: contig of 3322 bp in length  
\* 60131 60230: gap of unknown length  
\* 60231 62896: contig of 2666 bp in length  
\* 62897 62996: gap of unknown length  
\* 62997 65284: contig of 2288 bp in length  
\* 65285 65384: gap of unknown length  
\* 65385 68543: contig of 3159 bp in length  
\* 68544 68643: gap of unknown length  
\* 68644 71605: contig of 2962 bp in length  
\* 71606 73043: gap of unknown length  
\* 73044 73143: gap of unknown length  
\* 73144 75325: contig of 2182 bp in length  
\* 75326 75426: gap of unknown length  
\* 75427 77827: contig of 2402 bp in length  
\* 77828 77927: gap of unknown length  
\* 77928 79747: contig of 1820 bp in length  
\* 79748 79847: gap of unknown length  
\* 79848 82048: contig of 2201 bp in length  
\* 82049 82148: gap of unknown length  
\* 82149 84544: contig of 2396 bp in length  
\* 84545 84644: gap of unknown length  
\* 84645 86064: contig of 1420 bp in length  
\* 86065 86164: gap of unknown length  
\* 86165 88210: contig of 2046 bp in length  
\* 88211 88310: gap of unknown length  
\* 88311 89982: contig of 1672 bp in length  
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\* 90083 91934: contig of 1852 bp in length  
\* 91935 92034: gap of unknown length  
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\* 96506 98196: contig of 1691 bp in length  
\* 98197 98296: gap of unknown length  
\* 98297 100079: contig of 1783 bp in length  
\* 100080 100179: gap of unknown length  
\* 100180 101420: contig of 1241 bp in length  
\* 101421 101520: gap of unknown length  
\* 101521 103845: contig of 2325 bp in length  
\* 103846 103946: gap of unknown length  
\* 103947 105477: contig of 1532 bp in length  
\* 105478 105578: gap of unknown length  
\* 105579 106976: contig of 1398 bp in length  
\* 106977 108224: contig of 1149 bp in length  
\* 108225 108325: gap of unknown length  
\* 108326 109716: contig of 1392 bp in length  
\* 109717 109816: gap of unknown length  
\* 109817 111020: contig of 1204 bp in length  
\* 111021 111120: gap of unknown length  
\* 111121 113035: contig of 1915 bp in length  
\* 113036 113135: gap of unknown length  
\* 113137 114902: contig of 1767 bp in length  
\* 114903 115002: gap of unknown length  
\* 115003 116304: contig of 1302 bp in length  
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\* 117755 117854: gap of unknown length  
\* 117855 119554: contig of 1699 bp in length  
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\* 119654 120689: contig of 1035 bp in length  
\* 120689 120789: gap of unknown length  
\* 120789 121913: contig of 1125 bp in length  
\* 121914 122013: gap of unknown length  
\* 122014 123345: contig of 1332 bp in length  
\* 123346 123446: gap of unknown length  
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\* 125354 127037: contig of 1684 bp in length  
\* 127038 127137: gap of unknown length  
\* 127138 128572: contig of 1435 bp in length

\* 128573 128672: gap of unknown length  
\* 128673 129924: contig of 1252 bp in length  
\* 129925 130024: gap of unknown length  
\* 130025 131222: contig of 1198 bp in length  
\* 131223 131322: gap of unknown length  
\* 131323 132602: contig of 1280 bp in length  
\* 132603 132702: gap of unknown length  
\* 132703 134281: contig of 1579 bp in length  
\* 134282 134382: gap of unknown length  
\* 134383 135794: contig of 1413 bp in length  
\* 135795 135894: gap of unknown length  
\* 135895 137173: contig of 1279 bp in length  
\* 137174 137273: gap of unknown length  
\* 137274 138283: contig of 1010 bp in length  
\* 138284 138383: gap of unknown length

Query Match 100.0%; Score 15; DB 2; Length 150765;  
Best Local Similarity 100.0%; Pred. No. 6.5e-02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCTTCTCGCCCTGTT 15  
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Db 76250 CCTTCTCGCCCTGTT 76264

RESULT 15  
AX195074  
LOCUS AX195074 160755 bp DNA linear PAT 28-AUG-2001  
DEFINITION Sequence 544 from Patent WO0151659.  
ACCESSION AX195074  
VERSION AX195074.1 GI:15385721  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 160755)  
AUTHORS Chu,T., Blumenfeld,M. and Cohen,D.  
TITLE Biallelic markers derived from genomic regions carrying genes  
involved in central nervous system disorders  
JOURNAL Patent: WO 0151659-A 544 19-JUL-2001;  
GENSET (FR)

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Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTTCTCGCCCTGTT 15
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Db 63345 CCTTCTCGCCCTGTT 63359
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Search completed: December 11, 2002, 14:35:19  
Job time : 1782 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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158.965 Million cell updates/sec

Title: US-09-750-609-9

Perfect score: 15

Sequence: 1 cctctcgcctgtt 15

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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23: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	AAH28084	Probe for human no
2	15	100.0	920	AAH88259	CNS disorder-relat
3	15	100.0	920	AAH88264	CNS disorder-relat
4	15	100.0	980	AAH28088	Nucleotide sequenc
5	15	100.0	1044	AAH80746	DNA encoding novel
6	15	100.0	1854	AAH28082	Nucleotide sequenc
7	15	100.0	1854	AAH28086	Nucleotide sequenc
8	15	100.0	1983	AAQ28118	Human norepinepher
9	15	100.0	5161	ABK83862	Human cDNA differe

10	15	100.0	160755	23	AAH88704	Human DNA sequence
11	14	93.3	336	24	ABN18096	Human ORFX polynuc
12	14	93.3	655	24	ABQ56203	Human ovarian anti
13	14	93.3	708	22	AAH65499	C glutamicum codin
14	14	93.3	2036	23	ABL11823	Drosophila melanog
15	14	93.3	2397	12	AAQ14533	Tea gene (cDNA 20.
16	14	93.3	2397	15	AAQ63614	T-cell transembra
17	14	93.3	2397	20	AAV59846	Human T-cell early
18	14	93.3	5031	23	ABL11822	Drosophila melanog
19	14	93.3	349980	22	AAH68525	C glutamicum codin
20	13.4	89.3	15	22	AAH28085	Probe for human no
21	13.4	89.3	114	22	ABA40720	Probe #19186 for g
22	13.4	89.3	114	22	AAK24835	Human brain expres
23	13.4	89.3	114	22	AAI56840	Probe #25526 used
24	13.4	89.3	114	24	ABS24326	Human genome-deriv
25	13.4	89.3	324	19	AAV27204	Homo sapiens TSH r
26	13.4	89.3	328	22	ABA15500	Human nervous syst
27	13.4	89.3	331	24	ABN17269	Human ORFX polynuc
28	13.4	89.3	334	24	ABN24354	Human ORFX polynuc
29	13.4	89.3	352	21	AAC09241	Human secreted pro
30	13.4	89.3	374	22	AAK69418	Human immune/haema
31	13.4	89.3	374	22	AAK69419	Human immune/haema
32	13.4	89.3	375	22	ABA11654	Human nervous syst
33	13.4	89.3	389	22	ABA11693	Human nervous syst
34	13.4	89.3	400	22	AAK57066	Human immune/haema
35	13.4	89.3	411	12	AAQ11640	Human TSH-receptor
36	13.4	89.3	417	22	AAI81399	Human polynucleoti
37	13.4	89.3	445	23	ABV50337	Human prostate exp
38	13.4	89.3	450	22	AAI22903	Human breast cance
39	13.4	89.3	458	24	ABS23895	Human genome-deriv
40	13.4	89.3	509	23	AAH81898	DNA encoding novel
41	13.4	89.3	517	24	ABN73664	Bovine embryonic g
42	13.4	89.3	543	24	ABS11537	Human genome-deriv
43	13.4	89.3	549	23	AAH66052	DNA encoding novel
44	13.4	89.3	573	17	AAI16644	Hepatitis C virus
45	13.4	89.3	580	22	ABA31138	Probe #9604 for ge

# ALIGNMENTS

RESULT 1

AAH28084  
ID AAH28084 standard; DNA; 15 BP.

AC AAH28084;

XX 05-SEP-2001 (first entry)

DT Probe for human norepinephrine transporter gene wild type allele.

DE Norepinephrine transporter; orthostatic intolerance; gene therapy;

XX mental illness; hypertension; heart disease; stimulant abuse; cocaine;

KW amphetamine abuse; probe; ss.

XX Homo sapiens.

OS WO200148246-A1.

PN 05-JUL-2001.

PD 28-DEC-2000; 2000WO-US35491.

XX 29-DEC-1999; 99US-0173682.

XX 11-JAN-2000; 2000US-0175456.

XX (UYVA-) UNIV VANDERBILT.

XX Robertson D, Blakely RD;

XX WPI; 2001-425681/45.

PT Screening for susceptibility to sub-optimal norepinephrine transport,

PT particularly orthostatic intolerance in a subject by detecting a  
 PT polymorphism of norepinephrine transporter gene -  
 PS Claim 15; Page 69; 133pp; English.  
 XX  
 CC The present sequence represents a probe for the wild type allele of  
 CC a human norepinephrine transporter gene. The specification a method  
 CC for screening for susceptibility to sub-optimal norepinephrine transport  
 CC in a subject. The method comprises obtaining a biological sample from  
 CC the subject and detecting a polymorphism of a norepinephrine transporter  
 CC gene in the sample from the subject, the presence of the polymorphism  
 CC indicating the susceptibility of the subject to sub-optimal  
 CC norepinephrine transport. The method is useful for screening for  
 CC susceptibility of a subject to orthostatic intolerance. Norepinephrine  
 CC transporter genes are useful for gene therapy for modulating  
 CC norepinephrine transport in a target cell and treating susceptibility  
 CC to impaired norepinephrine transporter function, orthostatic intolerance  
 CC or other relevant diseases in humans and animals such as mental illness,  
 CC hypertension, heart disease, psycho stimulant abuse e.g. cocaine or  
 CC amphetamine abuse.  
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 SQ Sequence 15 BP; 0 A; 7 C; 2 G; 6 T; 0 other;  
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 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CCTTCTCGCCCTGTT 15  
 Db 1 CCTTCTCGCCCTGTT 15  
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 ID AAH88259 standard; DNA; 920 BP.  
 XX  
 AC AAH88259;  
 XX  
 DT 26-FEB-2002 (first entry)  
 XX  
 DE CNS disorder-related biallelic marker #10 from NET gene.  
 XX  
 KW Single nucleotide polymorphism; SNP; biallelic marker; human; ds;  
 KW central nervous system disorder; CNS; NET; norepinephrine transporter.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_feature 95  
 FT /\*tag= a  
 FT /standard\_name= "single nucleotide polymorphism"  
 XX  
 WO200151659-A2.  
 XX  
 PD 19-JUL-2001.  
 XX  
 PF 11-JAN-2001; 2001WO-IB00116.  
 XX  
 PR 13-JAN-2000; 2000US-0175854.  
 XX  
 PA (GEST ) GENSET.  
 XX  
 PI Chu T, Blumenfeld M, Cohen D;  
 XX WPI; 2001-483085/52.  
 XX  
 DR Isolated polynucleotides, useful for genotyping nucleic acids for  
 PT biallelic markers for the diagnosis of depression, comprises central  
 PT nervous system disorder related biallelic marker -  
 XX  
 Claim 1; Page 248; 519pp; English.  
 PS The present invention relates to biallelic markers derived from human

CC genes involved in central nervous system (CNS) disorders. The present  
 CC sequence is one such biallelic marker derived from human norepinephrine  
 CC transporter (NET) gene. This marker has a single nucleotide polymorphism  
 CC (SNP) and is useful in determining the genetic predisposition of  
 CC individuals to CNS disorders, by identifying the nucleotides at a set of  
 CC genetic markers in a biological sample, where the markers comprise at  
 CC least one CNS disorder related marker.  
 XX  
 SQ Sequence 920 BP; 204 A; 260 C; 225 G; 227 T; 4 other;  
 Query Match 100.0%; Score 15; DB 23; Length 920;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CCTTCTCGCCCTGTT 15  
 Db 170 CCTTCTCGCCCTGTT 184  
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 ID AAH88264 standard; DNA; 920 BP.  
 XX  
 AC AAH88264;  
 XX  
 DT 26-FEB-2002 (first entry)  
 XX  
 DE CNS disorder-related biallelic marker #15 from NET gene.  
 XX  
 KW Single nucleotide polymorphism; SNP; biallelic marker; human; ds;  
 KW central nervous system disorder; CNS; NET; norepinephrine transporter.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_feature 206  
 FT /\*tag= a  
 FT /standard\_name= "single nucleotide polymorphism"  
 XX  
 WO200151659-A2.  
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 PD 19-JUL-2001.  
 XX  
 PF 11-JAN-2001; 2001WO-IB00116.  
 XX  
 PR 13-JAN-2000; 2000US-0175854.  
 XX  
 PA (GEST ) GENSET.  
 XX  
 PI Chu T, Blumenfeld M, Cohen D;  
 XX WPI; 2001-483085/52.  
 XX  
 DR Isolated polynucleotides, useful for genotyping nucleic acids for  
 PT biallelic markers for the diagnosis of depression, comprises central  
 PT nervous system disorder related biallelic marker -  
 XX  
 Claim 1; Pages 251-252; 519pp; English.  
 XX  
 PS The present invention relates to biallelic markers derived from human  
 CC genes involved in central nervous system (CNS) disorders. The present  
 CC sequence is one such biallelic marker derived from human norepinephrine  
 CC transporter (NET) gene. This marker has a single nucleotide polymorphism  
 CC (SNP) and is useful in determining the genetic predisposition of  
 CC individuals to CNS disorders, by identifying the nucleotides at a set of  
 CC genetic markers in a biological sample, where the markers comprise at  
 CC least one CNS disorder related marker.  
 XX  
 SQ Sequence 920 BP; 204 A; 260 C; 225 G; 227 T; 4 other;  
 Query Match 100.0%; Score 15; DB 23; Length 920;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTGCGCCTGTT 15  
|||||  
Db 170 CCTTCTGCGCCTGTT 184

RESULT 4  
AAH28088  
ID AAH28088 standard; DNA; 980 BP.

XX

AC AAH28088;

XX

DT 05-SEP-2001 (first entry)

XX

DE Nucleotide sequence of a exon 9 of norepinephrine transporter gene.

XX

KW Norepinephrine transporter; orthostatic intolerance; gene therapy;  
KW mental illness; hypertension; heart disease; stimulant abuse; cocaine;  
KW amphetamine abuse; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT exon 129...257

FT /\*tag= a

FT intron 257...700

FT /\*tag= b

FT exon 701...802

FT /\*tag= c

XX

PN WO200148246-A1.

XX

PD 05-JUL-2001.

XX

PF 28-DEC-2000; 2000WO-US35491.

XX

PR 29-DEC-1999; 99US-0173682.

PR 11-JAN-2000; 2000US-0175456.

XX

PA (UYVA-) UNIV VANDERBILT.

XX

PI Robertson D, Blakely RD;

XX

DR WPI; 2001-425681/45.

XX

PT Screening for susceptibility to sub-optimal norepinephrine transport,  
PT particularly orthostatic intolerance in a subject by detecting a  
PT polymorphism of norepinephrine transporter gene

XX

PS Disclosure; Page 125; 133pp; English.

XX

CC The present sequence represents exon 9 of the human norepinephrine  
CC transporter gene. The specification a method for screening for  
CC susceptibility to sub-optimal norepinephrine (NE) transport in a  
CC subject. The method comprises obtaining a biological sample from the  
CC subject and detecting a polymorphism of a norepinephrine transporter  
CC gene in the sample from the subject, the presence of the polymorphism  
CC indicating the susceptibility of the subject to sub-optimal  
CC norepinephrine transport. The method is useful for screening for  
CC susceptibility of a subject to orthostatic intolerance. Norepinephrine  
CC transporter genes are useful for gene therapy for modulating  
CC norepinephrine transport in a target cell and treating susceptibility  
CC to impaired norepinephrine transporter function, orthostatic intolerance  
CC or other relevant diseases in humans and animals such as mental illness,  
CC hypertension, heart disease, psycho stimulant abuse e.g. cocaine or  
CC amphetamine abuse.

XX

SQ Sequence 980 BP; 218 A; 275 C; 246 G; 238 T; 3 other;

Query Match 100.0%; Score 15; DB 22; Length 980;  
Best Local Similarity 100.0%; Pred. No. 1.8e-02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTGCGCCTGTT 15  
|||||  
Db 230 CCTTCTGCGCCTGTT 244

RESULT 5

AA80746/c

ID AA80746 standard; cDNA; 1044 BP.

XX

AC AA80746;

XX

DT 13-FEB-2002 (first entry)

XX

DE DNA encoding novel human diagnostic protein #16550.

XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX

OS Homo sapiens.

XX

PN WO200175067-A2.

XX

PD 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US08631.

XX

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Drmanac RT, Liu C, Tang YT;

XX

DR WPI; 2001-639362/73.

XX

DR P-PSDB; ABG16559.

XX

PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity

XX

PS Claim 1; SEQ ID No 16550; 103pp; English.

XX

CC The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AAS64197-AAS94564 represent novel human  
CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX

SQ Sequence 1044 BP; 229 A; 303 C; 258 G; 254 T; 0 other;

Query Match 100.0%; Score 15; DB 23; Length 1044;  
Best Local Similarity 100.0%; Pred. No. 1.8e-02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTGCGCCTGTT 15  
|||||

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Db 97 CCTTCTCGCCCTGTT 83
RESULT 6
AAH28082
ID AAH28082 standard; DNA; 1854 BP.
XX
AC AAH28082;
XX
DT 05-SEP-2001 (first entry)
XX
DE Nucleotide sequence of a human norepinephrine transporter.
XX
KW Norepinephrine transporter; orthostatic intolerance; gene therapy;
KW mental illness; hypertension; heart disease; stimulant abuse; cocaine;
KW amphetamine abuse; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1854
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FT FT /product= "norepinephrine transporter"
XX
PN WO200148246-A1.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US35491.
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PR 29-DEC-1999; 99US-0173682.
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PR 11-JAN-2000; 2000US-0175456.
XX
PA (UYVA-) UNIV VANDERBILT.
XX
PI Robertson D, Blakely RD;
XX
DR WPI; 2001-425681/45.
DR P-PSDB; AAB84532.
XX
PT Screening for susceptibility to sub-optimal norepinephrine transporter,
PT particularly orthostatic intolerance in a subject by detecting a
PT polymorphism of norepinephrine transporter gene -
XX
PS Claim 75; Page 98-101; 133pp; English.
XX
CC The present sequence encodes a human norepinephrine transporter. The
CC specification a method for screening for susceptibility to sub-optimal
CC norepinephrine (NE) transport in a subject. The method comprises
CC obtaining a biological sample from the subject and detecting a
CC polymorphism of a norepinephrine transporter gene in the sample from
CC the subject, the presence of the polymorphism indicating the
CC susceptibility of the subject to sub-optimal norepinephrine transporter.
CC The method is useful for screening for susceptibility of a subject to
CC orthostatic intolerance. Norepinephrine transporter genes are useful
CC for gene therapy for modulating norepinephrine transporter in a target
CC cell and treating susceptibility to impaired norepinephrine transporter
CC function, orthostatic intolerance or other relevant diseases in humans
CC and animals such as mental illness, hypertension, heart disease, psycho
CC stimulant abuse e.g. cocaine or amphetamine abuse.
XX
SQ Sequence 1854 BP; 356 A; 554 C; 494 G; 450 T; 0 other;

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Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1362 CCTTCTCGCCCTGTT 1376

RESULT 7
AAQ28118
ID AAQ28118 standard; CDNA; 1983 BP.
XX
AC AAQ28118;
XX

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AAH28086
ID AAH28086 standard; DNA; 1854 BP.
XX
AC AAH28086;
XX
DT 05-SEP-2001 (first entry)
XX
DE Nucleotide sequence of a human norepinephrine transporter.
XX
KW Norepinephrine transporter; orthostatic intolerance; gene therapy;
KW mental illness; hypertension; heart disease; stimulant abuse; cocaine;
KW amphetamine abuse; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
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PN WO200148246-A1.
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PD 05-JUL-2001.
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PF 28-DEC-2000; 2000WO-US35491.
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PR 29-DEC-1999; 99US-0173682.
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PR 11-JAN-2000; 2000US-0175456.
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PI Robertson D, Blakely RD;
XX
DR WPI; 2001-425681/45.
DR P-PSDB; AAB84532.
XX
PT Screening for susceptibility to sub-optimal norepinephrine transporter,
PT particularly orthostatic intolerance in a subject by detecting a
PT polymorphism of norepinephrine transporter gene -
XX
PS Claim 75; Page 112-115; 133pp; English.
XX
CC The present sequence encodes a human norepinephrine transporter. The
CC specification a method for screening for susceptibility to sub-optimal
CC norepinephrine (NE) transport in a subject. The method comprises
CC obtaining a biological sample from the subject and detecting a
CC polymorphism of a norepinephrine transporter gene in the sample from
CC the subject, the presence of the polymorphism indicating the
CC susceptibility of the subject to sub-optimal norepinephrine transporter.
CC The method is useful for screening for susceptibility of a subject to
CC orthostatic intolerance. Norepinephrine transporter genes are useful
CC for gene therapy for modulating norepinephrine transporter in a target
CC cell and treating susceptibility to impaired norepinephrine transporter
CC function, orthostatic intolerance or other relevant diseases in humans
CC and animals such as mental illness, hypertension, heart disease, psycho
CC stimulant abuse e.g. cocaine or amphetamine abuse.
XX
SQ Sequence 1854 BP; 357 A; 553 C; 494 G; 450 T; 0 other;

Query Match 100.0%; Score 15; DB 22; Length 1854;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
| | | | | | | | | | | | | | |
Db 1362 CCTTCTCGCCCTGTT 1376

RESULT 8
AAQ28118
ID AAQ28118 standard; CDNA; 1983 BP.
XX
AC AAQ28118;
XX

```



XX DT 15-MAR-1993 (first entry)  
 XX DE Human norepinephrine transporter protein cDNA clone.  
 XX KW NT; noradrenaline; neuroblastoma; neutotransmitter; antidepressant;  
 XX KW ss.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 XX FT CDS 61..1914  
 XX /\*tag= a  
 XX  
 XX PN WO9217568-A.  
 XX PD 15-OCT-1992.  
 XX PF 20-FEB-1992; 92WO-US01376.  
 XX PR 28-MAR-1991; 91US-0676980.  
 XX PA (UYOR-) UNIV OREGON HEALTH SCI.  
 XX PI Amara SG, Blakely RD, Pacholczyk T;  
 XX DR WPI; 1992-366242/44.  
 XX DR P-PSDB; AAR26416.  
 XX  
 XX PT Complementary DNA clone encoding human norepinephrine transporter  
 XX PT protein - isolated from human neuroblastoma cells and useful for  
 XX PT determining action of e.g. antidepressant drugs  
 XX PS Claim 3; Fig 1; 37pp; English.  
 XX  
 CC Pools of clones from a human SK-N-SH cell (a human neuroblastoma  
 CC cell line) cDNA library were transfected into COS-1 cells. The  
 CC transfected clones were in the form of expression vectors (pXM)  
 CC having an SV-40 replication origin to enable amplification.  
 CC Transfectants of these cells expressing the norepinephrine  
 CC transporter were identified by employing an assay exploiting the  
 CC fact that the norepinephrine analogue m-iodobenzylguanidine (m-IBG)  
 CC is accumulated intracellularly by SK-N-SH cells expressing the  
 CC intact NT. The accumulated radiolabelled m-IBG allows direct  
 CC autoradiographic visualisation of transporter expressing  
 CC transfectants. DNA was rescued from positive colonies and the  
 CC resulting plasmid pools rescreened and subdivided until a single  
 CC clone was obtd. Transfected cells become capable of norepinephrine  
 CC uptake, which may be inhibited by various drugs, e.g. cocaine, to  
 CC a degree similar to the effect of such drugs on noradrenergic  
 CC neurons. The cloned cDNA makes possible well-controlled studies  
 CC of neurotransmitter transporter function in non-neuronal cells  
 CC without the abfuscating influence of other transporters in the  
 CC same cell. Such studies include the relative effects of various  
 CC (psychotropic) drugs such as antidepressants.  
 XX  
 SQ Sequence 1983 BP; 384 A; 602 C; 529 G; 468 T; 0 other;  
 Query Match 100.0%; Score 15; DB 13; Length 1983;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CCTTCGCGCCCTGTT 15  
 |||||  
 Db 1422 CCTTCGCGCCCTGTT 1436  
 RESULT 9  
 ABK83862/c  
 ID ABK83862 standard; cDNA; 5161 BP.  
 XX  
 AC ABK83862;  
 XX

DT 14-AUG-2002 (first entry)  
 XX Human cDNA differentially expressed in granulocytic cells #433.  
 XX  
 XX KW Human; ss; granulocytic cell; DNA chip; bacterial infection;  
 KW viral infection; parasitic infection; protozoal infection;  
 KW fungal infection; sterile inflammatory disease; psoriasis;  
 KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;  
 KW cardiac reperfusion injury; renal reperfusion injury; ARDS;  
 KW adult respiratory distress syndrome; inflammatory bowel disease;  
 KW Crohn's disease; ulcerative colitis; periodontal disease;  
 KW granulocyte activation; chronic inflammation; allergy.  
 XX  
 OS Homo sapiens.  
 XX WO200228999-A2.  
 XX PN 11-APR-2002.  
 XX PD 03-OCT-2001; 2001WO-US30821.  
 XX PF 03-OCT-2000; 2000US-237189P.  
 XX PR (GENE-) GENE LOGIC INC.  
 XX PA Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;  
 XX PI WPI; 2002-435328/46.  
 XX DR  
 XX  
 XX PT Detecting granulocyte activation by detecting differential expression  
 XX PT of genes associated with granulocyte activation, which serves as  
 XX PT diagnostic markers that is useful for monitoring disease states and  
 XX PT drug toxicity  
 XX PS Claim 1; SEQ ID No 433; 114pp; English.  
 XX  
 CC The invention relates to detecting (M1) granulocyte (GC) activation  
 CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by  
 CC DNA chip analysis as given in the specification, and comparing  
 CC the expression level to an expression level in an unactivated  
 CC GC, where differential expression of Gs is indicative of GCA.  
 CC Also included are modulating (M2) GA by contacting GC with an agent  
 CC that alters the expression of at least one gene in Gs; (2) screening (M3)  
 CC for an agent capable of modulating GCA or an inflammation (especially  
 CC chronic) in a tissue, an allergic response in a subject, exposure of a  
 CC subject to a pathogen or sterile inflammatory disease using the  
 CC gene expression profile; (3) detecting (M4) an inflammation (especially  
 CC chronic) in a tissue, an allergic response in a subject, exposure of a  
 CC subject to a pathogen or sterile inflammatory disease, by detecting the  
 CC level of expression in a sample of the tissue of gene(s) from Gs, where  
 CC the level of expression of the gene is indicative of inflammation;  
 CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,  
 CC an allergic response in a subject, exposure of a subject to a pathogen  
 CC or sterile inflammatory disease, by contacting a tissue having  
 CC inflammation with an agent that modulates the expression of gene(s)  
 CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for  
 CC modulating GA; M3 is useful for screening an agent capable of modulating  
 CC GCA preferably in an inflammation in a tissue; M4 is useful for  
 CC detecting an inflammation (especially chronic) in a tissue, an allergic  
 CC response in a subject, exposure of a subject to a pathogen or sterile  
 CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,  
 CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal  
 CC reperfusion injury, ARDS, adult respiratory distress syndrome,  
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,  
 CC periodontal disease; also bacterial infection, viral infection,  
 CC parasitic infection, protozoal infection, fungal infection and M5 is  
 CC useful for treating one of the above conditions. The present  
 CC sequence represents a gene differentially expressed in granulocytes.  
 CC Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX

```
SQ Sequence 5161 BP; 1254 A; 1420 C; 1363 G; 1124 T; 0 other;
Query Match 100.0%; Score 15; DB 24; Length 5161;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTGCCCTGTT 15
Db 2673 CCTTCTGCCCTGTT 2659

RESULT 10
AAH88704
ID AAH88704 standard; DNA; 160755 BP.
XX
AC AAH88704;
XX
DT 26-FEB-2002 (first entry)
XX
DE Human DNA sequence SEQ ID 544.
XX
KW Single nucleotide polymorphism; SNP; biallelic marker; human;
KW central nervous system disorder; CNS; ds.
XX
OS Homo sapiens.
XX
XX WO200151659-A2.
XX
XX 19-JUL-2001.
XX
PF 11-JAN-2001; 2001WO-IB00116.
XX
XX 13-JAN-2000; 2000US-0175854.
XX
PA (GEST ) GENSET.
XX
PI Chu T, Blumenfeld M, Cohen D;
XX
DR WPI; 2001-483085/52.
XX
XX Isolated polynucleotides, useful for genotyping nucleic acids for
PT biallelic markers for the diagnosis of depression, comprises central
PT nervous system disorder related biallelic marker -
XX
PS Disclosure: Page 476-519; 519pp; English.
XX
CC The present invention relates to biallelic markers derived from human
CC genes involved in central nervous system (CNS) disorders (see
CC AH88161-AAH88702). The markers have a single nucleotide polymorphism
CC (SNP) and are useful in determining the genetic predisposition of
CC individuals to CNS disorders, by identifying the nucleotides at a set of
CC genetic markers in a biological sample, where the markers comprise at
CC least one CNS disorder related marker. The present sequence was used
CC to illustrate the invention.
XX
SQ Sequence 160755 BP; 43057 A; 36601 C; 38189 G; 42727 T; 181 other;
Query Match 100.0%; Score 15; DB 23; Length 160755;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTGCCCTGTT 15
Db 63345 CCTTCTGCCCTGTT 63359

RESULT 11
ABN18096
ID ABN18096 standard; cDNA; 336 BP.
XX
AC ABN18096;
XX
XX 24-JUN-2002 (first entry)
```

```
XX Human ORFX polynucleotide sequence SEQ ID NO:4669.
DE
XX
KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
KW hypertension; hypothyroidism; cholesterol ester storage disease;
KW immune deficiency; immune disorder; infectious disease;
KW autoimmune disorder; rheumatoid arthritis; infectious disease;
KW myasthenia gravis; gene; ss.
XX
XX Homo sapiens.
OS
XX
PN WO200192523-A2.
XX
XX 06-DEC-2001.
PD
XX
XX 29-MAY-2001; 2001WO-US10836.
PF
XX
XX 30-MAY-2000; 2000US-206132p.
PR
XX 29-AUG-2000; 2000US-228716p.
PR
XX
PA (CURA-) CURAGEN CORP.
XX
XX Shimkets RA, Leach MD;
XX
XX WPI; 2002-106308/14.
DR
XX P-PSDB; ABP02344.
DR
XX
XX Novel human polypeptides and polynucleotides useful for diagnosing,
PT preventing and treating cardiovascular disease, neurodegenerative,
PT hyperproliferative disorders and autoimmune disorders -
XX
XX Disclosure: SEQ ID 4669; 1037pp; English.
PS
XX
CC The present invention describes substantially purified human proteins
CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
CC in the specification). ABN15762 to ABN27252 encode the human ORFX
CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
CC treating or preventing a pathology associated with an ORFX-associated
CC disorder in humans, and in the manufacture of a medicament for treating a
CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
CC sequences can be used in gene therapy. ORFX sequences can be used in the
CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
CC osteoarthritis, neurodegenerative disorders, disorders related to organ
CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
CC storage disease, various immune deficiencies and disorders, infectious
CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
CC bone degenerative disorders, or periodontal disease, and for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues and conditions resulting from
CC systemic cytokine damage.
CC
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX
SQ Sequence 336 BP; 61 A; 101 C; 109 G; 64 T; 1 other;
```

```
Query Match 93.3%; Score 14; DB 24; Length 336;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTCTGCCCTGTT 15
Db 82 CTTCTGCCCTGTT 95
```

RESULT 12  
ABQ56203/c  
ID ABQ56203 standard; cDNA; 655 BP.  
XX  
AC ABQ56203;  
XX  
XX  
DT 22-AUG-2002 (first entry)  
XX  
DE Human ovarian antigen HVVAW26 cDNA, SEQ ID NO:2083.  
XX  
KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;  
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;  
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;  
KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;  
KW inflammatory condition; immune disorder; blood disorder;  
KW cardiovascular disorder; respiratory disorder; neurological disorder;  
KW gastrointestinal disorder; urinary system disorder; drug screening;  
KW gene therapy; chromosome mapping; forensic analysis;  
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;  
KW antiinflammatory; gynaecological; reproductive; gene; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200200677-A1.  
XX  
PD 03-JAN-2002.  
XX  
PF 07-JUN-2001; 2001WO-US18569.  
XX  
PR 07-JUN-2000; 2000US-209467P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Birse CE, Rosen CA;  
XX  
DR WPI; 2002-147878/19.  
DR P-PSDB; ABP43126.  
XX  
XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,  
PT useful in the prevention, treatment and diagnosis of cancer (e.g.  
PT ovarian cancer), immune disorders, cardiovascular disorders and  
PT neurological diseases -  
XX  
XX Claim 1; SEQ ID NO 2083; 2922pp; English.  
XX  
XX The invention relates to 2175 novel human ovarian antigens (ABP41054-  
CC ABP43228) and to cDNAs encoding them (ABQ54111-ABQ56305), and also  
CC encompasses polypeptides 90% identical and polynucleotides 95% identical  
CC to the sequences of the invention. The invention additionally relates to  
CC recombinant vectors and host cells comprising human ovarian antigen  
CC polynucleotides, antibodies against human ovarian antigens, and the use  
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,  
CC treating, prognosing or preventing various ovary and/or breast-related  
CC disorders. Such conditions include ovarian cancer and breast cancer, and  
CC metastatic tumours of ovarian or breast origin, reproductive system  
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,  
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine  
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic  
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and  
CC vaginitis), immune disorders (e.g., congenital and acquired  
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),  
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,  
CC respiratory disorders, neurological disorders, gastrointestinal disorders  
CC and urinary system disorders. Ovarian antigen polypeptides and  
CC polynucleotides may also be used in screening for compounds which  
CC modulate ovarian antigen expression or activity. The polynucleotides may  
CC further be used for gene therapy, chromosome mapping, in the  
CC identification of individuals and in forensic analysis, and the  
CC polypeptides may be used as food additives or to prepare antibodies  
CC useful in disease diagnosis, drug targeting and phenotyping. The present  
CC sequence represents cDNA encoding a human ovarian antigen of the  
CC invention.  
XX Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 655 BP; 182 A; 168 C; 177 G; 116 T; 12 other;  
Query Match 93.3%; Score 14; DB 24; Length 655;  
Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 CTTCTCGCCCTGTT 15  
DB 556 CTTCTCGCCCTGTT 543  
RESULT 13  
AAH65499/c  
ID AAH65499 standard; DNA; 708 BP.  
AC AAH65499;  
XX  
DT 26-SEP-2001 (first entry)  
XX  
DE C glutamicum coding sequence fragment SEQ ID NO: 534.  
XX  
KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;  
KW organic acid synthesis; ds.  
XX  
OS Corynebacterium glutamicum.  
XX  
PN EP1108790-A2.  
XX  
PD 20-JUN-2001.  
XX  
PF 18-DEC-2000; 2000EP-0127688.  
XX  
PR 16-DEC-1999; 99JP-0377484.  
PR 07-APR-2000; 2000JP-0159162.  
PR 03-AUG-2000; 2000JP-0280988.  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;  
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;  
XX  
DR WPI; 2001-376931/40.  
DR P-PSDB; AAG90280.  
XX  
XX Novel polynucleotides derived from Coryneform bacteria, for identifying  
PT mutation point of a gene, measuring expression of a gene, analysing  
PT expression profile or pattern of a gene and identifying homologous gene  
PT  
XX  
PS Claim 8; SEQ ID NO: 534; 246pp + Sequence Listing; English.  
XX  
XX The present invention provides a number of nucleotide and protein  
CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These  
CC are useful for identifying the mutation point of a gene derived from a  
CC mutant of coryneform bacterium, measuring expression amount and  
CC analysing the expression profile or expression pattern of a gene derived  
CC from Coryneform bacterium, and identifying a homologue of a gene derived  
CC from coryneform bacterium. Coryneform bacteria are useful for producing  
CC amino acids, nucleic acids, vitamins, saccharides and organic acids,  
CC particularly L-lysine. The present sequence is a nucleic acid described  
CC in the exemplification of the invention.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from the  
CC European Patent Office.  
XX  
SQ Sequence 708 BP; 152 A; 212 C; 196 G; 148 T; 0 other;  
Query Match 93.3%; Score 14; DB 22; Length 708;  
Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



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OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 13:29:32 ; Search time 47 seconds  
(without alignments)  
97.876 Million cell updates/sec

Title: US-09-750-609-9  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	93.3	2397	1 US-07-686-322A-5	Sequence 5, Appli
2	14	93.3	2397	1 US-08-002-999-5	Sequence 5, Appli
3	14	93.3	2397	2 US-08-132-990A-5	Sequence 5, Appli
4	14	93.3	2397	5 PCR-US92-09382-5	Sequence 5, Appli
5	13.4	89.3	573	2 US-08-290-665A-137	Sequence 137, App
6	13.4	89.3	573	5 PCR-US95-10398-137	Sequence 137, App
7	13.4	89.3	630	3 US-08-612-973-29	Sequence 29, Appl
8	13.4	89.3	630	4 US-08-927-597-29	Sequence 29, Appl
9	13.4	89.3	738	4 US-09-605-785-747	Sequence 747, App
10	13.4	89.3	1458	4 US-09-105-537-9	Sequence 9, Appli
11	13.4	89.3	1475	4 US-08-961-527-320	Sequence 320, App
12	13.4	89.3	1565	3 US-09-320-878-24	Sequence 24, Appl
13	13.4	89.3	1678	3 US-08-650-766-2	Sequence 2, Appli
14	13.4	89.3	1954	3 US-08-922-635-2	Sequence 2, Appli
15	13.4	89.3	2169	1 US-08-379-496-1	Sequence 1, Appli
16	13.4	89.3	3318	3 US-08-650-766-3	Sequence 3, Appli
17	13.4	89.3	3318	3 US-08-922-635-3	Sequence 3, Appli
18	13.4	89.3	3385	3 US-08-650-766-1	Sequence 1, Appli
19	13.4	89.3	3385	3 US-08-922-635-1	Sequence 1, Appli
20	13.4	89.3	6405	4 US-09-281-481A-18	Sequence 18, Appl
21	13.4	89.3	9785	1 US-08-319-387-1	Sequence 1, Appli
22	13.4	89.3	10322	4 US-09-330-330-3	Sequence 3, Appli
23	13.4	89.3	13613	4 US-09-105-537-3	Sequence 3, Appli
24	13.4	89.3	15202	3 US-08-922-635-21	Sequence 21, Appl
25	13.4	89.3	4403765	4 US-09-103-840A-2	Sequence 2, Appli
26	13.4	89.3	4411529	4 US-09-103-840A-1	Sequence 1, Appli
27	13	86.7	485	4 US-09-400-208B-22	Sequence 22, Appl

c 28	13	86.7	491	4	US-09-400-208B-23	Sequence 23, Appl
c 29	13	86.7	497	4	US-09-400-208B-24	Sequence 24, Appl
c 30	13	86.7	2001	4	US-09-400-208B-4	Sequence 4, Appli
c 31	13	86.7	2023	4	US-09-491-522-6	Sequence 6, Appli
c 32	13	86.7	2450	4	US-09-491-522-2	Sequence 2, Appli
c 33	13	86.7	3240	4	US-09-171-337A-4	Sequence 4, Appli
c 34	13	86.7	3748	1	US-08-261-206A-76	Sequence 1, Appli
c 35	13	86.7	4657	3	US-09-254-325-1	Sequence 1, Appli
c 36	13	86.7	6692	4	US-09-491-522-1	Sequence 1, Appli
c 37	13	86.7	35100	1	US-08-306-691B-19	Sequence 19, Appl
c 38	13	86.7	35100	5	PCR-US93-06251-19	Sequence 19, Appl
c 39	12.4	82.7	23	4	US-09-177-650-37	Sequence 37, Appl
c 40	12.4	82.7	318	4	US-09-177-650-108	Sequence 108, App
c 41	12.4	82.7	358	1	US-07-925-920-1	Sequence 1, Appli
c 42	12.4	82.7	361	1	US-08-094-079-12	Sequence 12, Appl
c 43	12.4	82.7	361	1	US-08-094-079-18	Sequence 18, Appl
c 44	12.4	82.7	361	1	US-08-094-079-20	Sequence 20, Appl
c 45	12.4	82.7	361	1	US-08-094-079-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1  
US-07-686-322A-5  
; Sequence 5, Application US/07686322A  
; Patent No. 5312733  
; GENERAL INFORMATION:  
; APPLICANT: MacLeod Dr., Carol L.  
; TITLE OF INVENTION: No. 5312733el T-cell Lymphoma cDNA Clones  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patent Department, Fulbright & Jaworski  
; STREET: 1301 McKinney, Suit 5100  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77010-3095  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/686,322A  
; FILING DATE: 19910411  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/509684  
; FILING DATE: 13-APR-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Launer, Charlene A.  
; REGISTRATION NUMBER: 33,035  
; REFERENCE/DOCKET NUMBER: D-52332-CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (713) 651-3634  
; TELEFAX: (713) 651-5246  
; TELEX: Western Union 762829  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2397 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; ORIGINAL SOURCE:  
; ORGANISM: Mouse  
; STRAIN: AKR1 Jackson  
; INDIVIDUAL ISOLATE: SL12 cell line  
; TISSUE TYPE: Lymphoma  
; CELL TYPE: T-cell  
; CELL LINE: SL12.3 and SL12.4  
; IMMEDIATE SOURCE:

CLONE: 20.5  
US-07-686-322A-5

Query Match 93.3%; Score 14; DB 1; Length 2397;  
Best Local Similarity 100.0%; Pred. No. 84;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTCTCGCCCTGTT 15  
|||||

Db 1379 CTTCTCGCCCTGTT 1392

RESULT 2  
US-08-002-999-5  
; Sequence 5, Application us/08002999  
; Patent No. 5440017  
; GENERAL INFORMATION:  
; APPLICANT: MacLeod Dr., Carol L.  
; TITLE OF INVENTION: No. 5440017el T-cell Lymphoma cDNA Clones  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patent Department, Fulbright & Jaworski  
; STREET: 1301 McKinney, Suite 5100  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77010-3095  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/002,999  
; FILING DATE: 19930111  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/686,322  
; FILING DATE: 11-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Adler, Benjamin A.  
; REGISTRATION NUMBER: 35,423  
; REFERENCE/DOCKET NUMBER: D-5232-DIV  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (713) 651-5587  
; TELEFAX: (713) 651-5246  
; TELEX: Western Union 762829  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2397 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; ORIGINAL SOURCE:  
; ORGANISM: Mouse  
; STRAIN: AKR1 Jackson  
; INDIVIDUAL ISOLATE: SL12 cell line  
; TISSUE TYPE: Lymphoma  
; CELL TYPE: T-cell  
; CELL LINE: SL12.3 and SL12.4  
; IMMEDIATE SOURCE:  
; CLONE: 20.5  
US-08-002-999-5

Query Match 93.3%; Score 14; DB 1; Length 2397;  
Best Local Similarity 100.0%; Pred. No. 84;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTCTCGCCCTGTT 15  
|||||

Db 1379 CTTCTCGCCCTGTT 1392

RESULT 3  
US-08-132-990A-5  
; Sequence 5, Application US/08132990A  
; Patent No. 5834589  
; GENERAL INFORMATION:  
; APPLICANT: MERUELO, DANIEL  
; APPLICANT: YOSHIMOTO, TAKAYUKI  
; TITLE OF INVENTION: Human Retrovirus Receptor and DNA Coding Therefor  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/132,990A  
; FILING DATE: 07-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/084,729  
; FILING DATE: 29-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/05569  
; FILING DATE: 11-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/899,075  
; FILING DATE: 11-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/806,178  
; FILING DATE: 13-DEC-1991  
; APPLICATION NUMBER: 07/627,950  
; FILING DATE: 14-DEC-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 8105-004-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864  
; TELEX: 66441 PENNIE  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2397 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 410..1768  
US-08-132-990A-5

Query Match 93.3%; Score 14; DB 2; Length 2397;  
Best Local Similarity 100.0%; Pred. No. 84;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTCTCGCCCTGTT 15  
|||||

Db 1379 CTTCTCGCCCTGTT 1392

RESULT 4  
PCT-US92-09382-5  
; Sequence 5, Application PC/TUS9209382  
; GENERAL INFORMATION:

APPLICANT: MERUELO, DANIEL  
APPLICANT: YOSHIMOTO, TAKAYUKI  
TITLE OF INVENTION: Human Retrovirus Receptor and DNA Coding  
TITLE OF INVENTION: Therefor  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Broadway and Neimark  
STREET: 419 Seventh Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/09382  
FILING DATE: 19921213  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Livnat, Shmuel  
REGISTRATION NUMBER: 33,949  
REFERENCE/DOCKET NUMBER: MERUELO-1  
TELEPHONE: 202 628-5197  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2397 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 410..1768  
PCT-US92-09382-5

Query Match 93.3%; Score 14; DB 5; Length 2397;  
Best Local Similarity 100.0%; Pred. No. 84;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTCTCGCCCTGTT 15  
|||||

Db 1379 CTCTCGCCCTGTT 1392

## RESULT 5

US-08-290-665A-137  
Sequence 137, Application US/08290665A  
Patent No. 5882852

GENERAL INFORMATION:  
APPLICANT: BUKH, J., MILLER, R. H. AND  
APPLICANT: PURCELL, R. H.  
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED  
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND  
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS  
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE  
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES  
NUMBER OF SEQUENCES: 263  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/290,665A  
FILING DATE: 15-AUG-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: RICHARD W. BORK  
REGISTRATION NUMBER: 36,459  
REFERENCE/DOCKET NUMBER: 2026-4116  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 137:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 573 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
ORIGINAL SOURCE:  
ORGANISM: homosapiens  
INDIVIDUAL ISOLATE: S2  
US-08-290-665A-137

Query Match 89.3%; Score 13.4; DB 2; Length 573;  
Best Local Similarity 93.3%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTGCGCCCTGTT 15

|||||

Db 531 CCTTCTGCGCCCTGTT 545

## RESULT 6

PCT-US95-10398-137  
Sequence 137, Application PC/TUS9510398  
GENERAL INFORMATION:

APPLICANT: BUKH, J., MILLER, R. H. AND  
APPLICANT: PURCELL, R. H.  
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED  
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND  
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS  
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE  
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES  
NUMBER OF SEQUENCES: 263  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/10398  
FILING DATE: 15-AUG-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/086,428  
FILING DATE: 29 JUNE 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/290/665  
FILING DATE: 15 AUGUST 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: RICHARD W. BORK  
REGISTRATION NUMBER: 36,459  
REFERENCE/DOCKET NUMBER: 2026-4116  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849

TELEX: 421792  
INFORMATION FOR SEQ ID NO: 137:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 573 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
ORGANISM: homoplasmic  
INDIVIDUAL ISOLATE: S2  
PCT-US95-10398-137

Query Match 89.3%; Score 13.4; DB 5; Length 573;  
Best Local Similarity 93.3%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15  
|||||

Db 531 CCTTCTCGCCCTGTT 545

## RESULT 7

US-08-612-973-29  
Sequence 29, Application US/08612973  
Patent No. 6150134  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT  
APPLICANT: BOSMAN, FONS  
APPLICANT: DE MARTYNOFF, GUY  
APPLICANT: BUYSSE, MARIE-ANGE  
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHVE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/612,973  
FILING DATE: 11-MAR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BYRNE, THOMAS E.  
REGISTRATION NUMBER: 32,205  
REFERENCE/DOCKET NUMBER: 1487-10  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 630 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..627  
NAME/KEY: mat\_peptide  
LOCATION: 1..624  
US-08-612-973-29

Query Match 89.3%; Score 13.4; DB 3; Length 630;  
Best Local Similarity 93.3%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15

Db 177 CCTTCTCGCTCTGTT 191

## RESULT 8

US-08-927-597-29  
Sequence 29, Application US/08927597  
Patent No. 6245503  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT  
APPLICANT: BOSMAN, FONS  
APPLICANT: DE MARTYNOFF, GUY  
APPLICANT: BUYSSE, MARIE-ANGE  
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHVE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/927,597  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/612,973  
FILING DATE: 11-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BYRNE, THOMAS E.  
REGISTRATION NUMBER: 32,205  
REFERENCE/DOCKET NUMBER: 1487-10  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 630 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..627  
NAME/KEY: mat\_peptide  
LOCATION: 1..624  
US-08-927-597-29

Query Match 89.3%; Score 13.4; DB 4; Length 630;  
Best Local Similarity 93.3%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15

Db 177 CCTTCTCGCTCTGTT 191



## RESULT 9

US-09-605-785-747/c  
; Sequence 747, Application US/09605785  
; Patent No. 6321716

## GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqi  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.427C16  
; CURRENT APPLICATION NUMBER: US/09/605,785  
; CURRENT FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 835  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 747  
; LENGTH: 738  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(738)  
; OTHER INFORMATION: n=A,T,C or G  
US-09-605-785-747

Query Match 89.3%; Score 13.4; DB 4; Length 738;

Best Local Similarity 93.3%; Pred. No. 1.6e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15

Db 469 CCTTCTCTCCCTGTT 455

## RESULT 10

US-09-105-537-9  
; Sequence 9, Application US/09105537A  
; Patent No. 6265202

## GENERAL INFORMATION:

; APPLICANT: Sherman, D.H.  
; APPLICANT: Liu, H.  
; APPLICANT: Xue, Y.  
; APPLICANT: Zhao, L.  
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin  
; FILE REFERENCE: 600.438U51  
; CURRENT APPLICATION NUMBER: US/09/105,537A  
; CURRENT FILING DATE: 1998-06-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 9  
; LENGTH: 1458  
; TYPE: DNA  
; ORGANISM: Streptomyces venezuelae  
US-09-105-537-9

Query Match 89.3%; Score 13.4; DB 4; Length 1458;

Best Local Similarity 93.3%; Pred. No. 1.7e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15

Db 246 CCTTCTCGCCCTGTT 260

## RESULT 11

US-08-961-527-320/c  
; Sequence 320, Application US/08961527  
; Patent No. 6420135  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunsch  
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 391  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/961,527  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brookes, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PB340P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512

; INFORMATION FOR SEQ ID NO: 320:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1475 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

US-08-961-527-320

Query Match 89.3%; Score 13.4; DB 4; Length 1475;

Best Local Similarity 93.3%; Pred. No. 1.7e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15

Db 641 CCTTCTCGCCCTGTT 627

## RESULT 12

US-09-320-878-24

; Sequence 24, Application US/09320878A  
; Patent No. 6117659

## GENERAL INFORMATION:

; APPLICANT: ASHLEY, Gary  
; APPLICANT: BETLACH, Melanie C.  
; APPLICANT: BETLACH, Mary C.  
; APPLICANT: MCDANIEL, Robert  
; APPLICANT: TANG, Li  
; TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE  
; FILE REFERENCE: 300622002120  
; CURRENT APPLICATION NUMBER: US/09/320,878A  
; CURRENT FILING DATE: 1999-05-27  
; EARLIER APPLICATION NUMBER: CIP OF 09/141,908  
; EARLIER FILING DATE: 1998-08-28  
; EARLIER APPLICATION NUMBER: CIP OF 09/073,538

; EARLIER FILING DATE: 1998-05-06  
; EARLIER APPLICATION NUMBER: CIP OF 08/846,247  
; EARLIER FILING DATE: 1997-04-30  
; EARLIER APPLICATION NUMBER: 60/119,139  
; EARLIER FILING DATE: 1999-02-08  
; EARLIER APPLICATION NUMBER: 60/100,880  
; EARLIER FILING DATE: 1998-09-22  
; EARLIER APPLICATION NUMBER: 60/087,080  
; EARLIER FILING DATE: 1998-05-28  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 1565  
; TYPE: DNA  
; ORGANISM: Streptomyces venezuelae  
US-09-320-878-24

Query Match 89.3%; Score 13.4; DB 3; Length 1565;  
Best Local Similarity 93.3%; Pred. No. 1.7e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15  
||| ||||| ||||| |||||  
Db 295 CCTCTCGCCCTGTT 309

RESULT 13  
US-08-650-766-2/c  
; Sequence 2, Application US/08650766D  
; Patent No. 6015690  
; GENERAL INFORMATION:  
; APPLICANT: PILETZ, John E.  
; APPLICANT: IVANOV, Tina R.  
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A HUMAN IMIDAZOLINE RECEPTOR AND  
; TITLE OF INVENTION: METHOD FOR CLONING THE SAME  
; FILE REFERENCE: Corrected Sequence Listing  
; Patent No. 6015690  
; CURRENT APPLICATION NUMBER: US/08/650,766D  
; CURRENT FILING DATE: 1996-05-20  
; EARLIER APPLICATION NUMBER: US 60/012,600  
; EARLIER FILING DATE: 1996-03-01  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1678  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-08-650-766-2

Query Match 89.3%; Score 13.4; DB 3; Length 1678;  
Best Local Similarity 93.3%; Pred. No. 1.7e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15  
||| ||||| ||||| |||||  
Db 679 CCTCTCGCCCTGTT 665

RESULT 14  
US-08-922-635-2/c  
; Sequence 2, Application US/08922635A  
; Patent No. 6033871  
; GENERAL INFORMATION:  
; APPLICANT: PILETZ, John E.  
; APPLICANT: IVANOV, Tina R.  
; TITLE OF INVENTION: DNA MOLECULES ENCODING IMIDALINE RECEPTIVE POLYPEPTIDES  
; TITLE OF INVENTION: AND POLYPEPTIDES ENCODED THEREBY  
; FILE REFERENCE: Corrected Sequence Listing  
; Patent No. 6033871  
; CURRENT APPLICATION NUMBER: US/08/922,635A  
; CURRENT FILING DATE: 1997-09-03  
; EARLIER APPLICATION NUMBER: 08/650,766  
; EARLIER FILING DATE: 1996-05-20

; EARLIER APPLICATION NUMBER: 60/012,600  
; EARLIER FILING DATE: 1996-03-01  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1954  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-08-922-635-2

Query Match 89.3%; Score 13.4; DB 3; Length 1954;  
Best Local Similarity 93.3%; Pred. No. 1.7e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15  
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Db 679 CCTCTCGCCCTGTT 665

RESULT 15  
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; Sequence 1, Application US/08379496  
; Patent No. 5593833  
; GENERAL INFORMATION:  
; APPLICANT: MORRISON, Nigel A  
; APPLICANT: EISMAN, John A  
; APPLICANT: KELLY, Paul J  
; TITLE OF INVENTION: Assessment of Trans-Acting Factors Allelic  
; TITLE OF INVENTION: Variation  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz  
; STREET: Suite 701-E, 555 13th Street.N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/379,496  
; FILING DATE: 02-MAR-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ERNST, Barbara G  
; REGISTRATION NUMBER: 30,377  
; REFERENCE/DOCKET NUMBER: 1871-114  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202 783-6040  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2169 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-379-496-1

Query Match 89.3%; Score 13.4; DB 1; Length 2169;  
Best Local Similarity 93.3%; Pred. No. 1.7e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15  
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Db 164 CCTTCTCTCCCTGTT 150

Search completed: December 11, 2002, 15:30:43  
Job time : 52 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 14:35:52 ; Search time 52.5 Seconds  
(without alignments)  
111.409 Million cell updates/sec

Title: US-09-750-609-9  
Perfect score: 15  
Sequence: 1 ccttctgcctgtt 15

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Watch 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA.\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq.\*
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- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	13.4	89.3	543	10	US-09-864-761-15909
4	13.4	89.3	580	10	US-09-864-761-9604
5	13.4	89.3	592	10	US-09-864-761-12426
6	13.4	89.3	738	10	US-09-759-143-747
7	13.4	89.3	738	10	US-09-780-669-747
8	13.4	89.3	738	10	US-09-822-827-747
9	13.4	89.3	1458	9	US-09-860-846-9
10	13.4	89.3	1458	10	US-09-861-289-9
11	13.4	89.3	2109	10	US-09-815-242-6020
12	13.4	89.3	5828	9	US-09-430-029-1
13	13.4	89.3	5881	10	US-09-764-869-2353
14	13.4	89.3	9377	10	US-09-801-874-3
15	13.4	89.3	13613	9	US-09-860-846-3
16	13.4	89.3	13613	10	US-09-861-289-3
17	13.4	89.3	15016	10	US-09-880-107-3783
18	13.4	89.3	15857	10	US-09-764-864-1704
19	13.4	89.3	42450	10	US-09-815-048-3

20	13	86.7	3992	10	US-09-944-807-9	Sequence 9, Appli
c 21	13	86.7	4558	10	US-09-764-878-258	Sequence 258, App
c 22	13	86.7	4558	10	US-09-764-860-937	Sequence 937, App
c 23	12.4	82.7	138	10	US-09-783-530-6989	Sequence 6989, Ap
c 24	12.4	82.7	148	10	US-09-878-574-14438	Sequence 14438, A
c 25	12.4	82.7	173	10	US-09-974-300-7193	Sequence 7193, Ap
c 26	12.4	82.7	258	10	US-09-878-574-6987	Sequence 6987, Ap
c 27	12.4	82.7	262	10	US-09-923-876-3974	Sequence 3974, Ap
c 28	12.4	82.7	269	10	US-09-878-574-15063	Sequence 15063, A
c 29	12.4	82.7	337	10	US-09-983-965-906	Sequence 906, App
c 30	12.4	82.7	356	10	US-09-983-965-5128	Sequence 5128, Ap
c 31	12.4	82.7	357	10	US-09-777-564-881	Sequence 881, App
c 32	12.4	82.7	360	10	US-09-777-564-1626	Sequence 1626, Ap
c 33	12.4	82.7	368	10	US-09-777-564-553	Sequence 553, App
c 34	12.4	82.7	389	10	US-09-954-456-1577	Sequence 1577, Ap
c 35	12.4	82.7	389	10	US-09-880-107-3234	Sequence 3234, Ap
c 36	12.4	82.7	390	10	US-09-960-332-14333	Sequence 14333, A
c 37	12.4	82.7	413	10	US-09-983-965-968	Sequence 968, App
c 38	12.4	82.7	427	10	US-09-983-965-928	Sequence 928, App
c 39	12.4	82.7	447	10	US-09-784-423-17	Sequence 17, Appl
c 40	12.4	82.7	453	10	US-09-983-965-723	Sequence 723, App
c 41	12.4	82.7	456	10	US-09-770-444-528	Sequence 528, App
c 42	12.4	82.7	461	9	US-09-954-531-813	Sequence 813, App
c 43	12.4	82.7	467	10	US-09-867-701-10365	Sequence 10365, A
c 44	12.4	82.7	476	10	US-09-864-761-1452	Sequence 1452, Ap
c 45	12.4	82.7	477	10	US-09-969-708-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1

US-09-864-761-26040/C  
; Sequence 26040, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL  
; FILE REFERENCE: Aecomica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
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; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 26040
; LENGTH: 114
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006427.13
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
; OTHER INFORMATION: EST_HUMAN HIT: BF345368.1, EVALUE 5.00e-31
; OTHER INFORMATION: NT HIT: gill1430273, EVALUE 4.00e-31
; US-09-864-761-26040
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Query Match 89.3%; Score 13.4; DB 10; Length 114;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 CCTCTCGCCCTGTT 15
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Db 91 CCTCTCGCGCTGTT 77
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US-09-864-761-32413
; Sequence 32413, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
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; PRIOR FILING DATE: 2001-01-30
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; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 32413
; LENGTH: 458
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL121787.22
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.1
; OTHER INFORMATION: NT HIT: g16671607, EVALUE 2.00e-91
; OTHER INFORMATION: SWISSPROT HIT: P97303, EVALUE 1.00e-37
; OTHER INFORMATION: EST_HUMAN HIT: BE890758.1, EVALUE 4.30e-01
; US-09-864-761-32413
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Query Match 89.3%; Score 13.4; DB 10; Length 458;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 CCTCTCGCCCTGTT 15
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Db 259 CCTCTCGCCCTGTT 273
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## RESULT 3

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US-09-864-761-15909
; Sequence 15909, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
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; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
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; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 15909  
; LENGTH: 543  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AL121787.22  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.1  
US-09-864-761-15909

Query Match 89.3%; Score 13.4; DB 10; Length 543;  
Best Local Similarity 93.3%; Pred. No. 1.8e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTCTCGCCCTGTT 15  
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Db 295 CCTCTCGCCCTGTT 309

## RESULT 4

US-09-864-761-9604/c  
; Sequence 9604, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aeonica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
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; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 9604  
; LENGTH: 580  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AC006427.13  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5  
US-09-864-761-9604

Query Match 89.3%; Score 13.4; DB 10; Length 580;  
Best Local Similarity 93.3%; Pred. No. 1.8e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTCTCGCCCTGTT 15  
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Db 391 CCTCTCGCCCTGTT 377

## RESULT 5

US-09-864-761-12426  
; Sequence 12426, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL  
; FILE REFERENCE: Aeonica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
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; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
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; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 12426  
; LENGTH: 592  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AL138956.3  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.98  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.85  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.84  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.75  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.77  
US-09-864-761-12426

Query Match 89.3%; Score 13.4; DB 10; Length 592;  
Best Local Similarity 93.3%; Pred. No. 1.8e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15  
||||| |||||||  
Db 578 CCTTCTCGCCCTGTT 592

RESULT 6  
US-09-759-143-747/c  
; Sequence 747, Application US/09759143  
; Patent No. US200202248A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqui  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.427C23  
; CURRENT APPLICATION NUMBER: US/09/759,143  
; CURRENT FILING DATE: 2001-01-12  
; NUMBER OF SEQ ID NOS: 934  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 747  
; LENGTH: 738  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(738)  
; OTHER INFORMATION: n=A,T,C or G  
US-09-759-143-747

Query Match 89.3%; Score 13.4; DB 10; Length 738;  
Best Local Similarity 93.3%; Pred. No. 1.8e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CCTTCTCGCCCTGTT 15  
||||| |||||||  
Db 469 CCTTCTCTCCCTGTT 455

RESULT 7  
US-09-780-669-747/c  
; Sequence 747, Application US/09780669  
; Patent No. US20020051977A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqui  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepler, William  
; APPLICANT: Hural, John  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Houghton, Raymond L.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.427C24  
; CURRENT APPLICATION NUMBER: US/09/780,669  
; CURRENT FILING DATE: 2001-02-09  
; NUMBER OF SEQ ID NOS: 943  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 747  
; LENGTH: 738  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(738)  
; OTHER INFORMATION: n=A,T,C or G  
US-09-780-669-747

Query Match 89.3%; Score 13.4; DB 10; Length 738;  
Best Local Similarity 93.3%; Pred. No. 1.8e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15  
||||| |||||||  
Db 469 CCTTCTCTCCCTGTT 455

RESULT 8  
US-09-822-827-747/c  
; Sequence 747, Application US/09822827  
; Patent No. US20020081680A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.534C1  
; CURRENT APPLICATION NUMBER: US/09/822,827  
; CURRENT FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 982  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 747  
; LENGTH: 738

; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (1)...(738)  
; OTHER INFORMATION: n=A,T,C or G  
US-09-822-827-747

Query Match 89.3%; Score 13.4; DB 10; Length 738;  
Best Local Similarity 93.3%; Pred. No. 1.8e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15  
||||| |||||  
Db 469 CCTTCTCGCCCTGTT 455

## RESULT 9

US-09-860-846-9  
; Sequence 9, Application US/09860846  
; Patent No. US2002016472A1  
; GENERAL INFORMATION:  
; APPLICANT: Sherman, D.H.  
; APPLICANT: Liu, H.  
; APPLICANT: xue, Y.  
; APPLICANT: Zhao, L.  
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin  
; FILE REFERENCE: 600.438US1  
; CURRENT APPLICATION NUMBER: US/09/860,846  
; PRIOR FILING DATE: 2001-05-18  
; PRIOR APPLICATION NUMBER: 09/105,537  
; PRIOR FILING DATE: 1998-06-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 9  
; LENGTH: 1458  
; TYPE: DNA  
; ORGANISM: Streptomyces venezuelae  
US-09-860-846-9

Query Match 89.3%; Score 13.4; DB 9; Length 1458;  
Best Local Similarity 93.3%; Pred. No. 1.8e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15  
||||| |||||  
Db 246 CCTCTCGCCCTGTT 260

## RESULT 10

US-09-861-289-9  
; Sequence 9, Application US/09861289  
; Patent No. US20020110897A1  
; GENERAL INFORMATION:  
; APPLICANT: Sherman, D.H.  
; APPLICANT: Liu, H.  
; APPLICANT: xue, Y.  
; APPLICANT: Zhao, L.  
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin  
; FILE REFERENCE: 600.438US1  
; CURRENT APPLICATION NUMBER: US/09/861,289  
; PRIOR FILING DATE: 2001-05-18  
; PRIOR APPLICATION NUMBER: 09/105,537  
; PRIOR FILING DATE: 1998-06-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 9  
; LENGTH: 1458  
; TYPE: DNA  
; ORGANISM: Streptomyces venezuelae  
US-09-861-289-9

Query Match 89.3%; Score 13.4; DB 10; Length 1458;

Best Local Similarity 93.3%; Pred. No. 1.8e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15  
||||| |||||  
Db 246 CCTCTCGCCCTGTT 260

## RESULT 11

US-09-815-242-6020/c  
; Sequence 6020, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6020  
; LENGTH: 2109  
; TYPE: DNA  
; ORGANISM: Escherichia coli  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(2109)  
US-09-815-242-6020

Query Match 89.3%; Score 13.4; DB 10; Length 2109;  
Best Local Similarity 93.3%; Pred. No. 1.9e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15  
||||| |||||  
Db 1492 CCTTCTCGCCCTGTT 1478

## RESULT 12

US-09-430-029-1/c  
; Sequence 1, Application US/09430029  
; Patent No. US20020168738A1  
; GENERAL INFORMATION:  
; APPLICANT: Yano, Tetsuya; No. US20020168738A1oto, tsuyoshi; Imamura, Takeshi; Can  
; TITLE OF INVENTION: DNA Fragment Carrying Toluene Monooxygenase Gene,  
; TITLE OF INVENTION: Recombinant Plasmid, Transformed Microorganism,  
; TITLE OF INVENTION: Method for Degrading Chlorinated Aliphatic Hydrocarbon  
; TITLE OF INVENTION: Compounds and Aromatic Compounds, and  
; FILE REFERENCE: CFO13982U\$  
; CURRENT APPLICATION NUMBER: US/09/430,029

; CURRENT FILING DATE: 1999-10-29  
; EARLIER APPLICATION NUMBER: JP P1998-310801  
; EARLIER FILING DATE: 1998-10-30  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 5828  
; TYPE: DNA  
; ORGANISM: Burkholderia cepacia  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (234)..(443)  
; OTHER INFORMATION: comk  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (463)..(1455)  
; OTHER INFORMATION: comL  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1495)..(1761)  
; OTHER INFORMATION: comM  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1803)..(3350)  
; OTHER INFORMATION: comN  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (3428)..(3781)  
; OTHER INFORMATION: comO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (3810)..(4871)  
; OTHER INFORMATION: comP  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (4876)..(5229)  
; OTHER INFORMATION: comQ  
US-09-430-029-1

Query Match 89.3%; Score 13.4; DB 9; Length 5828;  
Best Local Similarity 93.3%; Pred. No. 2e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15  
|||||

DB 2013 CCTTCTCGCCCTGTT 1999

RESULT 13  
US-09-764-869-2353  
; Sequence 2353, Application US/09764869  
; Patent No. US20020061521A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC007  
; CURRENT APPLICATION NUMBER: US/09764,869  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 2442  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2353  
; LENGTH: 5881  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-764-869-2353

Query Match 89.3%; Score 13.4; DB 10; Length 5881;  
Best Local Similarity 93.3%; Pred. No. 2e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15  
|||||

DB 4343 CCTTCTCTCCCTGTT 4357

RESULT 14  
US-09-801-874-3/c  
; Sequence 3, Application US/09801874  
; Patent No. US20020048801A1  
; GENERAL INFORMATION:  
; APPLICANT: YAN, Chunhua et al.  
; TITLE OF INVENTION: ISOLATED HUMAN AMINOTRANSFERASE  
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN  
; TITLE OF INVENTION: AMINOTRANSFERASE PROTEINS,  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: CL000615  
; CURRENT APPLICATION NUMBER: US/09/801,874  
; CURRENT FILING DATE: 2001-03-09  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 9377  
; TYPE: DNA  
; ORGANISM: Human  
US-09-801-874-3

Query Match 89.3%; Score 13.4; DB 10; Length 9377;  
Best Local Similarity 93.3%; Pred. No. 2e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15  
|||||

DB 3421 CCTTCTCACCTGTT 3407

RESULT 15  
US-09-860-846-3/c  
; Sequence 3, Application US/09860846  
; Patent No. US2002016472A1  
; GENERAL INFORMATION:  
; APPLICANT: Sherman, D.H.  
; APPLICANT: Liu, H.  
; APPLICANT: Xue, Y.  
; APPLICANT: Zhao, L.  
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin  
; FILE REFERENCE: 600.438US1  
; CURRENT APPLICATION NUMBER: US/09/860,846  
; CURRENT FILING DATE: 2001-05-18  
; PRIOR APPLICATION NUMBER: 09/105,537  
; PRIOR FILING DATE: 1998-06-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 13613  
; TYPE: DNA  
; ORGANISM: Streptomyces venezuelae  
US-09-860-846-3

Query Match 89.3%; Score 13.4; DB 9; Length 13613;  
Best Local Similarity 93.3%; Pred. No. 2.1e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15  
|||||

DB 11394 CCTTCTCGCCCTGTT 11380

Search completed: December 11, 2002, 17:01:24  
Job time : 55.5 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: December 11, 2002, 13:27:12 ; Search time 1661 Seconds  
(without alignments)  
146.257 Million cell updates/sec

Title: US-09-750-609-9  
Perfect score: 15  
Sequence: 1 ccttcgcgcctgtt 15

Scoring table: IDENTITY\_NUC  
Gap 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues  
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

- 1: em\_estba:\*
- 2: em\_esthum:\*
- 3: em\_estin:\*
- 4: em\_estmu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_htc:\*
- 9: gb\_estl:\*
- 10: gb\_est2:\*
- 11: gb\_htc:\*
- 12: gb\_est3:\*
- 13: gb\_est4:\*
- 14: gb\_est5:\*
- 15: em\_estfun:\*
- 16: em\_estom:\*
- 17: gb\_gss:\*
- 18: em\_gss\_hum:\*
- 19: em\_gss\_inv:\*
- 20: em\_gss\_pln:\*
- 21: em\_gss\_vrt:\*
- 22: em\_gss\_fun:\*
- 23: em\_gss\_mam:\*
- 24: em\_gss\_mus:\*
- 25: em\_gss\_other:\*
- 26: em\_gss\_pro:\*
- 27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	15	100.0	309	14	T48892
c 2	15	100.0	313	17	BH019102
c 3	15	100.0	505	13	BM273267
c 4	15	100.0	513	17	BH019101
c 5	15	100.0	543	10	AV434035
c 6	15	100.0	551	13	BM142008

c 7	15	100.0	617	12	BF971415
c 8	15	100.0	626	9	AA102111
c 9	15	100.0	628	9	AA099915
c 10	15	100.0	653	13	BI997613
c 11	15	100.0	659	10	BE313934
c 12	15	100.0	676	12	BE776197
c 13	15	100.0	713	12	BF315344
c 14	15	100.0	830	12	PG444893
c 15	15	100.0	839	14	BQ609181
c 16	15	100.0	859	17	AG100084
c 17	15	100.0	939	12	BF180250
c 18	15	100.0	972	12	BG169177
c 19	15	100.0	1005	17	AG085931
c 20	15	100.0	1146	12	BG323915
c 21	14	93.3	226	10	BB068653
c 22	14	93.3	236	10	BB037017
c 23	14	93.3	257	10	BB054187
c 24	14	93.3	274	10	BB460985
c 25	14	93.3	279	10	BB464879
c 26	14	93.3	280	10	BB038101
c 27	14	93.3	282	9	AA140425
c 28	14	93.3	284	10	BB402819
c 29	14	93.3	288	10	BB163513
c 30	14	93.3	292	10	BB408502
c 31	14	93.3	297	10	AA436133
c 32	14	93.3	302	12	BF895478
c 33	14	93.3	308	17	CNS06WIC
c 34	14	93.3	313	10	BB045638
c 35	14	93.3	317	10	BB403227
c 36	14	93.3	318	14	BQ693297
c 37	14	93.3	319	10	BB464805
c 38	14	93.3	343	9	AA493073
c 39	14	93.3	360	14	BQ739202
c 40	14	93.3	362	14	W41213
c 41	14	93.3	370	10	BB872281
c 42	14	93.3	372	9	AI450145
c 43	14	93.3	400	14	BQ103252
c 44	14	93.3	403	12	BF743003
c 45	14	93.3	421	9	AI546215

ALIGNMENTS

RESULT 1  
LOCUS T48892/c  
DEFINITION yb07a09.r1 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:70456 5' similar to similar to SP:S28778 S28778 COLLAGEN ALPHA 1(XV) CHAIN - HUMAN, mRNA sequence.  
ACCESSION T48892  
VERSION T48892.1  
KEYWORDS GI:650752  
SOURCE EST.  
ORGANISM human.  
REFERENCE Homo sapiens  
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiuidae; Homo.  
1 (bases 1 to 309)  
Hallier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Neg,J., Travaakis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)  
97044478  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

High quality sequence stops: 239  
 Source: IMAGE Consortium, LLNL  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: M13RP1

High quality sequence stop: 239.

Location/Qualifiers

1. .309  
 /organism="Homo sapiens"  
 /db\_xref="CDB:491353"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:70456"  
 /clone\_lib="Stratagene placenta (#937225)"  
 /sex="male"  
 /lab\_host="SOLR cells (kanamycin resistant)"  
 /note="Organ: placenta; Vector: pBluescript SK-; Site\_1:  
 EcoRI; Site\_2: XhoI; Cloned unidirectionally. Primer:  
 Oligo dt. Caucasian. Average insert size: 1.2 kb; Uni-ZAP  
 XR Vector: -5' adaptor sequence: 5' GAATTCGGCAGCAG 3' -3',  
 adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTT 3'."

BASE COUNT 82 a 70 c 101 g 51 t 5 others

Query Match 100.0%; Score 15; DB 14; Length 309;  
 Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTCTCGCCCTGTT 15

|||||

Db 107 CCTCTCGCCCTGTT 93

#### RESULT 2

##### LOCUS

BM273267 313 bp DNA linear GSS 25-MAY-2001  
 L2358k.d.Hygr3.1 Leishmania major Friedlin Cosmid Genomic Library  
 Leishmania major genomic clone L2358k, DNA sequence.

##### DEFINITION

##### ACCESSION

##### VERSION

##### KEYWORDS

##### SOURCE

##### ORGANISM

Leishmania major.  
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;  
 Leishmania.

1 (bases 1 to 313)

Myler,P.J., Vogt,C., Cavthra,J., Klacking,M., Marty,A., Mack,J.,  
 Munden,H., Nguyen,D., Robertson,L., Sisk,E., Fazelinia,G., Aggarwal  
 ,G., Nelson,S., Seyler,A., Worthey,E. and Stuart,K.

Leishmania major Friedlin Cosmid End Sequences

Unpublished (2000)

Contact: Myler PJ

Seattle Biomedical Research Institute

4 Nickerson Street, Seattle, WA 98109-1651, USA

Tel: 206 284-8846

Fax: 206 284-0313

Email: mylerpj@bri.org

Seq primer: Hygr3

Class: cosmid ends.

Location/Qualifiers

1. .313

/organism="Leishmania major"

/strain="Friedlin"

/db\_xref="taxon:5664"

/clone="L2358k"

/clone\_lib="Leishmania major Friedlin Cosmid Genomic

Library"

/lab\_host="E. coli ED8767"

/note="Vector: cLHYG; Site\_1: BamHI; Genomic DNA from

Leishmania major Friedlin was partially digested with

Sau3AI, size selected, and ligated with BamHI-digested

cLHYG cosmid vector DNA. 9216 clones were picked and

arrayed. Library construction is described in Ivens et

al., Genomics Research, 8:135-145 (1998). The cLHYG

vector (Acc. NO. CVU59231) is described in Ryan et al,  
 Gene, 131:145-150 (1993)"

BASE COUNT 90 a 86 c 68 g 67 t 2 others

##### ORIGIN

Query Match 100.0%; Score 15; DB 17; Length 313;

Best Local Similarity 100.0%; Pred. No. 6.2e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTCTCGCCCTGTT 15

|||||

Db 57 CCTCTCGCCCTGTT 71

#### RESULT 3

##### BM273267/c

##### LOCUS

BM273267 505 bp mRNA linear EST 12-MAR-2002  
 lf28e01.y1 Melton Normalized Human Islet 4 M4-HIS 1 Homo sapiens  
 cDNA clone IMAGE:5677896 5' similar to SW:CALE\_HUMAN P39059  
 COLLAGEN ALPHA 1(XV) CHAIN PRECURSOR. [1]; mRNA sequence.

##### DEFINITION

##### ACCESSION

##### VERSION

##### KEYWORDS

##### SOURCE

##### ORGANISM

##### REFERENCE

##### AUTHORS

##### TITLE

##### JOURNAL

##### COMMENT

##### Other\_ESRs: lf28e01.xl

##### Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

##### Endocrine Pancreas Consortium

##### Harvard University, Howard Hughes Medical Institute

##### Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,

##### MA 02138

##### Tel: 617-495-1812

##### Fax: 617-495-8557

##### Email: dmelton@biohp.harvard.edu

##### Library was constructed by Dr. Douglas Melton DNA sequencing by:

##### Washington University Genome Sequencing Center For information on

##### obtaining a clone please contact: Juliana Brown

##### (brownefas.harvard.edu) This sequence now available from the IMAGE

##### consortium, for clone orders contact: info@image.llnl.gov

##### Seq primer: -40RP from Gibco

##### High quality sequence stop: 432.

##### Location/Qualifiers

##### 1. .505

##### /organism="Homo sapiens"

##### /db\_xref="taxon:9606"

##### /clone="IMAGE:5677896"

##### /clone\_lib="Melton Normalized Human Islet 4 M4-HIS 1"

##### /sex="Both"

##### /tissue\_type="Islets of Langerhans"

##### /dev\_stage="Adult"

##### /lab\_host="DH10B"

##### /note="Organ: Pancreas; Vector: pSPORT1; Site\_1: Not 1;

##### Site\_2: Sal 1; Starting library constructed using

##### SuperScript plasmid Library kit (Life Technologies). cDNA

##### made by oligo-dT priming. Size-selected by column

##### fractionation; average insert size 1.08 kb. Library was

##### amplified once on solid support and plasmid DNA from

##### library was prepared. The library DNA was normalized by

##### Method #4 from Bonaldo, Lennon, and Soares 1996 Genome

##### Research 6:791-806; 0.5 microgram single-stranded library

##### plasmid DNA was mixed with 5 micrograms PCR product

##### representing library inserts and hybridized to an Ecot of

20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."

BASE COUNT 133 a 138 c 148 g 86 t

Query Match 100.0%; Score 15; DB 13; Length 505;  
Best Local Similarity 100.0%; Pred. No. 6.9e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15  
|||||

Db 50 CCTTCTCGCCCTGTT 36

## RESULT 4

BH019101

LOCUS

DEFINITION L2357k.d.HyGT3.1 Leishmania major Friedlin Cosmid Genomic Library

Leishmania major genomic clone L2357k, DNA sequence.

ACCESSION BH019101

VERSION BH019101.1

KEYWORDS GSS.

SOURCE Leishmania major.

ORGANISM Leishmania major

REFERENCE 1 (bases 1 to 513)

AUTHORS Myler,P.J., Voigt,C., Cawthra,J., Klacking,M., Marty,A., Mack,J.,

Munden,H., Nguyen,D., Robertson,L., Sisk,E., Fazelinia,G., Aggarwal,

G., Nelson,S., Seyler,A., Worthey,E. and Stuart,K.

Leishmania major Friedlin Cosmid End Sequences

Unpublished (2000)

Contact: Myler PJ

Seattle Biomedical Research Institute

4 Nickerson Street, Seattle, WA 98109-1651, USA

Tel: 206 284-8846

Fax: 206 284-0313

Email: mylerpj@sbri.org

Seq primer: Hygt3

Class: cosmid ends.

Location/Qualifiers.

1. .513

/organism="Leishmania major"

/strain="Friedlin"

/db\_xref="taxon:5664"

/clone="L2357k"

/clone\_lib="Leishmania major Friedlin Cosmid Genomic Library"

/lab\_host="E. coli ED8767"

/note="Vector: cLHYG; Site\_1: BamHI; Genomic DNA from

Leishmania major Friedlin was partially digested with

Sau3AI, size selected, and ligated with BamHI-digested

cLHYG cosmid vector DNA. 9216 clones were picked and

arrayed. Library construction is described in Ivens et

al., Genomics research, 8:135-145 (1998). The cLHYG

vector (Acc.No. CV059231) is described in Ryan et al.,

Gene, 131:145-150 (1993)."

141 a 154 c 100 g 118 t

BASE COUNT 141 a 154 c 100 g 118 t

ORIGIN

Query Match 100.0%; Score 15; DB 17; Length 513;

Best Local Similarity 100.0%; Pred. No. 6.9e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15

|||||

Db 52 CCTTCTCGCCCTGTT 66

|||||

RESULT 5

AV434035

LOCUS

## DEFINITION

AV434035 Porphyra yezoensis TU-1 Porphyra yezoensis cDNA clone

PM037d06\_r 5', mRNA sequence.

ACCESSION AV434035

VERSION AV434035.1

KEYWORDS GI:8589260

SOURCE EST.

ORGANISM Porphyra yezoensis.

Porphyra yezoensis

Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae;

Porphyra.

REFERENCE 1 (bases 1 to 543)

AUTHORS Nikaido,I., Asamizu,E., Nakajima,M., Nakamura,Y., Saga,N. and

Tabata,S.

Generation of 10,154 expressed sequence tags from a leafy

gametophyte of a marine red alga, Porphyra yezoensis

DNA Res. 7, 223-227 (2000)

20363100

COMMENT Contact: Erika Asamizu

The First Laboratory for Plant Gene Research

Kazusa DNA Research Institute

Yana 1532-3, Kisarazu, Chiba 292-0812, Japan

Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

Location/Qualifiers

1. .543

/organism="Porphyra yezoensis"

/strain="TU-1"

/db\_xref="taxon:2788"

/clone="PM037d06\_r"

/clone\_lib="Porphyra yezoensis TU-1"

/note="Vector: pBluescriptII SK-; Site\_1: EcoRI; Site\_2:

XhoI"

55 a 163 c 190 g 135 t

BASE COUNT 55 a 163 c 190 g 135 t

ORIGIN

Query Match 100.0%; Score 15; DB 10; Length 543;

Best Local Similarity 100.0%; Pred. No. 7e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15

|||||

Db 423 CCTTCTCGCCCTGTT 437

|||||

RESULT 6

BH42008/c

LOCUS

DEFINITION BH42008

if25d08.y1 Melton Normalized Human Islet 4 M-HIS 1 Homo sapiens

cDNA clone IMAGE:5677479 5' similar to SW:CALE\_HUMAN P39059

COLLAGEN ALPHA 1(XV) CHAIN PRECURSOR. [1] ; mRNA sequence.

551 bp mRNA linear EST 12-MAR-2002

ACCESSION BH42008

VERSION BH42008.1

KEYWORDS GI:17152075

SOURCE EST.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 551)

AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,

Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,

Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,

Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas

M., Gibbons M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.

, Jackson,Y. and Bowers,Y.

Endocrine Pancreas Consortium

Unpublished (2000)

Other ESTs: if25d08.x1

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,

MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Douglas Melton DNA sequencing by:  
Washington University Genome Sequencing Center For information on  
obtaining a clone please contact: Juliana Brown  
(brownjefas.harvard.edu) This sequence now available from the IMAGE  
consortium, for clone orders contact: info@image.llnl.gov  
Seq primer: -48RP from Gibco  
High quality sequence stop: 414.  
Location/Qualifiers

## FEATURES

source

```
1. .551
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:5677479"
/clone_host="Melton Normalized Human Islet 4 N4-HIS 1"
/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
```

```
/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
Site_2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
method #4 from Bernaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an EcoT of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."
```

BASE COUNT 145 a 148 c 159 g 99 t

ORIGIN

```
Query Match 100.0%; Score 15; DB 13; Length 551;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 CCTTCTCGCCCTGTT 15

|||||

Db 50 CCTTCTCGCCCTGTT 36

## RESULT 7

BF971415/c

```
LOCUS 617 bp mRNA linear EST 22-JAN-2001
DEFINITION 602272934F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4361024 5',
mRNA sequence.
```

ACCESSION BF971415

VERSION BF971415.1 GI:12338630

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

REFERENCE 1 (bases 1 to 617)

AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L1AM10003 Row: c column: 09

High quality sequence stop: 614.

Location/Qualifiers

1. .617

/organism="Homo sapiens"

## FEATURES

source

```
/db_xref="taxon:9606"
/clone_lib="IMAGE:4361024"
/tissue_type="adrenal cortex carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
Not1; Site_2: Sal1; Cloned unidirectionally; oligo-dT
primed. Average insert size 1.229 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
```

BASE COUNT 157 a 158 c 195 g 107 t

ORIGIN

```
Query Match 100.0%; Score 15; DB 12; Length 617;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 CCTTCTCGCCCTGTT 15

|||||

Db 375 CCTTCTCGCCCTGTT 361

## RESULT 8

AA102111

LOCUS

DEFINITION

```
AA102111 626 bp mRNA linear EST 11-MAY-1997
zk87h09.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone
IMAGE:489857 3', similar to SW:CAIE_HUMAN P39059 COLLAGEN ALPHA 1(XV
) CHAIN PRECURSOR. ; mRNA sequence.
```

ACCESSION AA102111

VERSION AA102111.1 GI:1646031

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

REFERENCE 1 (bases 1 to 626)

AUTHORS Hillier,L., Lennon,G., Becker,M., Bernaldo,M.F., Chiapelli,B.,  
Chissoe,S., Dietrich,N., DuBucq,T., Favello,A., Gish,W., Hawkins  
,B., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore  
Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaskis,E.,  
Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.  
Generation and analysis of 280,000 human expressed sequence tags  
Genome Res. 6 (9), 807-828 (1996)

97044478

CONTACT: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: [est@watson.wustl.edu](mailto:est@watson.wustl.edu)

This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.

Insert length: 867 Std Error: 0.00

Seq primer: -40M13 fwd. from Amersham

High quality sequence stop: 453.

Location/Qualifiers

1. .626

/organism="Homo sapiens"

/db\_xref="GDB:380444"

/db\_xref="taxon:9606"

/clone="IMAGE:489857"

/clone\_lib="Soares\_pregnant\_uterus\_NbHPU"

/sex="female"

/dev\_stage="adult"

/lab\_host="DH10B"

```
/note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not 1;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5',
AACTGGAAGAAATTCGCCGCCCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
```



```

VERSION BE313934.1 GI:9134434
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 659)
JOURNAL NIH-MGC http://mgc.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: Incyte Genomics, Inc.
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM122 row: c column: 04
High quality sequence stop: 618.
FEATURES
source
1. .659
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3162555"
/clone_lib="NIH_MGC_19"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/Note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 125 a 203 c 166 g 165 t
ORIGIN
Query Match 100.0%; Score 15; DB 10; Length 659;
Best Local Similarity 100.0%; Pred. No. 7.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
|||||
Db 42 CCTTCTCGCCCTGTT 56

RESULT 12
BE776197/c
LOCUS BE776197
DEFINITION MV-12-R-02 PinfestansMY Phytophthora infestans cDNA, mRNA sequence.
ACCESSION BE776197
VERSION BE776197.1 GI:10229852
KEYWORDS EST.
SOURCE potato late blight agent.
ORGANISM Phytophthora infestans
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.
1 (bases 1 to 676)
Kamoun,S., Hraber,P.T., Sobral,B.W.S., Nuss,D. and Govers,F.
Initial assessment of gene diversity for the oomycete pathogen
Phytophthora infestans based on expressed sequences
Fungal Genet. Biol. 28 (2), 94-106 (1999)
20056376
Contact: Govers F
Laboratory of Phytopathology
Wageningen University
Binnenhaven 9, P.O.Box 8025, 6700 EE, Wageningen, The Netherlands
Tel: 31 317 483 138
Fax: 31 317 483 412
Email: Francine.Govers@medew.fyto.wau.nl.
Location/Qualifiers

FEATURES
source
1. .676
/organism="Phytophthora infestans"
/strain="DDR7602, A1 mating type"
/db_xref="taxon:4787"
/clone_lib="PinfestansMY"
/dev_stage="4-week old vegetative, non-sporulating
mycelium in synthetic medium"
/lab_host="E. coli, strain DH5-alpha"
/Note="vector: pSPORT1; Site_1: SalI; Site_2: NotI; Total
RNA was isolated from mycelium of P. infestans DDR7602
cultured for 4 weeks in synthetic medium. EST clones were
named by their position in the microtiter plate, preceded
by the prefix MY (for mycelial) and the successive number
of the microtiter plate (e.g. MY-06-A-04)."
BASE COUNT 144 a 180 c 198 g 151 t
ORIGIN
Query Match 100.0%; Score 15; DB 12; Length 676;
Best Local Similarity 100.0%; Pred. No. 7.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
|||||
Db 110 CCTTCTCGCCCTGTT 96

RESULT 13
BF315344/c
LOCUS BF315344
DEFINITION 601902627F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135278 5',
mRNA sequence.
ACCESSION BF315344
VERSION BF315344.1 GI:11263579
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 713)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM1039 row: e column: 07
High quality sequence stop: 644.
FEATURES
Location/Qualifiers
1. .713
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4135278"
/clone_lib="NIH_MGC_19"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/Note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 189 a 169 c 203 g 152 t
ORIGIN
Query Match 100.0%; Score 15; DB 12; Length 713;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;

```

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15  
|||||  
Db 274 CCTTCTCGCCCTGTT 260

RESULT 14  
BG444893/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

830 bp mRNA linear EST 15-MAR-2001  
GA\_Ea0025P19f Gossypium arboreum 7-10 dpa fiber library Gossypium  
arboreum cDNA clone GA\_Ea0025P19f, mRNA sequence.  
BG444893  
EST.  
BG444893.1 GI:13354545  
Gossypium arboreum.  
Gossypium arboreum.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.  
1 (bases 1 to 830)  
Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry  
, D., Wood, T.C., Leslie, A. and Wilkins, T.A.  
An integrated analysis of the genetics, development, and evolution  
of the cotton fiber  
Unpublished (2000)  
Contact: Wing RA  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: rwing@clemson.edu  
Seq primer: TAATACGACTACTATAGG  
High quality sequence stop: 182.

FEATURES  
source  
1..830  
/organism="Gossypium arboreum"  
/strain="AKA"  
/cultivar="8400"  
/db\_xref="taxon:29729"  
/clone="GA\_Ea0025P19f"  
/clone\_lib="Gossypium arboreum 7-10 dpa fiber library"  
/tissue\_type="Fibers isolated from bolls harvested 7-10  
dpa"  
/lab\_host="E. coli"  
/note="Vector: pBK-CMV; Site\_1: EcoRI; Site\_2: XhoI"

BASE.COUNT 218 a 111 c 385 g 116 t  
ORIGIN

Query Match 100.0%; Score 15; DB 12; Length 830;  
Best Local Similarity 100.0%; Pred. No. 7.7e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15  
|||||  
Db 752 CCTTCTCGCCCTGTT 738

RESULT 15  
BQ609181  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

839 bp mRNA linear EST 25-JUN-2002  
BRY\_5105 wheat EST endosperm library Triticum aestivum cDNA 5',  
mRNA sequence.  
BQ609181  
BQ609181.1 GI:21558520  
EST.  
bread wheat.  
Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae  
; Triticeae; Triticum.  
1 (bases 1 to 839)

AUTHORS  
TITLE  
JOURNAL  
COMMENT

Clarke, B., Lambrecht, M. and Rhee, S.  
Assessing the utility of Arabidopsis genomic information for  
interpreting wheat EST sequences  
Unpublished (2002)  
Contact: Lambrecht M  
The Arabidopsis Information Resource  
Carnegie Institution of Washington, Dept. of Plant Biology  
260 Panama Street, Stanford, CA 94305, USA  
Tel: 1 650 325 1521 x 251  
Fax: 1 650 325 3748  
Email: rhee@coma.stanford.edu.

FEATURES  
source  
1..839  
Location/Qualifiers  
/organism="Triticum aestivum"  
/cultivar="Wyuna"  
/db\_xref="taxon:4565"  
/clone\_lib="wheat EST endosperm library"  
/tissue\_type="endosperm"  
/dev\_stage="developing endosperm tissue 8, 10 and 12 DPA  
(days post anthesis)"  
/note="Vector: Bluescript II SK(-)"

BASE COUNT 36 a 409 c 68 g 326 t  
ORIGIN

Query Match 100.0%; Score 15; DB 14; Length 839;  
Best Local Similarity 100.0%; Pred. No. 7.7e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15  
|||||  
Db 399 CCTTCTCGCCCTGTT 413

Search completed: December 11, 2002, 15:28:53  
Job time : 1664 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 13:30:57 : Search time 2560.5 Seconds  
(without alignments)  
147.290 Million cell updates/sec

Title: US-09-750-609-9  
Perfect score: 15  
Sequence: 1 cttctcgccctgtt 15.

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	15	100.0	15	29	US-09-750-609-9
3	15	100.0	15	61	US-60-173-682-9
4	15	100.0	257	18	US-09-440-302A-470
5	15	100.0	257	18	US-09-440-302B-470
6	15	100.0	258	18	US-09-440-302-470
7	15	100.0	258	18	US-09-442-366A-309
8	15	100.0	472	27	US-09-698-012-481
9	15	100.0	510	20	US-09-534-856-18784
10	15	100.0	592	67	US-60-230-445-2923
11	15	100.0	601	35	US-09-948-933-4005
12	15	100.0	601	35	US-09-948-933-4006
13	15	100.0	601	35	US-09-948-933-4007
14	15	100.0	601	35	US-09-948-933-4008
15	15	100.0	817	24	US-09-634-306B-7016
16	15	100.0	817	24	US-09-634-306B-7017
17	15	100.0	817	38	US-10-027-632-7016
18	15	100.0	817	38	US-10-027-632-7017
19	15	100.0	920	61	US-60-175-854-99
20	15	100.0	920	61	US-60-175-854-104
21	15	100.0	980	1	PCT-US000-35491-15
					Sequence 9, Appli
					Sequence 9, Appli
					Sequence 470, App
					Sequence 470, App
					Sequence 309, App
					Sequence 481, App
					Sequence 18784, A
					Sequence 2923, Ap
					Sequence 4005, Ap
					Sequence 4006, Ap
					Sequence 4007, Ap
					Sequence 4008, Ap
					Sequence 7016, Ap
					Sequence 7017, Ap
					Sequence 99, Appli
					Sequence 104, App
					Sequence 15, Appli

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22      15 100.0 980 1 PCT-US02-25060-1
23      15 100.0 980 29 US-09-750-609-15
24      15 100.0 980 42 US-10-213-948-1
25      15 100.0 980 61 US-06-173-682-15
26      15 100.0 1044 1 PCT-US01-08631-16550
27      15 100.0 1093 29 US-09-758-468-90
28      15 100.0 1093 42 US-10-211-625-90
29      15 100.0 1209 39 US-10-098-754-16300
30      15 100.0 1462 16 US-09-270-849B-35413
31      15 100.0 1573 65 US-06-213-177-929
32      15 100.0 1591 65 US-06-213-177-926
33      15 100.0 1597 65 US-06-213-177-928
34      15 100.0 1606 65 US-06-213-177-927
35      15 100.0 1831 65 US-06-213-177-1027
36      15 100.0 1854 1 PCT-US00-35491-1
37      15 100.0 1854 1 PCT-US00-35491-11
38      15 100.0 1854 29 US-09-750-609-1
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44      15 100.0 1983 18 US-09-440-302B-1067
45      15 100.0 2049 61 US-06-172-373-18619, A

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## ALIGNMENTS

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RESULT 1
PCT-US00-35491-9
; Sequence 9, Application PC/TUS0035491
; GENERAL INFORMATION:
; APPLICANT: Robertson, David
; APPLICANT: Blakely, Randy D.
; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
; FILE REFERENCE: Attorney Docket No. 1242-27 PCT
; CURRENT APPLICATION NUMBER: PCT/US00/35491
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 60/175,456
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/173,682
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US00-35491-9

Query Match 100.0%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
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DB 1 CCTTCTCGCCCTGTT 15

RESULT 2
US-09-750-609-9
; Sequence 9, Application US/09750609
; GENERAL INFORMATION:
; APPLICANT: Robertson, David
; APPLICANT: Blakely, Randy D.
; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
; FILE REFERENCE: Attorney Docket No. 1242-27-2-2
; CURRENT APPLICATION NUMBER: US/09750,609
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 60/175,456

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; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/173,682
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-750-609-9

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Query Match 100.0%; Score 15; DB 29; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CCTTCTCGCCCTGTT 15
   |||||
DB 1 CCTTCTCGCCCTGTT 15

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## RESULT 3

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US-60-173-682-9
; Sequence 9, Application US/60173682
; GENERAL INFORMATION:
; APPLICANT: Robertson, David
; APPLICANT: Blakely, Randy D.
; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
; FILE REFERENCE: Attorney Docket No. 1242-27
; CURRENT APPLICATION NUMBER: US/60/173,682
; CURRENT FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-173-682-9

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Query Match 100.0%; Score 15; DB 61; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CCTTCTCGCCCTGTT 15
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DB 1 CCTTCTCGCCCTGTT 15

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## RESULT 4

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US-09-440-302A-470
; Sequence 470, Application US/09440302A
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashov, Matvey E.
; TITLE OF INVENTION: Human Neurobiology Array
; FILE REFERENCE: CLON-006CIP11
; CURRENT APPLICATION NUMBER: US/09/440,302A
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 1193
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 470
; LENGTH: 257
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleic Acid Probe
US-09-440-302A-470

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Query Match 100.0%; Score 15; DB 18; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CCTTCTCGCCCTGTT 15  
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Db 45 CCTTCTCGCCCTGTT 59

## RESULT 5

US-09-440-302B-470  
; Sequence 470, Application US/09440302B  
; GENERAL INFORMATION:  
; APPLICANT: Chenchik, Alex  
; APPLICANT: Lukashev, Matvey E.  
; TITLE OF INVENTION: Human Neurobiology Array  
; FILE REFERENCE: CLON-006CIP11  
; CURRENT APPLICATION NUMBER: US/09/440,302B  
; CURRENT FILING DATE: 1999-11-17  
; PRIOR APPLICATION NUMBER: 09/053,375  
; PRIOR FILING DATE: 1998-03-31  
; NUMBER OF SEQ ID NOS: 1193  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 470  
; LENGTH: 257  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Nucleic Acid Probe  
US-09-440-302B-470

Query Match 100.0%; Score 15; DB 18; Length 257;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15  
|||||  
Db 45 CCTTCTCGCCCTGTT 59

## RESULT 6

US-09-440-302-470  
; Sequence 470, Application US/09440302  
; GENERAL INFORMATION:  
; APPLICANT: Chenchik, Alex  
; APPLICANT: Lukashev, Matvey E.  
; TITLE OF INVENTION: Human Neurobiology Array  
; FILE REFERENCE: CLON-006CIP11  
; CURRENT APPLICATION NUMBER: US/09/440,302  
; CURRENT FILING DATE: 1999-11-17  
; PRIOR APPLICATION NUMBER: 09/053,375  
; PRIOR FILING DATE: 1998-03-31  
; NUMBER OF SEQ ID NOS: 597  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 470  
; LENGTH: 258  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Nucleic Acid Probe  
US-09-440-302-470

Query Match 100.0%; Score 15; DB 18; Length 258;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15  
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Db 45 CCTTCTCGCCCTGTT 59

## RESULT 7

US-09-442-366A-309  
; Sequence 309, Application US/09442366A  
; GENERAL INFORMATION:  
; APPLICANT: Chenchik, Alex

; APPLICANT: Lukashev, Matvey E.  
; TITLE OF INVENTION: Human Array  
; FILE REFERENCE: CLON-006CIP13  
; CURRENT APPLICATION NUMBER: US/09/442,366A  
; CURRENT FILING DATE: 1999-11-17  
; PRIOR APPLICATION NUMBER: 09/053,375  
; PRIOR FILING DATE: 1998-03-31  
; NUMBER OF SEQ ID NOS: 2216  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 309  
; LENGTH: 258  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic gene fragment  
US-09-442-366A-309

Query Match 100.0%; Score 15; DB 18; Length 258;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15  
|||||  
Db 45 CCTTCTCGCCCTGTT 59

## RESULT 8

US-09-698-012-481/c  
; Sequence 481, Application US/09698012  
; GENERAL INFORMATION:  
; APPLICANT: Gearing, David P.  
; APPLICANT: Holtzman, Douglas A.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES  
; TITLE OF INVENTION: THEREFOR  
; FILE REFERENCE: 1600.2002-001  
; CURRENT APPLICATION NUMBER: US/09/698,012  
; CURRENT FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: 60/162,166  
; PRIOR FILING DATE: 1999-10-28  
; NUMBER OF SEQ ID NOS: 9719  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 481  
; LENGTH: 472  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-698-012-481

Query Match 100.0%; Score 15; DB 27; Length 472;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15  
|||||  
Db 76 CCTTCTCGCCCTGTT 62

## RESULT 9

US-09-534-856-18784/c  
; Sequence 18784, Application US/09534856  
; GENERAL INFORMATION:  
; APPLICANT: Seilhamer, Jeffrey J.  
; APPLICANT: Deleage, Angelo M.  
; APPLICANT: Stuart, Susan G.  
; APPLICANT: Stuve, Laura L.  
; APPLICANT: Mullahy, Sara J.  
; APPLICANT: Naughton, Rebecca E.  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING STRUCTURAL, SECRETED,  
; FILE REFERENCE: PD-1015 CIP  
; CURRENT APPLICATION NUMBER: US/09/534,856  
; CURRENT FILING DATE: 2000-03-24  
; Prior application data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 26334

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; SOFTWARE: PERL Program
; SEQ ID NO 18784
; LENGTH: 510
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID No: hu01124269
; NAME/KEY: unsure
; LOCATION: 488
; OTHER INFORMATION: a, t, c, g, or other
US-09-534-856-18784

Query Match      100.0%; Score 15; DB 20; Length 510;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
    |||||
Db 185 CCTTCTCGCCCTGTT 171

RESULT 10
US-60-230-445-2923
; Sequence 2923. Application US/60230445
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000765
; CURRENT APPLICATION NUMBER: US/60/230,445
; CURRENT FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 3051
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2923
; LENGTH: 592
; TYPE: DNA
; ORGANISM: HUMAN
US-60-230-445-2923

Query Match      100.0%; Score 15; DB 67; Length 592;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
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Db 44 CCTTCTCGCCCTGTT 58

RESULT 11
US-09-948-933-4005/c
; Sequence 4005. Application US/09948933
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL000787
; CURRENT APPLICATION NUMBER: US/09/948,933
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231,399
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 6404
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4005
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-948-933-4005

Query Match      100.0%; Score 15; DB 35; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
    |||||
Db 226 CCTTCTCGCCCTGTT 212

RESULT 12
US-09-948-933-4006/c
; Sequence 4006. Application US/09948933
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL000787
; CURRENT APPLICATION NUMBER: US/09/948,933
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231,399
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 6404
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4006
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-948-933-4006

Query Match      100.0%; Score 15; DB 35; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
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Db 126 CCTTCTCGCCCTGTT 112

RESULT 13
US-09-948-933-4007/c
; Sequence 4007. Application US/09948933
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL000787
; CURRENT APPLICATION NUMBER: US/09/948,933
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231,399
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 6404
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4007
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-948-933-4007

Query Match      100.0%; Score 15; DB 35; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
    |||||
Db 226 CCTTCTCGCCCTGTT 212

RESULT 14
US-09-948-933-4008/c
; Sequence 4008. Application US/09948933
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
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Job time : 2562.5 secs

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GenCore version 5.1.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run On: December 11, 2002, 13:38:27 ; Search time 88 seconds  
(without alignments)  
122.513 Million cell updates/sec

Title: US-09-750-609-9  
Perfect score: 15  
Sequence: 1 ccttctgcctgtt 15

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	15	100.0	4338	5	US-09-724-676-24273
5	15	100.0	4848	5	US-09-724-676-24268
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7	15	100.0	5222	6	US-10-133-937-67
8	15	100.0	5589	5	US-09-724-676-24272
9	15	100.0	5589	5	US-09-724-676-24272
10	15	100.0	5642	5	US-09-724-676-24271
11	15	100.0	5642	5	US-09-724-676-24271
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14	15	100.0	6152	5	US-09-724-676-24266
15	15	100.0	6152	5	US-09-724-676-24266
16	13.4	89.3	236	6	US-10-284-498-14
17	13.4	89.3	352	6	US-09-513-999C-13316
18	13.4	89.3	1458	6	US-10-271-889-52
19	13.4	89.3	1565	6	US-10-201-365-22
20	13.4	89.3	1565	6	US-10-160-539A-24
21	13.4	89.3	2177	6	US-10-161-493-75
22	13.4	89.3	2520	6	US-10-264-237-1036
23	13.4	89.3	5128	6	US-10-284-499-2
24	13.4	89.3	5132	6	US-10-293-017-5
25	13.4	89.3	7430	1	PCT-US02-32727-4
26	13.4	89.3	7430	6	US-10-057-498-4

C	27	13.4	89.3	9377	6	US-10-274-994-3
	28	13.4	89.3	11547	1	PCT-US02-32727-86
	29	13.4	89.3	11547	6	US-10-057-498-86
C	30	13.4	89.3	13613	6	US-10-271-889-46
C	31	13.4	89.3	45000	1	PCT-US02-36692-12
C	32	13	86.7	1936	5	US-09-724-676-32136
C	33	13	86.7	1936	5	US-09-724-676A-32136
C	34	13	86.7	3590	5	US-09-724-676-24360
C	35	13	86.7	3590	5	US-09-724-676A-24360
C	36	13	86.7	276820	1	PCT-US02-32700-9
C	37	13	86.7	276820	6	US-10-271-416-9
C	38	12.4	82.7	237	5	US-09-513-999C-35434
C	39	12.4	82.7	248	5	US-09-620-607B-1245
C	40	12.4	82.7	261	5	US-09-513-999C-35759
C	41	12.4	82.7	319	5	US-09-513-999C-29349
C	42	12.4	82.7	353	5	US-09-513-999C-22349
C	43	12.4	82.7	354	5	US-09-513-999C-3109
C	44	12.4	82.7	476	6	US-10-203-138A-1480
C	45	12.4	82.7	480	5	US-09-724-676-45475

ALIGNMENTS

RESULT 1  
US-09-724-676-47407  
; Sequence 47407, Application US/09724676  
; GENERAL INFORMATION:  
; APPLICANT: CompuGen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 CompuGen  
; CURRENT APPLICATION NUMBER: US/09/724.676  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 47407  
; LENGTH: 2876  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676-47407

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Best Local Similarity 100.0%; Pred. No. 51;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTGCGCCTGTT 15  
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Db 1422 CCTTCTGCGCCTGTT 1436

RESULT 2  
US-09-724-676A-47407  
; Sequence 47407, Application US/09724676A  
; GENERAL INFORMATION:  
; APPLICANT: CompuGen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 CompuGen  
; CURRENT APPLICATION NUMBER: US/09/724.676A  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 47407  
; LENGTH: 2876  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676A-47407

Query Match 100.0%; Score 15; DB 5; Length 2876;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTGCGCCTGTT 15  
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Db 1422 CCTTCTCGCCCTGTT 1436

RESULT 3  
US-09-724-676-24273/c  
; Sequence 24273, Application US/09724676  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 24273  
; LENGTH: 4338  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676-24273

Query Match 100.0%; Score 15; DB 5; Length 4338;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15  
|||||

Db 2821 CCTTCTCGCCCTGTT 2807

RESULT 4  
US-09-724-676A-24273/c  
; Sequence 24273, Application US/09724676A  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676A  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 24273  
; LENGTH: 4338  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676A-24273

Query Match 100.0%; Score 15; DB 5; Length 4338;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15  
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Db 2821 CCTTCTCGCCCTGTT 2807

RESULT 5  
US-09-724-676-24268/c  
; Sequence 24268, Application US/09724676  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 24268  
; LENGTH: 4848  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676-24268

Query Match 100.0%; Score 15; DB 5; Length 4848;

Best Local Similarity 100.0%; Pred. No. 53;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15  
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Db 3331 CCTTCTCGCCCTGTT 3317

RESULT 6  
US-09-724-676A-24268/c  
; Sequence 24268, Application US/09724676A  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676A  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 24268  
; LENGTH: 4848  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676A-24268

Query Match 100.0%; Score 15; DB 5; Length 4848;  
Best Local Similarity 100.0%; Pred. No. 53;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15  
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Db 3331 CCTTCTCGCCCTGTT 3317

RESULT 7  
US-10-133-937-67/c  
; Sequence 67, Application US/10133937  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Javed  
; APPLICANT: Ringner, Markus  
; APPLICANT: Peterson, Carsten  
; APPLICANT: Meltzer, Paul  
; TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,  
; DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND  
; TITLE OF INVENTION: OTHER BIOLOGICAL STATES  
; FILE REFERENCE: 11613.56US01  
; CURRENT APPLICATION NUMBER: US/10/133.937  
; CURRENT FILING DATE: 2002-11-04  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 67  
; LENGTH: 5222  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-133-937-67

Query Match 100.0%; Score 15; DB 6; Length 5222;  
Best Local Similarity 100.0%; Pred. No. 53;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15  
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Db 2749 CCTTCTCGCCCTGTT 2735

RESULT 8  
US-09-724-676-24272/c  
; Sequence 24272, Application US/09724676  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676



; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 24272  
; LENGTH: 5589  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676-24272

Query Match 100.0%; Score 15; DB 5; Length 5589;  
Best Local Similarity 100.0%; Pred. No. 53;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15  
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Db 2821 CCTTCTCGCCCTGTT 2807

## RESULT 9

US-09-724-676A-24272/c  
; Sequence 24272, Application US/09724676A  
; GENERAL INFORMATION:

; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724, 676A  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 24272  
; LENGTH: 5589  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676A-24272

Query Match 100.0%; Score 15; DB 5; Length 5589;  
Best Local Similarity 100.0%; Pred. No. 53;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15  
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Db 2821 CCTTCTCGCCCTGTT 2807

## RESULT 10

US-09-724-676-24271/c  
; Sequence 24271, Application US/09724676  
; GENERAL INFORMATION:

; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724, 676  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 24271  
; LENGTH: 5642  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676-24271

Query Match 100.0%; Score 15; DB 5; Length 5642;  
Best Local Similarity 100.0%; Pred. No. 53;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15  
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Db 2821 CCTTCTCGCCCTGTT 2807

## RESULT 11

US-09-724-676A-24271/c  
; Sequence 24271, Application US/09724676A

; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724, 676A  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 24271  
; LENGTH: 5642  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676A-24271

Query Match 100.0%; Score 15; DB 5; Length 5642;  
Best Local Similarity 100.0%; Pred. No. 53;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15  
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Db 2821 CCTTCTCGCCCTGTT 2807

## RESULT 12

US-09-724-676-24267/c  
; Sequence 24267, Application US/09724676  
; GENERAL INFORMATION:

; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724, 676  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 24267  
; LENGTH: 6099  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676-24267

Query Match 100.0%; Score 15; DB 5; Length 6099;  
Best Local Similarity 100.0%; Pred. No. 53;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15  
|||||  
Db 3331 CCTTCTCGCCCTGTT 3317

## RESULT 13

US-09-724-676A-24267/c  
; Sequence 24267, Application US/09724676A  
; GENERAL INFORMATION:

; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724, 676A  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 24267  
; LENGTH: 6099  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676A-24267

Query Match 100.0%; Score 15; DB 5; Length 6099;  
Best Local Similarity 100.0%; Pred. No. 53;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15  
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Db 3331 CCTTCTCGCCCTGTT 3317

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; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24266
; LENGTH: 6152
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-24266

Query Match      100.0%; Score 15; DB 5; Length 6152;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
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Db 3331 CCTTCTCGCCCTGTT 3317

RESULT 15
US-09-724-676A-24266/c
; Sequence 24266, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24266
; LENGTH: 6152
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-24266

Query Match      100.0%; Score 15; DB 5; Length 6152;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
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Db 3331 CCTTCTCGCCCTGTT 3317

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GenCore version 5.1.3  
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Title: US-09-750-609-9

Perfect score: 15

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- 73: /cgn2\_6/ptodata/2/pna/US6029\_COMB.seq.\*
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- 77: /cgn2\_6/ptodata/2/pna/US6033\_COMB.seq.\*
- 78: /cgn2\_6/ptodata/2/pna/US6034\_COMB.seq.\*
- 79: /cgn2\_6/ptodata/2/pna/US6035\_COMB.seq.\*
- 80: /cgn2\_6/ptodata/2/pna/US6036\_COMB.seq.\*
- 81: /cgn2\_6/ptodata/2/pna/US6037\_COMB.seq.\*
- 82: /cgn2\_6/ptodata/2/pna/US6038\_COMB.seq.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	15	100.0	15	1	PCT-US00-35491-9
2	15	100.0	15	29	US-09-750-609-9
3	15	100.0	15	61	US-60-173-682-9
4	15	100.0	257	18	US-09-440-302A-470
5	15	100.0	257	18	US-09-440-302B-470
6	15	100.0	258	18	US-09-440-302-470
7	15	100.0	258	18	US-09-442-366A-309
8	15	100.0	472	27	US-09-698-012-481
9	15	100.0	510	20	US-09-534-856-18784
10	15	100.0	592	67	US-60-230-445-2923
11	15	100.0	601	35	US-09-948-933-4006
12	15	100.0	601	35	US-09-948-933-4006
13	15	100.0	601	35	US-09-948-933-4007
14	15	100.0	601	35	US-09-948-933-4008
15	15	100.0	817	24	US-09-634-306B-7016
16	15	100.0	817	24	US-09-634-306B-7017
17	15	100.0	817	38	US-10-027-632-7016
18	15	100.0	817	38	US-10-027-632-7017
19	15	100.0	920	61	US-60-175-854-99
20	15	100.0	920	61	US-60-175-854-104
21	15	100.0	980	1	PCT-US00-35491-15

22	15	100.0	980	1	PCT-US02-25060-1	Sequence 1, Appli	95	14	93.3	271	16	US-09-250-002B-711	Sequence 711, App
23	15	100.0	980	29	US-09-750-609-15	Sequence 15, Appl	96	14	93.3	271	20	US-09-534-846B-24502	Sequence 24502, A
24	15	100.0	980	42	US-10-213-948-1	Sequence 1, Appli	97	14	93.3	272	16	US-09-250-002B-1380	Sequence 1380, Ap
25	15	100.0	980	61	US-60-173-682-15	Sequence 15, Appl	98	14	93.3	272	20	US-09-534-846B-24519	Sequence 24519, A
c 26	15	100.0	1044	1	PCT-US01-08631-16550	Sequence 16550, A	99	14	93.3	272	19	US-09-500-900-1749	Sequence 1749, Ap
c 27	15	100.0	1093	29	US-09-758-168-90	Sequence 90, Appl	100	14	93.3	274	20	US-09-534-846B-24528	Sequence 24528, A
c 28	15	100.0	1093	42	US-10-211-625-90	Sequence 90, Appl	101	14	93.3	274	56	US-60-120-015-1749	Sequence 1749, Ap
c 29	15	100.0	1209	39	US-10-098-754-16300	Sequence 16300, A	102	14	93.3	275	20	US-09-534-846B-24498	Sequence 24498, A
c 30	15	100.0	1462	16	US-09-270-849B-35413	Sequence 35413, A	103	14	93.3	281	15	US-09-148-483-204	Sequence 204, App
c 31	15	100.0	1573	65	US-60-213-177-929	Sequence 929, App	104	14	93.3	281	15	US-09-534-846B-24514	Sequence 24514, A
c 32	15	100.0	1591	65	US-60-213-177-926	Sequence 926, App	105	14	93.3	281	49	US-60-058-920-204	Sequence 204, App
c 33	15	100.0	1597	65	US-60-213-177-928	Sequence 928, App	106	14	93.3	289	18	US-09-420-691-1257	Sequence 1257, Ap
c 34	15	100.0	1606	65	US-60-213-177-927	Sequence 927, App	107	14	93.3	289	20	US-09-534-846B-24518	Sequence 24518, A
c 35	15	100.0	1831	65	US-60-213-177-1027	Sequence 1027, Ap	108	14	93.3	291	20	US-09-534-846B-24503	Sequence 24503, A
c 36	15	100.0	1854	1	PCT-US00-35491-1	Sequence 1, Appli	109	14	93.3	291	58	US-60-141-584-356	Sequence 356, App
c 37	15	100.0	1854	1	PCT-US00-35491-11	Sequence 11, Appl	110	14	93.3	293	20	US-09-534-846B-940	Sequence 940, App
c 38	15	100.0	1854	29	US-09-750-609-11	Sequence 11, Appli	111	14	93.3	298	20	US-09-534-846B-24517	Sequence 24517, A
c 39	15	100.0	1854	29	US-09-750-609-11	Sequence 11, Appli	112	14	93.3	302	18	US-09-420-691-1364	Sequence 1364, Ap
c 40	15	100.0	1854	61	US-60-173-682-1	Sequence 1, Appli	113	14	93.3	302	20	US-09-534-846B-24499	Sequence 24499, A
c 41	15	100.0	1854	61	US-60-173-682-11	Sequence 11, Appl	114	14	93.3	309	15	US-09-128-809-600	Sequence 600, App
c 42	15	100.0	1983	3	US-07-676-980B-1	Sequence 1, Appli	115	14	93.3	309	24	US-09-534-846B-24512	Sequence 1056, Ap
c 43	15	100.0	1983	18	US-09-440-302A-1067	Sequence 1067, Ap	116	14	93.3	345	24	US-09-625-102-1056	Sequence 861, App
c 44	15	100.0	1983	18	US-09-440-302B-1067	Sequence 1067, Ap	117	14	93.3	359	28	US-09-704-424-861	Sequence 861, App
c 45	15	100.0	2049	61	US-60-172-373-18619	Sequence 18619, A	118	14	93.3	372	13	US-08-971-197-5159	Sequence 5159, Ap
c 46	15	100.0	2128	67	US-60-230-445-2244	Sequence 2244, Ap	119	14	93.3	372	13	US-08-971-197-5159	Sequence 5159, Ap
c 47	15	100.0	2136	35	US-09-948-933-117	Sequence 117, App	120	14	93.3	426	57	US-60-138-830-146	Sequence 146, App
c 48	15	100.0	5161	18	US-09-442-589B-881	Sequence 881, App	121	14	93.3	435	5	US-08-187-634-8	Sequence 8, Appli
c 49	15	100.0	5204	36	US-09-971-392-159	Sequence 159, App	122	14	93.3	435	57	US-60-132-861-1244	Sequence 1244, Ap
c 50	15	100.0	5204	67	US-60-237-652-159	Sequence 159, App	123	14	93.3	435	57	US-60-125-817-5173	Sequence 5173, Ap
c 51	15	100.0	5204	71	US-60-278-258-10692	Sequence 10692, A	124	14	93.3	446	22	US-09-570-582B-108	Sequence 108, App
c 52	15	100.0	5205	76	US-60-324-185-14003	Sequence 14003, A	125	14	93.3	486	22	US-09-570-582B-108	Sequence 108, App
c 53	15	100.0	5297	25	US-09-644-867-7621	Sequence 7621, Ap	126	14	93.3	487	25	US-09-654-617-174767	Sequence 174767, A
c 54	15	100.0	5497	26	US-09-663-693-1074	Sequence 1074, Ap	127	14	93.3	487	25	US-09-684-016-174767	Sequence 174767, A
c 55	15	100.0	5497	27	US-09-698-010-14461	Sequence 14461, A	128	14	93.3	500	18	US-09-404-520-22058	Sequence 22058, A
c 56	15	100.0	5497	27	US-09-698-012-8717	Sequence 8717, Ap	129	14	93.3	514	27	US-09-698-012-4153	Sequence 4153, Ap
c 57	15	100.0	5497	28	US-09-699-997-11832	Sequence 11832, A	130	14	93.3	526	52	US-60-082-300-12476	Sequence 12476, A
c 58	15	100.0	5497	28	US-09-710-285-2191	Sequence 2191, Ap	131	14	93.3	537	25	US-09-654-617-33652	Sequence 33652, A
c 59	15	100.0	5497	28	US-09-716-473-2179	Sequence 2179, Ap	132	14	93.3	537	27	US-09-684-016-33652	Sequence 33652, A
c 60	15	100.0	5497	29	US-09-726-175-3362	Sequence 3362, Ap	133	14	93.3	552	20	US-09-534-847-23771	Sequence 23771, A
c 61	15	100.0	5497	29	US-09-726-175-1305	Sequence 1305, Ap	134	14	93.3	556	20	US-09-534-847-23674	Sequence 23674, A
c 62	15	100.0	5547	61	US-60-172-373-9131	Sequence 9131, Ap	135	14	93.3	562	20	US-09-534-847-23613	Sequence 23613, A
c 63	15	100.0	12331	24	US-09-620-392-35471	Sequence 35471, A	136	14	93.3	592	57	US-60-132-861-2848	Sequence 2848, Ap
c 64	15	100.0	29748	19	US-09-528-237A-279	Sequence 279, App	137	14	93.3	595	20	US-09-534-847-23636	Sequence 23636, A
c 65	15	100.0	50050	35	US-09-948-933-535	Sequence 535, App	138	14	93.3	655	1	PCT-US01-18569-2083	Sequence 2083, Ap
c 66	15	100.0	63038	24	US-09-620-392-37557	Sequence 37557, A	139	14	93.3	655	43	US-60-126-265-706	Sequence 706, App
c 67	15	100.0	108634	31	US-09-702-134-6961	Sequence 6961, Ap	140	14	93.3	656	56	US-09-634-306B-199074	Sequence 199074, A
c 68	15	100.0	108634	31	US-09-815-264-6252	Sequence 6252, A	141	14	93.3	659	24	US-09-634-306B-199075	Sequence 199075, A
c 69	14	93.3	215	20	US-09-534-846B-35357	Sequence 35357, A	142	14	93.3	659	24	US-09-634-306B-199076	Sequence 199076, A
c 70	14	93.3	215	53	US-60-096-664-879	Sequence 879, App	143	14	93.3	659	38	US-10-027-632-199074	Sequence 199074, A
c 71	14	93.3	228	15	US-09-113-753-13	Sequence 13, Appl	144	14	93.3	659	38	US-10-027-632-199075	Sequence 199075, A
c 72	14	93.3	228	20	US-09-534-846B-24527	Sequence 24527, A	145	14	93.3	664	62	US-60-180-489-3756	Sequence 3756, Ap
c 73	14	93.3	228	49	US-60-052-200-13	Sequence 13, Appl	146	14	93.3	664	62	US-60-180-489-3756	Sequence 3756, Ap
c 74	14	93.3	231	12	US-08-843-950-124	Sequence 124, App	147	14	93.3	674	23	US-09-604-693A-287	Sequence 287, App
c 75	14	93.3	231	21	US-09-540-229-54274	Sequence 54274, A	148	14	93.3	708	29	US-09-634-306B-199075	Sequence 199075, A
c 76	14	93.3	231	45	US-60-015-716-124	Sequence 124, App	149	14	93.3	742	18	US-09-408-626-534	Sequence 534, App
c 77	14	93.3	242	15	US-09-113-753-325	Sequence 325, App	150	14	93.3	831	23	US-09-604-693A-285	Sequence 285, App
c 78	14	93.3	242	20	US-09-534-846B-24524	Sequence 24524, A	151	14	93.3	1062	57	US-60-138-103-2116	Sequence 2116, Ap
c 79	14	93.3	242	49	US-60-052-200-325	Sequence 325, App	152	14	93.3	1322	42	US-10-219-999-18257	Sequence 18257, A
c 80	14	93.3	248	15	US-09-114-053-1084	Sequence 1084, Ap	153	14	93.3	1371	80	US-60-360-039-27932	Sequence 27932, A
c 81	14	93.3	248	18	US-09-420-691-4257	Sequence 4257, Ap	154	14	93.3	1437	80	US-60-360-039-23840	Sequence 23840, A
c 82	14	93.3	248	20	US-09-534-846B-24522	Sequence 24522, A	155	14	93.3	1553	80	US-60-360-039-23840	Sequence 23840, A
c 83	14	93.3	253	16	US-09-250-002B-833	Sequence 833, App	156	14	93.3	1582	16	US-09-270-767-15487	Sequence 15487, A
c 84	14	93.3	253	20	US-09-534-846B-24525	Sequence 24525, A	157	14	93.3	1989	4	US-08-074-893-1	Sequence 1, Appli
c 85	14	93.3	255	15	US-09-112-577-248	Sequence 248, App	158	14	93.3	1992	4	US-08-074-893-3	Sequence 3, Appli
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c 88	14	93.3	258	17	US-09-304-517A-151972	Sequence 151972, A	161	14	93.3	2036	61	US-60-173-464-12259	Sequence 12259, A
c 89	14	93.3	258	17	US-09-371-146A-151972	Sequence 151972, A	162	14	93.3	2036	63	US-60-191-637-15019	Sequence 15019, A
c 90	14	93.3	258	37	US-09-985-678-151972	Sequence 151972, A	163	14	93.3	2036	63	US-60-191-681-11854	Sequence 11854, A
c 91	14	93.3	265	15	US-09-129-873-3790	Sequence 3790, Ap	164	14	93.3	2397	3	US-07-627-950A-5	Sequence 5, Appli
c 92	14	93.3	265	20	US-09-534-846B-24496	Sequence 24496, A	165	14	93.3	2397	5	US-08-187-634-1	Sequence 1, Appli
c 93	14	93.3	270	16	US-09-250-002B-526	Sequence 526, App	166	14	93.3	2397	13	US-08-912-332-5	Sequence 5, Appli
c 94	14	93.3	270	20	US-09-534-846B-24495	Sequence 24495, A	167	14	93.3	2397	13	US-08-912-332-5	Sequence 5, Appli

c 168	14	93.3	3478	80	US-60-360-207-10993	Sequence 10993, A	c 241	13	86.7	99	26	US-09-669-817A-834	Sequence 834, App
c 169	14	93.3	3475	80	US-60-360-207-8748	Sequence 8748, Ap	242	13	86.7	117	23	US-09-619-643-12724	Sequence 12724, A
c 170	14	93.3	3479	18	US-09-404-520-15283	Sequence 15283, A	243	13	86.7	117	25	US-09-654-617-340657	Sequence 340657,
c 171	14	93.3	5031	23	US-09-614-150-14974	Sequence 14974, A	244	13	86.7	117	27	US-09-684-016-340857	Sequence 340857,
c 172	14	93.3	5031	60	US-60-167-217-15040	Sequence 15040, A	245	13	86.7	117	58	US-60-145-485-7789	Sequence 7789, Ap
c 173	14	93.3	5031	61	US-60-173-464-12258	Sequence 12258, A	246	13	86.7	135	60	US-60-164-378-482	Sequence 482, App
c 174	14	93.3	5031	63	US-60-191-637-15018	Sequence 15018, A	247	13	86.7	160	16	US-09-270-849B-23230	Sequence 23230, A
c 175	14	93.3	5031	63	US-60-191-681-11853	Sequence 11853, A	248	13	86.7	197	25	US-09-654-617-237248	Sequence 237248,
c 176	14	93.3	8005	64	US-60-207-361-6	Sequence 6, Appl1	249	13	86.7	197	27	US-09-684-016-237248	Sequence 237248,
c 177	14	93.3	23369	24	US-09-620-392-21337	Sequence 21337, A	250	13	86.7	204	30	US-09-760-466-159	Sequence 159, App
c 178	14	93.3	28237	19	US-09-528-237A-692	Sequence 692, App	251	13	86.7	204	30	US-09-760-466-629	Sequence 629, App
c 179	14	93.3	32383	68	US-60-248-592-44	Sequence 44, Appl	252	13	86.7	204	30	US-09-760-495-444	Sequence 444, App
c 180	14	93.3	32768	67	US-60-234-446-211	Sequence 211, App	253	13	86.7	204	40	US-10-143-775-454	Sequence 444, App
c 181	14	93.3	35442	28	US-09-702-134-6392	Sequence 6392, A	254	13	86.7	204	42	US-10-212-083-159	Sequence 159, App
c 182	14	93.3	35442	31	US-09-815-264-80318	Sequence 80318, A	255	13	86.7	204	42	US-10-212-083-629	Sequence 629, App
c 183	14	93.3	45355	33	US-09-897-516-436	Sequence 436, App	256	13	86.7	223	33	US-09-865-439A-56447	Sequence 56447, A
c 184	14	93.3	45355	33	US-09-897-516-437	Sequence 437, App	257	13	86.7	223	34	US-60-207-458-100610	Sequence 100610,
c 185	14	93.3	45355	33	US-09-897-516-438	Sequence 438, App	258	13	86.7	224	31	US-09-821-837-6070	Sequence 6070, Ap
c 186	14	93.3	45355	33	US-09-897-516-3725	Sequence 3725, Ap	259	13	86.7	233	16	US-09-298-328A-751	Sequence 751, App
c 187	14	93.3	45355	33	US-09-897-516-3726	Sequence 3726, Ap	260	13	86.7	233	52	US-60-085-147-751	Sequence 751, App
c 188	14	93.3	45355	33	US-09-897-516-3727	Sequence 3727, Ap	261	13	86.7	234	17	US-09-362-510-24581	Sequence 24581, A
c 189	14	93.3	45355	33	US-09-897-516-3728	Sequence 3728, Ap	262	13	86.7	234	17	US-09-362-510A-24581	Sequence 24581, A
c 190	14	93.3	45355	33	US-09-897-516-3729	Sequence 3729, Ap	263	13	86.7	234	34	US-09-904-013-24581	Sequence 24581, A
c 191	14	93.3	45355	33	US-09-897-516-3730	Sequence 3730, Ap	264	13	86.7	244	69	US-60-252-833-32705	Sequence 32705, A
c 192	14	93.3	45355	33	US-09-897-516-3731	Sequence 3731, Ap	265	13	86.7	250	21	US-09-540-212A-56729	Sequence 56729, A
c 193	14	93.3	45355	33	US-09-897-516-3732	Sequence 3732, Ap	266	13	86.7	258	16	US-09-270-849B-163161	Sequence 163161,
c 194	14	93.3	45355	33	US-09-897-516-3733	Sequence 3733, Ap	267	13	86.7	262	14	US-09-092-505-2737	Sequence 2737, Ap
c 195	14	93.3	45355	33	US-09-897-516-3734	Sequence 3734, Ap	268	13	86.7	262	21	US-09-540-212A-31327	Sequence 31327, A
c 196	14	93.3	45355	33	US-09-897-516-3735	Sequence 3735, Ap	269	13	86.7	265	27	US-09-692-257A-9085	Sequence 9085, Ap
c 197	14	93.3	45355	33	US-09-897-516-3736	Sequence 3736, Ap	270	13	86.7	265	60	US-60-162-747-8591	Sequence 8591, Ap
c 198	14	93.3	45355	33	US-09-897-516-3737	Sequence 3737, Ap	271	13	86.7	269	17	US-09-313-294A-3136	Sequence 3136, Ap
c 199	14	93.3	45355	33	US-09-897-516-3738	Sequence 3738, Ap	272	13	86.7	269	52	US-60-086-722-3136	Sequence 3136, Ap
c 200	14	93.3	45355	33	US-09-897-516-3739	Sequence 3739, Ap	273	13	86.7	272	26	US-09-663-779-7346	Sequence 7346, Ap
c 201	14	93.3	45355	33	US-09-897-516-3740	Sequence 3740, Ap	274	13	86.7	272	57	US-60-138-103-13500	Sequence 13500, A
c 202	14	93.3	45355	33	US-09-897-516-3741	Sequence 3741, Ap	275	13	86.7	278	62	US-60-185-215-4073	Sequence 4073, Ap
c 203	14	93.3	45355	33	US-09-897-516-3742	Sequence 3742, Ap	276	13	86.7	281	32	US-09-834-366-36983	Sequence 36983, A
c 204	14	93.3	45355	33	US-09-897-516-3743	Sequence 3743, Ap	277	13	86.7	281	63	US-60-197-873-36983	Sequence 36983, A
c 205	14	93.3	45355	33	US-09-897-516-3744	Sequence 3744, Ap	278	13	86.7	282	26	US-09-669-817A-24620	Sequence 24620, A
c 206	14	93.3	45355	65	US-60-215-161-436	Sequence 436, App	279	13	86.7	283	21	US-09-540-213-30696	Sequence 30696, A
c 207	14	93.3	45355	65	US-60-215-161-437	Sequence 437, App	280	13	86.7	283	69	US-60-256-867-1671	Sequence 1671, Ap
c 208	14	93.3	45355	65	US-60-215-161-438	Sequence 438, App	281	13	86.7	286	65	US-60-213-178-972	Sequence 972, App
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c 210	14	93.3	45355	65	US-60-215-161-3725	Sequence 3725, Ap	283	13	86.7	299	25	US-09-654-617-314284	Sequence 314284,
c 211	14	93.3	45355	65	US-60-215-161-3727	Sequence 3727, Ap	284	13	86.7	299	27	US-09-684-016-314284	Sequence 314284,
c 212	14	93.3	45355	65	US-60-215-161-3728	Sequence 3728, Ap	285	13	86.7	302	64	US-60-207-458-6136	Sequence 6136, Ap
c 213	14	93.3	45355	65	US-60-215-161-3729	Sequence 3729, Ap	286	13	86.7	308	25	US-09-654-617-280771	Sequence 280771,
c 214	14	93.3	45355	65	US-60-215-161-3730	Sequence 3730, Ap	287	13	86.7	308	27	US-09-684-016-280771	Sequence 280771,
c 215	14	93.3	45355	65	US-60-215-161-3731	Sequence 3731, Ap	288	13	86.7	310	17	US-09-394-745-324	Sequence 324, App
c 216	14	93.3	45355	65	US-60-215-161-3732	Sequence 3732, Ap	289	13	86.7	310	22	US-09-565-306-6	Sequence 6, Appl1
c 217	14	93.3	45355	65	US-60-215-161-3733	Sequence 3733, Ap	290	13	86.7	314	69	US-60-253-652-15165	Sequence 15165, A
c 218	14	93.3	45355	65	US-60-215-161-3734	Sequence 3734, Ap	291	13	86.7	339	69	US-60-256-867-1730	Sequence 1730, Ap
c 219	14	93.3	45355	65	US-60-215-161-3735	Sequence 3735, Ap	292	13	86.7	350	26	US-09-666-355A-5732	Sequence 5732, Ap
c 220	14	93.3	45355	65	US-60-215-161-3736	Sequence 3736, Ap	293	13	86.7	358	17	US-09-362-510-13987	Sequence 13987, A
c 221	14	93.3	45355	65	US-60-215-161-3737	Sequence 3737, Ap	294	13	86.7	358	17	US-09-362-510A-13987	Sequence 13987, A
c 222	14	93.3	45355	65	US-60-215-161-3738	Sequence 3738, Ap	295	13	86.7	358	34	US-09-904-013-13987	Sequence 13987, A
c 223	14	93.3	45355	65	US-60-215-161-3739	Sequence 3739, Ap	296	13	86.7	361	17	US-09-397-424-2325	Sequence 2325, Ap
c 224	14	93.3	45355	65	US-60-215-161-3740	Sequence 3740, Ap	297	13	86.7	361	17	US-09-397-424A-2325	Sequence 2325, Ap
c 225	14	93.3	45355	65	US-60-215-161-3741	Sequence 3741, Ap	298	13	86.7	368	25	US-09-654-617-310872	Sequence 310872,
c 226	14	93.3	45355	65	US-60-215-161-3742	Sequence 3742, Ap	299	13	86.7	368	27	US-09-684-016-310872	Sequence 310872,
c 227	14	93.3	45355	65	US-60-215-161-3743	Sequence 3743, Ap	300	13	86.7	374	1	PCT-US01-01354-24230	Sequence 24230, A
c 228	14	93.3	45355	65	US-60-215-161-3744	Sequence 3744, Ap	301	13	86.7	374	1	PCT-US01-01354-24231	Sequence 24231, A
c 229	14	93.3	70665	1	PCT-US02-02176-850	Sequence 850, App	302	13	86.7	374	16	US-09-235-076-37637	Sequence 37637, A
c 230	14	93.3	264792	68	US-60-245-228-44	Sequence 44, Appl	303	13	86.7	374	16	US-09-277-227-16269	Sequence 16269, A
c 231	14	93.3	1090936	14	US-09-012-031-308	Sequence 308, App	304	13	86.7	374	17	US-09-332-782-37637	Sequence 37637, A
c 232	14	93.3	1090936	14	US-09-012-031B-308	Sequence 308, App	305	13	86.7	374	29	US-09-737-223-37637	Sequence 37637, A
c 233	14	93.3	1090936	14	US-09-012-031C-308	Sequence 308, App	306	13	86.7	374	30	US-09-764-905-24230	Sequence 24230, A
c 234	14	93.3	1090936	17	US-09-335-032-12210	Sequence 12210, A	307	13	86.7	374	34	US-09-909-627-16269	Sequence 16269, A
c 235	13	86.7	24	42	US-10-239-316-56	Sequence 56, Appl	308	13	86.7	374	34	US-09-918-995-37637	Sequence 37637, A
c 236	13	86.7	25	36	US-09-954-427-66715	Sequence 66715, A	309	13	86.7	374	34	US-10-092-399-24230	Sequence 24230, A
c 237	13	86.7	25	67	US-60-233-166-66715	Sequence 66715, A	310	13	86.7	374	39	US-10-092-399-24231	Sequence 24231, A
c 238	13	86.7	25	79	US-60-353-987-809837	Sequence 809837,	311	13	86.7	379	19	US-09-521-640-63009	Sequence 63009, A
c 239	13	86.7	70	33	US-09-874-708A-31751	Sequence 31751, A	312	13	86.7	379	23	US-09-605-698-8174	Sequence 8174, Ap
c 240	13	86.7	70	65	US-60-211-750-31307	Sequence 31307, A	313	13	86.7	379			

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316	13	86.7	386	61	US-60-171-432-10979	Sequence 10979, A	c 389	13	86.7	483	22	US-09-572-409-26925	Sequence 26925, A
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318	13	86.7	390	58	US-60-140-769-11531	Sequence 11531, A	391	13	86.7	484	35	US-09-933-524-110397	Sequence 110397, A
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321	13	86.7	393	16	US-09-248-797-22456	Sequence 22456, A	c 394	13	86.7	485	18	US-09-400-122A-22	Sequence 22, Appl
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323	13	86.7	393	26	US-09-669-817A-27412	Sequence 27412, A	c 396	13	86.7	489	62	US-60-182-467-1094	Sequence 1094, Ap
324	13	86.7	393	27	US-09-684-016-426485	Sequence 426485, A	397	13	86.7	489	62	US-60-182-467-1094	Sequence 1094, Ap
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327	13	86.7	400	30	US-09-764-905-2126	Sequence 2126, Ap	c 400	13	86.7	496	64	US-60-207-458-137089	Sequence 137089, A
328	13	86.7	400	39	US-10-092-399-2126	Sequence 2126, Ap	c 401	13	86.7	497	18	US-09-400-122A-24	Sequence 24, Appl
329	13	86.7	402	31	US-09-821-837-6779	Sequence 6779, Ap	c 402	13	86.7	498	61	US-60-170-870-610	Sequence 610, App
330	13	86.7	408	57	US-60-135-952-4795	Sequence 4795, Ap	c 403	13	86.7	499	26	US-09-669-817A-29366	Sequence 29366, A
331	13	86.7	414	27	US-09-692-257A-548	Sequence 548, App	c 404	13	86.7	501	28	US-09-710-282-336	Sequence 336, App
332	13	86.7	414	60	US-60-162-747-510	Sequence 510, App	c 405	13	86.7	501	38	US-10-029-386-11356	Sequence 11356, A
333	13	86.7	415	19	US-09-528-409-85841	Sequence 85841, A	c 406	13	86.7	501	38	US-10-029-386-11356	Sequence 11356, A
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339	13	86.7	416	56	US-60-128-436-112	Sequence 112, App	412	13	86.7	508	32	US-60-197-873-9089	Sequence 9089, Ap
340	13	86.7	418	26	US-09-669-817A-26056	Sequence 26056, A	c 413	13	86.7	510	25	US-09-654-617-127482	Sequence 127482, A
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342	13	86.7	420	57	US-60-132-861-243	Sequence 243, App	c 415	13	86.7	512	52	US-60-082-300-1817	Sequence 1817, Ap
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351	13	86.7	426	26	US-09-675-784A-2644	Sequence 2644, Ap	424	13	86.7	526	63	US-60-196-713-1031	Sequence 1031, Ap
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353	13	86.7	426	27	US-09-808-383-1314	Sequence 1314, Ap	426	13	86.7	526	63	US-60-196-713-1033	Sequence 1033, Ap
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355	13	86.7	435	21	US-09-540-215-2493	Sequence 2493, Ap	428	13	86.7	526	63	US-60-196-714-147	Sequence 147, App
356	13	86.7	435	21	US-09-654-617-417934	Sequence 417934, A	429	13	86.7	526	63	US-60-196-714-303	Sequence 303, App
357	13	86.7	435	26	US-09-669-817A-40152	Sequence 40152, A	c 430	13	86.7	531	19	US-09-526-263A-1118	Sequence 1118, App
358	13	86.7	435	27	US-09-684-016-417934	Sequence 417934, A	c 431	13	86.7	531	19	US-09-526-263A-1118	Sequence 1118, App
359	13	86.7	436	18	US-09-421-016-25908	Sequence 25908, A	432	13	86.7	536	39	US-60-196-714-362	Sequence 362, App
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362	13	86.7	436	22	US-09-552-087B-18094	Sequence 18094, A	c 435	13	86.7	544	42	US-10-256-174-300	Sequence 300, App
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370	13	86.7	445	13	US-08-975-985-2116	Sequence 2116, Ap	c 443	13	86.7	570	18	US-09-417-507-18190	Sequence 18190, A
371	13	86.7	445	62	US-60-182-094-445	Sequence 445, App	c 444	13	86.7	572	22	US-09-565-309A-8768	Sequence 8768, Ap
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373	13	86.7	447	16	US-09-252-991A-11703	Sequence 11703, A	c 446	13	86.7	580	61	US-60-172-375-8217	Sequence 8217, Ap
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376	13	86.7	455	16	US-09-248-797-33261	Sequence 33261, A	c 449	13	86.7	582	22	US-09-565-309A-8766	Sequence 391883, A
377	13	86.7	455	17	US-09-332-782-14723	Sequence 14723, A	c 450	13	86.7	582	22	US-09-565-309A-8766	Sequence 391883, A
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379	13	86.7	455	34	US-09-918-995-14723	Sequence 14723, A	c 452	13	86.7	610	19	US-09-505-532-17429	Sequence 359, App
380	13	86.7	455	34	US-09-925-564-33261	Sequence 33261, A	c 453	13	86.7	610	31	US-09-819-091A-17429	Sequence 17429, A
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382	13	86.7	464	28	US-09-704-424-25504	Sequence 25504, A	c 455	13	86.7	624	63	US-60-196-718-1250	Sequence 1250, Ap
383	13	86.7	466	25	US-09-873-402A-75923	Sequence 75923, A	c 456	13	86.7	624	64	US-60-207-458-26435	Sequence 26435, A
384	13	86.7	466	25	US-09-654-617-185194	Sequence 185194, A	c 457	13	86.7	625	61	US-60-170-869-155	Sequence 155, App
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461	13	86.7	636	60	US-60-162-356-307	Sequence 307, App	534	13	86.7	1261	65	US-60-212-656-621	Sequence 621, App
462	13	86.7	636	60	US-60-163-232-830	Sequence 830, App	535	13	86.7	1261	67	US-60-230-435-2363	Sequence 2363, App
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464	13	86.7	636	60	US-60-169-842-2170	Sequence 2170, App	537	13	86.7	1323	1	PCT-US02-13142-6086	Sequence 6086, App
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466	13	86.7	643	69	US-60-256-867-1769	Sequence 1769, App	539	13	86.7	1336	23	US-09-614-150-4055	Sequence 4055, App
467	13	86.7	644	69	US-60-256-867-1738	Sequence 1738, App	540	13	86.7	1336	23	US-09-619-049-227	Sequence 227, App
468	13	86.7	647	39	US-09-317-311C-117	Sequence 117, App	541	13	86.7	1336	61	US-60-171-627-332	Sequence 332, App
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c 470	13	86.7	650	25	US-09-654-617-271571	Sequence 271571,	543	13	86.7	1336	63	US-60-191-637-4070	Sequence 4070, App
c 471	13	86.7	650	27	US-09-684-016-271571	Sequence 271571,	544	13	86.7	1336	63	US-60-191-681-3254	Sequence 3254, App
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476	13	86.7	685	52	US-60-082-300-6301	Sequence 6301, App	549	13	86.7	1425	16	US-09-252-991A-11848	Sequence 11848, A
c 477	13	86.7	690	29	US-09-739-449-6263	Sequence 6263, App	550	13	86.7	1440	34	US-09-902-540-9640	Sequence 9640, App
c 478	13	86.7	690	31	US-09-803-110-6263	Sequence 6263, App	551	13	86.7	1446	16	US-09-252-991A-11593	Sequence 11593, A
c 479	13	86.7	702	80	US-60-360-207-33052	Sequence 33052, A	552	13	86.7	1501	31	US-09-815-264-25351	Sequence 25351, A
c 480	13	86.7	716	18	US-09-471-275-10264	Sequence 10264, A	553	13	86.7	1501	31	US-09-815-264-32361	Sequence 32361, A
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c 482	13	86.7	738	18	US-09-417-507-11581	Sequence 11581, A	555	13	86.7	1535	65	US-60-213-178-22	Sequence 22, Appl
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484	13	86.7	738	75	US-60-316-362-2086	Sequence 2086, App	557	13	86.7	1581	38	US-10-015-127-8942	Sequence 8942, App
c 485	13	86.7	740	18	US-09-404-520-25007	Sequence 25007, A	558	13	86.7	1584	80	US-60-360-039-41456	Sequence 41456, A
c 486	13	86.7	753	26	US-09-675-784A-2277	Sequence 2277, A	559	13	86.7	1599	18	US-09-417-507-8698	Sequence 8698, App
c 487	13	86.7	765	34	US-03-902-540-9484	Sequence 9484, App	560	13	86.7	1716	18	US-09-404-520-25338	Sequence 25338, A
c 488	13	86.7	796	1	PCT-US02-13142-1086	Sequence 1086, App	561	13	86.7	1717	19	US-09-513-996A-54344	Sequence 54344, A
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c 491	13	86.7	805	23	US-09-614-150-3653	Sequence 3653, App	564	13	86.7	1779	80	US-60-360-207-37859	Sequence 37859, A
c 492	13	86.7	805	63	US-60-191-637-3665	Sequence 3665, App	565	13	86.7	1880	66	US-60-229-515-1407	Sequence 1407, App
c 493	13	86.7	808	60	US-60-167-217-3718	Sequence 3718, App	566	13	86.7	1880	66	US-60-229-515-1565	Sequence 1565, App
c 494	13	86.7	809	80	US-60-360-039-37023	Sequence 37023, A	567	13	86.7	1899	65	US-60-213-178-57	Sequence 57, Appl
c 495	13	86.7	815	18	US-09-404-520-21560	Sequence 21560, A	568	13	86.7	2001	13	US-08-951-984-4	Sequence 4, Appl
c 496	13	86.7	850	18	US-09-404-520-13362	Sequence 13362, A	569	13	86.7	2001	18	US-09-400-122A-4	Sequence 4, Appl
c 497	13	86.7	850	18	US-09-404-520-21306	Sequence 21306, A	570	13	86.7	2001	18	US-09-400-122A-4	Sequence 4, Appl
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c 502	13	86.7	915	80	US-60-360-039-37915	Sequence 37915, A	575	13	86.7	2126	23	US-09-614-150-13685	Sequence 13685, A
c 503	13	86.7	915	80	US-60-360-039-38486	Sequence 38486, A	576	13	86.7	2126	60	US-60-167-217-13753	Sequence 13753, A
c 504	13	86.7	915	80	US-60-360-039-38660	Sequence 38660, A	577	13	86.7	2126	61	US-60-173-464-11185	Sequence 11185, A
c 505	13	86.7	924	19	US-09-514-000-3965	Sequence 3965, App	578	13	86.7	2168	28	US-09-708-427-76744	Sequence 76744, A
c 506	13	86.7	933	29	US-09-739-449-6367	Sequence 6367, App	579	13	86.7	2205	69	US-60-258-273-227	Sequence 227, App
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c 508	13	86.7	952	18	US-09-404-520-7813	Sequence 7813, App	581	13	86.7	2224	63	US-60-191-681-10819	Sequence 10819, A
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c 510	13	86.7	960	80	US-60-360-039-27084	Sequence 27084, A	583	13	86.7	2250	1	PCT-US01-08656-3711	Sequence 3711, App
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c 513	13	86.7	1029	31	US-09-513-996A-26435	Sequence 26435, A	586	13	86.7	2292	31	US-09-826-509-398	Sequence 398, App
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c 523	13	86.7	1140	80	US-60-360-039-45095	Sequence 45095, A	596	13	86.7	2450	12	US-08-886-333-2	Sequence 2, Appl
c 524	13	86.7	1143	30	US-09-782-816A-55	Sequence 55, Appl	597	13	86.7	2469	3	US-07-722-620-38	Sequence 28, Appl
c 525	13	86.7	1173	33	US-09-887-272A-4693	Sequence 4693, App	598	13	86.7	2469	15	US-09-186-350A-54	Sequence 54, Appl
c 526	13	86.7	1182	41	US-10-155-881-23516	Sequence 23516, A	599	13	86.7	2512	18	US-09-417-507-18181	Sequence 18181, A
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c 529	13	86.7	1206	38	US-10-015-127-5712	Sequence 5712, App	602	13	86.7	2553	1	PCT-US01-14827-5132	Sequence 5132, App
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c 609	13	86.7	2694	18	US-09-404-520-3874	Sequence 3874, Ap	c 682	13	86.7	3867	22	US-09-577-410-7484	Sequence 7484, Ap
c 610	13	86.7	2708	34	US-09-902-540-2864	Sequence 2864, Ap	c 683	13	86.7	3882	68	US-60-245-228-588	Sequence 588, Ap
c 611	13	86.7	2733	61	US-60-173-464-7365	Sequence 7365, Ap	684	13	86.7	3915	60	US-60-167-245-293	Sequence 293, Ap
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c 618	13	86.7	2827	65	US-60-213-178-1186	Sequence 1186, Ap	691	13	86.7	3992	18	US-09-442-384A-735	Sequence 735, Ap
c 619	13	86.7	2874	17	US-09-391-631-4197	Sequence 4197, Ap	692	13	86.7	3992	35	US-09-442-384B-735	Sequence 735, Ap
c 620	13	86.7	2897	80	US-60-360-207-13554	Sequence 13554, Ap	693	13	86.7	3992	38	US-09-944-807-9	Sequence 9, Appl
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c 628	13	86.7	3015	23	US-09-614-150-3652	Sequence 3652, Ap	701	13	86.7	4340	60	US-60-167-217-4376	Sequence 4376, Ap
c 629	13	86.7	3015	63	US-60-191-637-3664	Sequence 3664, Ap	702	13	86.7	4340	61	US-60-173-464-3567	Sequence 3567, Ap
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c 633	13	86.7	3032	63	US-60-191-681-7102	Sequence 7102, Ap	c 706	13	86.7	4402	23	US-09-614-150-2810	Sequence 2810, Ap
c 634	13	86.7	3096	23	US-09-614-150-18176	Sequence 18176, A	c 707	13	86.7	4402	63	US-60-191-637-2816	Sequence 2816, Ap
c 635	13	86.7	3096	61	US-60-173-464-14968	Sequence 14968, A	c 708	13	86.7	4402	63	US-60-191-681-2255	Sequence 2255, Ap
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c 639	13	86.7	3168	80	US-60-360-207-11302	Sequence 11302, A	712	13	86.7	4471	24	US-09-620-392-56261	Sequence 56261, A
c 640	13	86.7	3215	23	US-09-614-150-21409	Sequence 21409, A	713	13	86.7	4490	60	US-60-167-217-1249	Sequence 1249, Ap
c 641	13	86.7	3215	63	US-60-191-637-21471	Sequence 21471, A	714	13	86.7	4490	61	US-60-173-464-994	Sequence 994, Ap
c 642	13	86.7	3215	63	US-60-191-681-16923	Sequence 16923, A	c 715	13	86.7	4490	1	PCT-US01-08631-22684	Sequence 22684, A
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c 645	13	86.7	3323	1	PCT-US02-13142-5086	Sequence 5086, Ap	c 718	13	86.7	4558	30	US-09-764-860-937	Sequence 937, Ap
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c 647	13	86.7	3338	23	US-09-614-150-7166	Sequence 7166, Ap	c 720	13	86.7	4558	39	US-10-074-095-937	Sequence 937, Ap
c 648	13	86.7	3338	63	US-60-191-637-7187	Sequence 7187, Ap	c 721	13	86.7	4558	39	US-10-074-095-937	Sequence 937, Ap
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c 650	13	86.7	3422	60	US-60-167-217-4114	Sequence 4114, Ap	c 723	13	86.7	4558	61	US-60-172-373-2934	Sequence 2934, Ap
c 651	13	86.7	3486	23	US-09-614-150-4054	Sequence 4054, Ap	c 724	13	86.7	4599	61	US-60-173-464-17583	Sequence 17583, A
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c 653	13	86.7	3486	61	US-60-171-627-331	Sequence 226, Ap	c 726	13	86.7	4765	38	US-09-785-276A-23256	Sequence 23256, A
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c 656	13	86.7	3486	63	US-60-191-681-3253	Sequence 3253, Ap	c 729	13	86.7	5071	60	US-60-167-217-9139	Sequence 9139, Ap
c 657	13	86.7	3537	1	PCT-US02-13142-6240	Sequence 6240, Ap	c 730	13	86.7	5299	23	US-09-614-150-9076	Sequence 9076, Ap
c 658	13	86.7	3537	40	US-10-128-714-6240	Sequence 6240, Ap	c 731	13	86.7	5299	63	US-60-191-637-9105	Sequence 9105, Ap
c 659	13	86.7	3537	40	US-10-128-714-6240	Sequence 7240, Ap	c 732	13	86.7	5299	63	US-60-191-681-7101	Sequence 7101, Ap
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c 661	13	86.7	3549	23	US-09-614-150-26666	Sequence 26666, A	c 734	13	86.7	5494	61	US-60-173-464-14967	Sequence 14967, A
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c 664	13	86.7	3549	63	US-60-191-681-21447	Sequence 21447, A	c 737	13	86.7	5537	40	PCT-US02-13142-5240	Sequence 5240, Ap
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c 666	13	86.7	3564	23	US-09-614-150-26663	Sequence 26663, A	c 739	13	86.7	5828	18	US-09-430-029-1	Sequence 1, Appl
c 667	13	86.7	3564	63	US-60-191-637-26835	Sequence 26835, A	c 740	13	86.7	5902	23	US-09-614-150-13684	Sequence 13684, A
c 668	13	86.7	3564	63	US-60-191-681-21444	Sequence 21444, A	c 741	13	86.7	5902	23	US-60-167-217-13752	Sequence 13752, A
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c 670	13	86.7	3611	61	US-60-173-464-2335	Sequence 2335, Ap	c 743	13	86.7	5902	63	US-60-191-637-13725	Sequence 13725, A
c 671	13	86.7	3614	60	US-60-167-217-2859	Sequence 2859, Ap	c 744	13	86.7	5902	63	US-60-191-681-10818	Sequence 10818, A
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c 673	13	86.7	3639	61	US-60-172-373-6629	Sequence 6629, Ap	c 746	13	86.7	6390	1	PCT-US01-08631-15469	Sequence 15469, A
c 674	13	86.7	3671	18	US-09-471-275-6778	Sequence 6778, Ap	c 747	13	86.7	6390	30	US-09-760-475-30710	Sequence 3710, Ap
c 675	13	86.7	3754	23	US-09-614-150-26669	Sequence 26669, A	c 748	13	86.7	6494	30	US-09-760-475-30710	Sequence 3710, Ap
c 676	13	86.7	3754	63	US-60-191-637-26841	Sequence 26841, A	c 749	13	86.7	6632	59	US-60-150-584-520	Sequence 520, Ap
c 677	13	86.7	3754	63	US-60-191-681-21450	Sequence 21450, A	c 750	13	86.7	6689	23	US-09-614-150-26668	Sequence 26668, A
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c 756	13	86.7	6772	76	US-60-324-185-12521	Sequence 12521, A	829	13	86.7	25048	34	US-09-902-540-1239	Sequence 1239, Ap
c 757	13	86.7	6916	23	US-09-614-150-26665	Sequence 26665, A	c 830	13	86.7	27739	28	US-09-702-134-8361	Sequence 8361, Ap
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c 790	13	86.7	10726	63	US-60-191-681-5611	Sequence 5611, Ap	862	13	86.7	54740	19	US-09-514-000-393	Sequence 393, App
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c 796	13	86.7	11992	63	US-60-191-681-2254	Sequence 2254, Ap	868	13	86.7	62010	31	US-09-815-264-67166	Sequence 67166, A
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c 800	13	86.7	15562	28	US-09-702-134-23299	Sequence 23299, A	c 872	13	86.7	92491	31	US-09-803-736-1414	Sequence 1414, Ap
c 801	13	86.7	15562	31	US-09-815-264-74056	Sequence 74056, A	873	13	86.7	141476	68	US-60-243-468-302	Sequence 302, App
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c 804	13	86.7	17592	34	US-09-902-540-1138	Sequence 1138, Ap	c 876	13	86.7	184961	19	US-09-528-237A-954	Sequence 954, App
c 805	13	86.7	18683	67	US-60-236-804-36	Sequence 36, Appl	c 877	13	86.7	190117	69	US-60-257-537-312	Sequence 312, App
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c 807	13	86.7	19665	24	US-09-620-392-68716	Sequence 68716, A	879	13	86.7	223100	41	US-10-174-014-12	Sequence 12, Appl
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c 815	13	86.7	22312	61	US-60-173-464-12480	Sequence 12480, A	887	13	86.7	1555893	18	US-09-458-180-1	Sequence 1, Appli
c 816	13	86.7	22313	23	US-09-614-150-15187	Sequence 15187, A	888	13	86.7	1555893	33	US-09-895-611D-1	Sequence 1, Appli
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c 968	12	80.0	184	69	US-60-253-653-15293	Sequence 15293, A							
c 969	12	80.0	188	13	US-08-959-395-4735	Sequence 4735, Ap							
c 970	12	80.0	188	20	US-08-532-315-26461	Sequence 26461, A							

## ALIGNMENTS

RESULT 1  
PCT-US00-35491-9  
; SEQUENCE 9, Application PC/TUS0035491  
; GENERAL INFORMATION:  
; APPLICANT: Robertson, David D.  
; APPLICANT: Blakely, Randy D.  
; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND  
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO  
; FILE REFERENCE: Attorney Docket No. 1242-27 PCT  
; CURRENT APPLICATION NUMBER: PCT/US00/35491  
; CURRENT FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: 60/175,456  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: 60/173,682  
; PRIOR FILING DATE: 1999-12-29  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US00-35491-9

Query Match 100.0%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15  
| | | | | | | | | | | | | | | | |  
Db 1 CCTTCTCGCCCTGTT 15

RESULT 2  
US-09-750-609-9  
; SEQUENCE 9, Application US/09750609  
; GENERAL INFORMATION:  
; APPLICANT: Robertson, David  
; APPLICANT: Blakely, Randy D.

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; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
; FILE REFERENCE: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
; CURRENT APPLICATION NUMBER: US/09/750,609
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 60/175,456
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/173,682
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-750-609-9

Query Match      100.0%; Score 15; DB 29; Length 15;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
   |||||
Db 1 CCTTCTCGCCCTGTT 15

RESULT 3
US-60-173-682-9
; Sequence 9, Application US/60173682
; GENERAL INFORMATION:
; APPLICANT: Robertson, David
; APPLICANT: Blakely, Randy D.
; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
; FILE REFERENCE: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
; CURRENT APPLICATION NUMBER: US/60/173,682
; CURRENT FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-173-682-9

Query Match      100.0%; Score 15; DB 61; Length 15;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
   |||||
Db 1 CCTTCTCGCCCTGTT 15

RESULT 4
US-09-440-302A-470
; Sequence 470, Application US/09440302A
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashev, Matvey E.
; TITLE OF INVENTION: Human Neurobiology Array
; FILE REFERENCE: CLON-006CIP11
; CURRENT APPLICATION NUMBER: US/09/440,302A
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 1193
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 470
; LENGTH: 257
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleic Acid Probe
US-09-440-302A-470

Query Match      100.0%; Score 15; DB 18; Length 257;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
   |||||
Db 1 CCTTCTCGCCCTGTT 15

RESULT 5
US-09-440-302B-470
; Sequence 470, Application US/09440302B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashev, Matvey E.
; TITLE OF INVENTION: Human Neurobiology Array
; FILE REFERENCE: CLON-006CIP11
; CURRENT APPLICATION NUMBER: US/09/440,302B
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 1193
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 470
; LENGTH: 257
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleic Acid Probe
US-09-440-302B-470

Query Match      100.0%; Score 15; DB 18; Length 257;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
   |||||
Db 1 CCTTCTCGCCCTGTT 15

RESULT 6
US-09-440-302-470
; Sequence 470, Application US/09440302
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashev, Matvey E.
; TITLE OF INVENTION: Human Neurobiology Array
; FILE REFERENCE: CLON-006CIP11
; CURRENT APPLICATION NUMBER: US/09/440,302
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 597
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 470
; LENGTH: 258
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleic Acid Probe
US-09-440-302-470

Query Match      100.0%; Score 15; DB 18; Length 258;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
   |||||
Db 1 CCTTCTCGCCCTGTT 15
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; OTHER INFORMATION: Nucleic Acid Probe
US-09-440-302A-470

Query Match      100.0%; Score 15; DB 18; Length 257;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
   |||||
Db 1 CCTTCTCGCCCTGTT 15

RESULT 5
US-09-440-302B-470
; Sequence 470, Application US/09440302B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashev, Matvey E.
; TITLE OF INVENTION: Human Neurobiology Array
; FILE REFERENCE: CLON-006CIP11
; CURRENT APPLICATION NUMBER: US/09/440,302B
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 1193
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 470
; LENGTH: 257
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleic Acid Probe
US-09-440-302B-470

Query Match      100.0%; Score 15; DB 18; Length 257;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
   |||||
Db 1 CCTTCTCGCCCTGTT 15

RESULT 6
US-09-440-302-470
; Sequence 470, Application US/09440302
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashev, Matvey E.
; TITLE OF INVENTION: Human Neurobiology Array
; FILE REFERENCE: CLON-006CIP11
; CURRENT APPLICATION NUMBER: US/09/440,302
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 597
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 470
; LENGTH: 258
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleic Acid Probe
US-09-440-302-470

Query Match      100.0%; Score 15; DB 18; Length 258;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
   |||||
Db 1 CCTTCTCGCCCTGTT 15
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RESULT 7  
US-09-442-366A-309  
; Sequence 309, Application US/09442366A  
; GENERAL INFORMATION:  
; APPLICANT: Chenchik, Alex  
; APPLICANT: Lukashov, Matvey E.  
; TITLE OF INVENTION: Human Array  
; FILE REFERENCE: CLON-006CIP13  
; CURRENT APPLICATION NUMBER: US/09/442,366A  
; CURRENT FILING DATE: 1999-11-17  
; PRIOR APPLICATION NUMBER: 09/053,375  
; PRIOR FILING DATE: 1998-03-31  
; NUMBER OF SEQ ID NOS: 2216  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 309  
; LENGTH: 258  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic gene fragment  
US-09-442-366A-309

Query Match 100.0%; Score 15; DB 18; Length 258;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15  
|||||  
DB 45 CCTTCTCGCCCTGTT 59

RESULT 8  
US-09-698-012-481/c  
; Sequence 481, Application US/09698012  
; GENERAL INFORMATION:  
; APPLICANT: Gearing, David P.  
; APPLICANT: Holtzman, Douglas A.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES  
; TITLE OF INVENTION: THEREFOR  
; FILE REFERENCE: 1600.2002-001  
; CURRENT APPLICATION NUMBER: US/09/698,012  
; CURRENT FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: 60/162,166  
; PRIOR FILING DATE: 1999-10-28  
; NUMBER OF SEQ ID NOS: 9719  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 481  
; LENGTH: 472  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-698-012-481

Query Match 100.0%; Score 15; DB 27; Length 472;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15  
|||||  
DB 76 CCTTCTCGCCCTGTT 62

RESULT 9  
US-09-534-856-18784/c  
; Sequence 18784, Application US/09534856  
; GENERAL INFORMATION:  
; APPLICANT: Seilhamer, Jeffrey J.  
; APPLICANT: Deleage, Angelo M.  
; APPLICANT: Stuart, Susan G.  
; APPLICANT: Stuve, Laura L.  
; APPLICANT: Mullahy, Sara J.  
; APPLICANT: Naughton, Rebecca E.  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING STRUCTURAL, SECRETED, AND

; TITLE OF INVENTION: EXTRACELLULAR MOLECULES  
; FILE REFERENCE: PD-1015 CIP  
; CURRENT APPLICATION NUMBER: US/09/534,856  
; CURRENT FILING DATE: 2000-03-24  
; Prior application data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 26334  
; SOFTWARE: PERL Program  
; SEQ ID NO 18784  
; LENGTH: 510  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; OTHER INFORMATION: Inceyte ID No: hu01124269  
; NAME/KEY: unsure  
; LOCATION: 488  
; OTHER INFORMATION: a, t, c, g, or other  
US-09-534-856-18784

Query Match 100.0%; Score 15; DB 20; Length 510;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15  
|||||  
DB 185 CCTTCTCGCCCTGTT 171

RESULT 10  
US-60-230-445-2923  
; Sequence 2923, Application US/60230445  
; GENERAL INFORMATION:  
; APPLICANT: Beasley, Ellen  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
; FILE REFERENCE: CL000765  
; CURRENT APPLICATION NUMBER: US/60/230,445  
; CURRENT FILING DATE: 2000-09-06  
; NUMBER OF SEQ ID NOS: 3051  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2923  
; LENGTH: 592  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-60-230-445-2923

Query Match 100.0%; Score 15; DB 67; Length 592;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15  
|||||  
DB 44 CCTTCTCGCCCTGTT 58

RESULT 11  
US-09-948-933-4005/c  
; Sequence 4005, Application US/09948933  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF  
; FILE REFERENCE: CL000787  
; CURRENT APPLICATION NUMBER: US/09/948,933  
; CURRENT FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/231,399  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 6404  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4005  
; LENGTH: 601

; TYPE: DNA  
; ORGANISM: Human  
US-09-948-933-4005

Query Match 100.0%; Score 15; DB 35; Length 601;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15  
|||||

Db 27 CCTTCTCGCCCTGTT 13  
|||||

## RESULT 12

US-09-948-933-4006/c

; Sequence 4006, Application US/09948933

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF

; TITLE OF INVENTION: DETECTION AND USES THEREOF

; FILE REFERENCE: CL000787

; CURRENT APPLICATION NUMBER: US/09/948,933

; CURRENT FILING DATE: 2001-09-10

; PRIOR APPLICATION NUMBER: 60/231,399

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 6404

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4006

; LENGTH: 601

; TYPE: DNA

; ORGANISM: Human

US-09-948-933-4006

Query Match

Best Local Similarity 100.0%; Score 15; DB 35; Length 601;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15  
|||||

Db 126 CCTTCTCGCCCTGTT 112  
|||||

## RESULT 13

US-09-948-933-4007/c

; Sequence 4007, Application US/09948933

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF

; TITLE OF INVENTION: DETECTION AND USES THEREOF

; FILE REFERENCE: CL000787

; CURRENT APPLICATION NUMBER: US/09/948,933

; CURRENT FILING DATE: 2001-09-10

; PRIOR APPLICATION NUMBER: 60/231,399

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 6404

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4007

; LENGTH: 601

; TYPE: DNA

; ORGANISM: Human

US-09-948-933-4007

Query Match

Best Local Similarity 100.0%; Score 15; DB 35; Length 601;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15  
|||||

Db 226 CCTTCTCGCCCTGTT 212  
|||||

## RESULT 14

US-09-948-933-4008/c

; Sequence 4008, Application US/09948933

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH CARDIOVASCULAR DISEASE AND LIPID DISORDERS, METHODS OF

; TITLE OF INVENTION: DETECTION AND USES THEREOF

; FILE REFERENCE: CL000787

; CURRENT APPLICATION NUMBER: US/09/948,933

; CURRENT FILING DATE: 2001-09-10

; PRIOR APPLICATION NUMBER: 60/231,399

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 6404

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4008

; LENGTH: 601

; TYPE: DNA

; ORGANISM: Human

US-09-948-933-4008

Query Match

Best Local Similarity 100.0%; Score 15; DB 35; Length 601;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15  
|||||

Db 337 CCTTCTCGCCCTGTT 323  
|||||

## RESULT 15

US-09-634-306B-7016/c

; Sequence 7016, Application US/09634306B

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; TITLE OF INVENTION: Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/09/634,306B

; CURRENT FILING DATE: 2002-02-21

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7016

; LENGTH: 817

; TYPE: DNA

; ORGANISM: Human

US-09-634-306B-7016

Query Match

Best Local Similarity 100.0%; Score 15; DB 24; Length 817;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCGCCCTGTT 15  
|||||

Db 138 CCTTCTCGCCCTGTT 124  
|||||

Search completed: December 11, 2002, 20:27:12

Job time : 2589 secs

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 17:10:08 ; Search time 88.5 Seconds  
(without alignments)  
121.821 Million cell updates/sec

Title: US-09-750-609-9  
Perfect score: 15  
Sequence: 1'ccttctgcgcctgtt 15

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 407964 seqs, 359371392 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 815928

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Pending\_Patents\_NA\_New.\*  
1: /cgn2\_6/ptodata/1/pna/US06\_PCT\_NEW\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq.\*  
7: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	2876	5	US-09-724-676-47407 Sequence 47407, A
2	15	100.0	2876	5	US-09-724-676A-47407 Sequence 47407, A
3	15	100.0	4338	5	US-09-724-676-24273 Sequence 24273, A
4	15	100.0	4338	5	US-09-724-676A-24273 Sequence 24273, A
5	15	100.0	4848	5	US-09-724-676-24268 Sequence 24268, A
6	15	100.0	4848	5	US-09-724-676A-24268 Sequence 24268, A
7	15	100.0	5222	6	US-10-133-937-67 Sequence 67, Appl
8	15	100.0	5589	5	US-09-724-676A-24272 Sequence 24272, A
9	15	100.0	5589	5	US-09-724-676A-24272 Sequence 24272, A
10	15	100.0	5642	5	US-09-724-676-24271 Sequence 24271, A
11	15	100.0	5642	5	US-09-724-676A-24271 Sequence 24271, A
12	15	100.0	6099	5	US-09-724-676-24267 Sequence 24267, A
13	15	100.0	6099	5	US-09-724-676A-24267 Sequence 24267, A
14	15	100.0	6152	5	US-09-724-676-24266 Sequence 24266, A
15	15	100.0	6152	5	US-09-724-676A-24266 Sequence 24266, A
16	13	86.7	1936	5	US-09-724-676-32136 Sequence 32136, A
17	13	86.7	1936	5	US-09-724-676A-32136 Sequence 32136, A
18	13	86.7	3590	5	US-09-724-676-24360 Sequence 24360, A
19	13	86.7	3590	5	US-09-724-676A-24360 Sequence 24360, A
20	13	86.7	7430	1	PCT-US02-32727-4 Sequence 4, Appl
21	13	86.7	7430	6	US-10-057-498-4 Sequence 4, Appl
22	13	86.7	276820	1	PCT-US02-32700-9 Sequence 9, Appl
23	13	86.7	276820	6	US-10-271-416-9 Sequence 9, Appl
24	12	80.0	152	6	US-10-203-138A-5521 Sequence 5521, Ap
25	12	80.0	187	5	US-09-513-999C-18000 Sequence 18000, A
26	12	80.0	237	5	US-09-513-999C-35434 Sequence 35434, A

Sequence 1966, Ap  
Sequence 35759, A  
Sequence 3109, Ap  
Sequence 32746, A  
Sequence 3420, Ap  
Sequence 27979, A  
Sequence 338, App  
Sequence 15535, A  
Sequence 15535, A  
Sequence 45475, A  
Sequence 212, App  
Sequence 23454, A  
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102	12	80.0	1240	5	US-09-724-676-23424	Sequence 23424, A	175	12	80.0	1765	5	US-09-724-676A-23416	Sequence 23416, A
103	12	80.0	1240	5	US-09-724-676A-23424	Sequence 23424, A	176	12	80.0	1781	5	US-09-724-676-23428	Sequence 23428, A
104	12	80.0	1267	5	US-09-724-676-23410	Sequence 23410, A	177	12	80.0	1781	5	US-09-724-676A-23428	Sequence 23428, A
105	12	80.0	1267	5	US-09-724-676A-23410	Sequence 23410, A	178	12	80.0	1830	5	US-09-724-676-23420	Sequence 23420, A
106	12	80.0	1295	5	US-09-724-676-39263	Sequence 39263, A	179	12	80.0	1830	5	US-09-724-676A-23420	Sequence 23420, A
107	12	80.0	1295	5	US-09-724-676A-39263	Sequence 39263, A	180	12	80.0	1870	5	US-09-724-676-7693	Sequence 7693, Ap
108	12	80.0	1324	5	US-09-724-676A-23417	Sequence 23417, A	181	12	80.0	1870	5	US-09-724-676A-7693	Sequence 7693, Ap
109	12	80.0	1324	5	US-09-724-676A-23417	Sequence 23417, A	182	12	80.0	1934	5	US-09-724-676-35064	Sequence 35064, A
110	12	80.0	1326	5	US-09-724-676-39266	Sequence 39266, A	183	12	80.0	1934	5	US-09-724-676A-35064	Sequence 35064, A
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112	12	80.0	1331	5	US-09-724-676-23433	Sequence 23433, A	185	12	80.0	1952	5	US-09-724-676A-23407	Sequence 23407, A
113	12	80.0	1331	5	US-09-724-676-39262	Sequence 39262, A	186	12	80.0	1954	6	US-10-203-138A-4807	Sequence 4807, Ap
114	12	80.0	1331	5	US-09-724-676-39262	Sequence 39262, A	187	12	80.0	1955	5	US-09-724-676-35065	Sequence 35065, A
115	12	80.0	1331	5	US-09-724-676A-23433	Sequence 23433, A	188	12	80.0	1955	5	US-09-724-676A-35065	Sequence 35065, A
116	12	80.0	1331	5	US-09-724-676A-39262	Sequence 39262, A	189	12	80.0	1983	5	US-09-724-676-35057	Sequence 35057, A
117	12	80.0	1331	5	US-09-724-676A-39262	Sequence 39262, A	190	12	80.0	1983	5	US-09-724-676A-35057	Sequence 35057, A
118	12	80.0	1340	5	US-09-724-676-23429	Sequence 23429, A	191	12	80.0	2009	5	US-09-724-676-23414	Sequence 23414, A
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120	12	80.0	1358	5	US-09-724-676-23437	Sequence 23437, A	193	12	80.0	2031	5	US-09-724-676-35058	Sequence 35058, A
121	12	80.0	1358	5	US-09-724-676A-23437	Sequence 23437, A	194	12	80.0	2031	5	US-09-724-676A-35058	Sequence 35058, A
122	12	80.0	1362	5	US-09-724-676-23411	Sequence 23411, A	195	12	80.0	2163	5	US-09-724-676-17044	Sequence 17044, A
123	12	80.0	1362	5	US-09-724-676-39265	Sequence 39265, A	196	12	80.0	2163	5	US-09-724-676A-17044	Sequence 17044, A
124	12	80.0	1362	5	US-09-724-676-39267	Sequence 39267, A	197	12	80.0	2247	6	US-10-240-965-271	Sequence 271, App
125	12	80.0	1362	5	US-09-724-676A-23411	Sequence 23411, A	198	12	80.0	2247	6	US-09-724-676-17043	Sequence 17043, A
126	12	80.0	1362	5	US-09-724-676A-39265	Sequence 39265, A	199	12	80.0	2319	5	US-09-724-676A-17043	Sequence 17043, A
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128	12	80.0	1380	5	US-09-724-676-23425	Sequence 23425, A	201	12	80.0	2326	5	US-09-724-676A-35060	Sequence 35060, A
129	12	80.0	1380	5	US-09-724-676A-23425	Sequence 23425, A	202	12	80.0	2347	5	US-09-724-676-35061	Sequence 35061, A
130	12	80.0	1389	5	US-09-724-676-23421	Sequence 23421, A	203	12	80.0	2347	5	US-09-724-676A-35061	Sequence 35061, A
131	12	80.0	1389	5	US-09-724-676A-23421	Sequence 23421, A	204	12	80.0	2451	5	US-09-724-676-7694	Sequence 7694, Ap
132	12	80.0	1415	5	US-09-724-676-23444	Sequence 23444, A	205	12	80.0	2451	5	US-09-724-676A-7694	Sequence 7694, Ap
133	12	80.0	1415	5	US-09-724-676A-23444	Sequence 23444, A	206	12	80.0	2454	6	US-10-240-965-108	Sequence 108, App
134	12	80.0	1419	5	US-09-724-676-23418	Sequence 23418, A	207	12	80.0	2485	6	US-10-152-319A-1901	Sequence 1901, Ap
135	12	80.0	1419	5	US-09-724-676A-23418	Sequence 23418, A	208	12	80.0	2556	6	US-10-240-965-202	Sequence 202, App
136	12	80.0	1467	5	US-09-724-676-39287	Sequence 39287, A	209	12	80.0	2793	6	US-10-152-319A-1649	Sequence 1649, Ap
137	12	80.0	1467	5	US-09-724-676A-39287	Sequence 39287, A	210	12	80.0	2976	6	US-10-194-163-36	Sequence 36, Appl
138	12	80.0	1480	5	US-09-724-676-23448	Sequence 23448, A	211	12	80.0	3010	5	US-09-724-676-7222	Sequence 7222, Ap
139	12	80.0	1480	5	US-09-724-676A-23448	Sequence 23448, A	212	12	80.0	3010	5	US-09-724-676A-7222	Sequence 7222, Ap
140	12	80.0	1498	5	US-09-724-676-39260	Sequence 39260, A	213	12	80.0	3063	5	US-09-724-676-33577	Sequence 33577, A
141	12	80.0	1498	5	US-09-724-676A-39260	Sequence 39260, A	214	12	80.0	3063	5	US-09-724-676A-33577	Sequence 33577, A
142	12	80.0	1502	5	US-09-724-676-23412	Sequence 23412, A	215	12	80.0	3067	5	US-09-724-676-33579	Sequence 33579, A
143	12	80.0	1502	5	US-09-724-676A-23412	Sequence 23412, A	216	12	80.0	3067	5	US-09-724-676A-33579	Sequence 33579, A
144	12	80.0	1503	5	US-09-724-676-39286	Sequence 39286, A	217	12	80.0	3102	5	US-09-724-676-7225	Sequence 7225, Ap
145	12	80.0	1503	5	US-09-724-676-39286	Sequence 39286, A	218	12	80.0	3102	5	US-09-724-676A-7225	Sequence 7225, Ap
146	12	80.0	1503	5	US-09-724-676A-39286	Sequence 39286, A	219	12	80.0	3105	5	US-09-724-676-35040	Sequence 35040, A
147	12	80.0	1503	5	US-09-724-676A-39288	Sequence 39288, A	220	12	80.0	3105	5	US-09-724-676A-35040	Sequence 35040, A
148	12	80.0	1511	5	US-09-724-676-23408	Sequence 23408, A	221	12	80.0	3289	5	US-09-724-676-35078	Sequence 35078, A
149	12	80.0	1511	5	US-09-724-676A-23408	Sequence 23408, A	222	12	80.0	3289	5	US-09-724-676A-35078	Sequence 35078, A
150	12	80.0	1534	5	US-09-724-676-39259	Sequence 39259, A	223	12	80.0	3629	6	US-10-289-757-9	Sequence 9, Appl1
151	12	80.0	1534	5	US-09-724-676-39259	Sequence 39259, A	224	12	80.0	3633	6	US-10-289-757-130	Sequence 130, App
152	12	80.0	1534	5	US-09-724-676A-39259	Sequence 39259, A	225	12	80.0	3735	6	US-10-289-757-11	Sequence 11, Appl
153	12	80.0	1537	5	US-09-724-676-23430	Sequence 23430, A	226	12	80.0	3743	6	US-10-289-757-132	Sequence 132, App
154	12	80.0	1537	5	US-09-724-676A-23430	Sequence 23430, A	227	12	80.0	3888	5	US-09-724-676-33578	Sequence 33578, A
155	12	80.0	1559	5	US-09-724-676-23419	Sequence 23419, A	228	12	80.0	3888	5	US-09-724-676A-33578	Sequence 33578, A
156	12	80.0	1559	5	US-09-724-676A-23419	Sequence 23419, A	229	12	80.0	3952	5	US-09-724-676-35074	Sequence 35074, A
157	12	80.0	1559	5	US-09-724-676A-23419	Sequence 23419, A	230	12	80.0	3952	5	US-09-724-676A-35074	Sequence 35074, A
158	12	80.0	1568	5	US-09-724-676-23415	Sequence 23415, A	231	12	80.0	4000	5	US-09-724-676-35075	Sequence 35075, A
159	12	80.0	1568	5	US-09-724-676A-23415	Sequence 23415, A	232	12	80.0	4000	5	US-09-724-676A-35075	Sequence 35075, A
160	12	80.0	1586	5	US-09-724-676-23422	Sequence 23422, A	233	12	80.0	4117	6	US-10-152-319A-1994	Sequence 1994, Ap
161	12	80.0	1586	5	US-09-724-676A-23422	Sequence 23422, A	234	12	80.0	4295	5	US-09-724-676-35076	Sequence 35076, A
162	12	80.0	1591	5	US-09-724-676-35062	Sequence 35062, A	235	12	80.0	4295	5	US-09-724-676A-35076	Sequence 35076, A
163	12	80.0	1591	5	US-09-724-676A-35062	Sequence 35062, A	236	12	80.0	4316	5	US-09-724-676-35077	Sequence 35077, A
164	12	80.0	1602	5	US-09-724-676-23434	Sequence 23434, A	237	12	80.0	4316	5	US-09-724-676A-35077	Sequence 35077, A
165	12	80.0	1602	5	US-09-724-676A-23434	Sequence 23434, A	238	12	80.0	4344	5	US-09-724-676-35069	Sequence 35069, A
166	12	80.0	1622	5	US-09-724-676-27210	Sequence 27210, A	239	12	80.0	4344	5	US-09-724-676A-35069	Sequence 35069, A
167	12	80.0	1622	5	US-09-724-676A-27210	Sequence 27210, A	240	12	80.0	4392	5	US-09-724-676-35071	Sequence 35071, A
168	12	80.0	1639	5	US-09-724-676-35063	Sequence 35063, A	241	12	80.0	4392	5	US-09-724-676A-35071	Sequence 35071, A
169	12	80.0	1639	5	US-09-724-676A-35063	Sequence 35063, A	242	12	80.0	4336	5	US-09-724-676-24735	Sequence 24735, A
170	12	80.0	1659	5	US-09-724-676-23442	Sequence 23442, A	243	12	80.0	4336	5	US-09-724-676A-24735	Sequence 24735, A
171	12	80.0	1659	5	US-09-724-676A-23442	Sequence 23442, A	244	12	80.0	4687	5	US-09-724-676-35072	Sequence 35072, A
172	12	80.0	1708	5	US-09-724-676-23409	Sequence 23409, A	245	12	80.0	4687	5	US-09-724-676A-35072	Sequence 35072, A



c 246	12	80.0	4708	5	US-09-724-676-35073	Sequence 35073, A	319	11	73.3	874	5	US-09-724-676-11829	Sequence 11829, A
c 247	12	80.0	4708	5	US-09-724-676A-35073	Sequence 35073, A	320	11	73.3	874	5	US-09-724-676A-11829	Sequence 11829, A
c 248	12	80.0	4733	5	US-09-724-676-17573	Sequence 17573, A	321	11	73.3	883	5	US-09-724-676-11824	Sequence 11824, A
c 249	12	80.0	4733	5	US-09-724-676A-17573	Sequence 17573, A	322	11	73.3	883	5	US-09-724-676A-11824	Sequence 11824, A
c 250	12	80.0	4942	5	US-09-724-676-17571	Sequence 17571, A	c 323	11	73.3	886	5	US-09-724-676-45866	Sequence 45866, A
c 251	12	80.0	4942	5	US-09-724-676A-17571	Sequence 17571, A	c 324	11	73.3	896	5	US-09-724-676A-45866	Sequence 45866, A
c 252	12	80.0	5343	5	US-09-724-676-17572	Sequence 17572, A	c 325	11	73.3	903	5	US-09-724-676-45852	Sequence 45852, A
c 253	12	80.0	5343	5	US-09-724-676A-17572	Sequence 17572, A	c 326	11	73.3	903	5	US-09-724-676A-45852	Sequence 45852, A
c 254	12	80.0	5648	6	US-10-152-319A-1694	Sequence 1694, Ap	c 327	11	73.3	937	5	US-09-724-676-10938	Sequence 10938, A
c 255	12	80.0	7753	5	US-09-724-676-42420	Sequence 42420, A	c 328	11	73.3	937	5	US-09-724-676A-10938	Sequence 10938, A
c 256	12	80.0	7753	5	US-09-724-676A-42420	Sequence 42420, A	c 329	11	73.3	956	5	US-09-724-676-45854	Sequence 45854, A
c 257	12	80.0	7791	5	US-09-724-676A-42419	Sequence 42419, A	c 330	11	73.3	956	5	US-09-724-676A-45854	Sequence 45854, A
c 258	12	80.0	7791	5	US-09-724-676-42422	Sequence 42422, A	c 331	11	73.3	978	5	US-09-724-676-34072	Sequence 34072, A
c 259	12	80.0	7880	5	US-09-724-676A-42418	Sequence 42418, A	c 332	11	73.3	978	5	US-09-724-676A-34072	Sequence 34072, A
c 260	12	80.0	7880	5	US-09-724-676A-42422	Sequence 42422, A	c 333	11	73.3	992	5	US-09-724-676A-18324	Sequence 18324, A
c 261	12	80.0	7918	5	US-09-724-676-42421	Sequence 42421, A	c 334	11	73.3	992	5	US-09-724-676A-18324	Sequence 18324, A
c 262	12	80.0	7918	5	US-09-724-676A-42421	Sequence 42421, A	c 335	11	73.3	1009	1	PCT-US02-32727-215	PCT-US02-32727-215
c 263	12	80.0	9589	5	US-09-724-676-42416	Sequence 42416, A	c 336	11	73.3	1009	6	US-10-057-498-215	US-10-057-498-215
c 264	12	80.0	9589	5	US-09-724-676A-42416	Sequence 42416, A	c 337	11	73.3	1038	5	US-09-724-676-11828	Sequence 11828, A
c 265	12	80.0	9716	5	US-09-724-676A-42418	Sequence 42418, A	c 338	11	73.3	1038	5	US-09-724-676A-11828	Sequence 11828, A
c 266	12	80.0	9716	5	US-09-724-676A-42418	Sequence 42418, A	c 339	11	73.3	1047	5	US-09-724-676-11823	Sequence 11823, A
c 267	12	80.0	9754	5	US-09-724-676-42417	Sequence 42417, A	c 340	11	73.3	1047	5	US-09-724-676A-11823	Sequence 11823, A
c 268	12	80.0	9754	5	US-09-724-676A-42417	Sequence 42417, A	c 341	11	73.3	1056	5	US-09-724-676-18322	Sequence 18322, A
c 269	12	80.0	9905	6	US-10-270-144-3	Sequence 3, Appl1	c 342	11	73.3	1056	5	US-09-724-676A-18322	Sequence 18322, A
c 270	12	80.0	18522	1	PCT-US02-32727-55	Sequence 55, Appl1	c 343	11	73.3	1058	6	US-10-264-237-839	US-10-264-237-839
c 271	12	80.0	18522	6	US-10-057-498-55	Sequence 55, Appl1	c 344	11	73.3	1092	5	US-09-724-676-18321	Sequence 18321, A
c 272	11	73.3	139	6	US-10-203-138A-9135	Sequence 9135, Ap	c 345	11	73.3	1092	5	US-09-724-676A-18321	Sequence 18321, A
c 273	11	73.3	161	5	US-09-513-999C-17838	Sequence 17838, A	c 346	11	73.3	1139	5	US-09-724-676-10940	Sequence 10940, A
c 274	11	73.3	161	5	US-09-513-999C-17841	Sequence 17841, A	c 347	11	73.3	1139	5	US-09-724-676A-10940	Sequence 10940, A
c 275	11	73.3	164	5	US-09-513-999C-17419	Sequence 17419, A	c 348	11	73.3	1150	6	US-10-125-923A-519	US-10-125-923A-519
c 276	11	73.3	170	5	US-09-513-999C-18312	Sequence 18312, A	c 349	11	73.3	1150	6	US-10-205-892-519	US-10-205-892-519
c 277	11	73.3	183	5	US-09-513-999C-16261	Sequence 16261, A	c 350	11	73.3	1150	6	US-10-174-575-519	US-10-174-575-519
c 278	11	73.3	207	5	US-09-134-000C-2208	Sequence 2208, Ap	c 351	11	73.3	1154	5	US-09-724-676-11827	Sequence 11827, A
c 279	11	73.3	208	6	US-10-266-131-1622	Sequence 1062, Ap	c 352	11	73.3	1154	5	US-09-724-676A-11827	Sequence 11827, A
c 280	11	73.3	214	5	US-09-513-999C-18050	Sequence 18050, A	c 353	11	73.3	1156	5	US-09-724-676-18323	Sequence 18323, A
c 281	11	73.3	228	6	US-10-203-138A-9011	Sequence 9011, Ap	c 354	11	73.3	1156	5	US-09-724-676A-18323	Sequence 18323, A
c 282	11	73.3	236	6	US-10-284-499-14	Sequence 14, Appl1	c 355	11	73.3	1163	5	US-09-724-676-11822	Sequence 11822, A
c 283	11	73.3	245	5	US-09-513-999C-31986	Sequence 31986, A	c 356	11	73.3	1163	5	US-09-724-676A-11822	Sequence 11822, A
c 284	11	73.3	251	5	US-09-513-999C-8420	Sequence 8420, Ap	c 357	11	73.3	1198	5	US-09-724-676-10939	Sequence 10939, A
c 285	11	73.3	276	5	US-09-513-999C-3085	Sequence 3085, Ap	c 358	11	73.3	1198	5	US-09-724-676A-10939	Sequence 10939, A
c 286	11	73.3	280	5	US-09-513-999C-27084	Sequence 27084, A	c 359	11	73.3	1237	5	US-09-724-676-11602	Sequence 11602, A
c 287	11	73.3	358	5	US-09-513-999C-27013	Sequence 27013, A	c 360	11	73.3	1237	5	US-09-724-676A-11602	Sequence 11602, A
c 288	11	73.3	362	6	US-10-203-138A-3875	Sequence 3875, Ap	c 361	11	73.3	1340	5	US-09-724-676-10937	Sequence 10937, A
c 289	11	73.3	370	6	US-10-203-138A-4002	Sequence 4002, Ap	c 362	11	73.3	1340	5	US-09-724-676A-10937	Sequence 10937, A
c 290	11	73.3	389	5	US-09-513-999C-958	Sequence 958, Ap	c 363	11	73.3	1361	5	US-09-724-676-41740	Sequence 41740, A
c 291	11	73.3	390	1	PCT-US02-34777-1055	Sequence 1055, Ap	c 364	11	73.3	1361	5	US-09-724-676A-41740	Sequence 41740, A
c 292	11	73.3	390	6	US-10-283-017-1055	Sequence 1055, Ap	c 365	11	73.3	1368	5	US-09-724-676-44696	Sequence 44696, A
c 293	11	73.3	393	5	US-09-513-999C-32667	Sequence 32667, A	c 366	11	73.3	1368	5	US-09-724-676A-44696	Sequence 44696, A
c 294	11	73.3	397	5	US-09-513-999C-2451	Sequence 2451, Ap	c 367	11	73.3	1399	5	US-09-724-676-10950	Sequence 10950, A
c 295	11	73.3	420	5	US-09-513-999C-1119	Sequence 1119, Ap	c 368	11	73.3	1399	5	US-09-724-676A-10950	Sequence 10950, A
c 296	11	73.3	426	5	US-09-513-999C-16404	Sequence 16404, A	c 369	11	73.3	1429	5	US-09-724-676-34071	Sequence 34071, A
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c 300	11	73.3	489	6	US-10-203-138A-2458	Sequence 2458, Ap	c 373	11	73.3	1458	6	US-10-271-889-52	US-10-271-889-52
c 301	11	73.3	540	6	US-10-152-319A-138	Sequence 138, Ap	c 374	11	73.3	1521	5	US-09-724-676-47839	Sequence 47839, A
c 302	11	73.3	560	5	US-09-724-676-45863	Sequence 45863, A	c 375	11	73.3	1521	5	US-09-724-676-47839	Sequence 47839, A
c 303	11	73.3	560	5	US-09-724-676A-45863	Sequence 45863, A	c 376	11	73.3	1564	6	US-10-237-021-61	US-10-237-021-61
c 304	11	73.3	570	5	US-09-724-676-44825	Sequence 44825, A	c 377	11	73.3	1565	6	US-10-201-365-22	US-10-201-365-22
c 305	11	73.3	570	5	US-09-134-000C-2207	Sequence 2207, Ap	c 378	11	73.3	1565	6	US-10-160-539A-24	US-10-160-539A-24
c 306	11	73.3	570	5	US-09-724-676A-44825	Sequence 44825, A	c 379	11	73.3	1608	1	PCT-US02-06147-6	PCT-US02-06147-6
c 307	11	73.3	578	5	US-09-724-676-45860	Sequence 45860, A	c 380	11	73.3	1616	5	US-09-724-676-41734	Sequence 41734, A
c 308	11	73.3	578	5	US-09-724-676A-45860	Sequence 45860, A	c 381	11	73.3	1616	5	US-09-724-676A-41734	Sequence 41734, A
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c 310	11	73.3	697	5	US-09-513-999C-3863	Sequence 3863, Ap	c 383	11	73.3	1672	5	US-09-724-676A-5016	Sequence 5016, Ap
c 311	11	73.3	736	5	US-09-724-676-10941	Sequence 10941, A	c 384	11	73.3	1695	5	US-09-724-676-44695	Sequence 44695, A
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c 314	11	73.3	768	6	US-10-258-951-30	Sequence 30, Appl1	c 387	11	73.3	1737	5	US-09-724-676-5014	Sequence 5014, Ap
c 315	11	73.3	791	5	US-09-724-676-45858	Sequence 45858, A	c 388	11	73.3	1737	5	US-09-724-676A-5014	Sequence 5014, Ap
c 316	11	73.3	791	5	US-09-724-676A-45858	Sequence 45858, A	c 389	11	73.3	1753	6	US-10-177-390-19	US-10-177-390-19
c 317	11	73.3	840	5	US-09-724-676-45864	Sequence 45864, A	c 390	11	73.3	1772	5	US-09-724-676-47376	Sequence 47376, A
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C 398	11	73.3	1920	5	US-09-724-676-44694	Sequence 44694, A	C 471	11	73.3	2740	5	US-09-724-676A-34070	Sequence 34070, A
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C 434	11	73.3	2281	6	US-10-205-892-253	Sequence 253, App	C 507	11	73.3	3349	5	US-09-724-676A-47858	Sequence 47858, A
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c 564	11	73.3	4084	5	US-09-724-676A-32179	Sequence 32179, A	c 637	11	73.3	5506	5	US-09-724-676-7038	Sequence 7038, Ap
c 565	11	73.3	4107	5	US-09-724-676-45543	Sequence 45543, A	c 638	11	73.3	5506	5	US-09-724-676A-7038	Sequence 7038, Ap
c 566	11	73.3	4107	5	US-09-724-676A-45543	Sequence 45543, A	c 639	11	73.3	5542	5	US-09-724-676-7035	Sequence 7035, Ap
c 567	11	73.3	4134	5	US-09-724-676-7108	Sequence 7108, Ap	c 640	11	73.3	5542	5	US-09-724-676-7041	Sequence 7041, Ap
c 568	11	73.3	4134	5	US-09-724-676A-7108	Sequence 7108, Ap	c 641	11	73.3	5542	5	US-09-724-676A-7035	Sequence 7035, Ap
c 569	11	73.3	4147	5	US-09-724-676-32194	Sequence 32194, A	c 642	11	73.3	5542	5	US-09-724-676A-7041	Sequence 7041, Ap
c 570	11	73.3	4147	5	US-09-724-676A-32194	Sequence 32194, A	c 643	11	73.3	5576	6	US-10-240-453-136	Sequence 136, App
c 571	11	73.3	4157	5	US-09-404-026-9	Sequence 9, Appl	c 644	11	73.3	5626	5	US-09-724-676-7083	Sequence 7083, Ap
c 572	11	73.3	4166	5	US-09-724-676-32201	Sequence 32201, A	c 645	11	73.3	5626	5	US-09-724-676A-7083	Sequence 7083, Ap
c 573	11	73.3	4166	5	US-09-724-676-45538	Sequence 45538, A	c 646	11	73.3	5662	5	US-09-724-676-7022	Sequence 7022, Ap
c 574	11	73.3	4166	5	US-09-724-676A-32201	Sequence 32201, A	c 647	11	73.3	5662	5	US-09-724-676-7054	Sequence 7054, Ap
c 575	11	73.3	4166	5	US-09-724-676A-45538	Sequence 45538, A	c 648	11	73.3	5662	5	US-09-724-676A-7022	Sequence 7022, Ap
c 576	11	73.3	4170	5	US-09-724-676-7105	Sequence 7105, Ap	c 649	11	73.3	5662	5	US-09-724-676A-7054	Sequence 7054, Ap
c 577	11	73.3	4170	5	US-09-724-676-7111	Sequence 7111, Ap	c 650	11	73.3	5705	5	US-09-724-676-7049	Sequence 7049, Ap
c 578	11	73.3	4170	5	US-09-724-676A-7105	Sequence 7105, Ap	c 651	11	73.3	5705	5	US-09-724-676A-7049	Sequence 7049, Ap
c 579	11	73.3	4170	5	US-09-724-676A-7111	Sequence 7111, Ap	c 652	11	73.3	5741	5	US-09-724-676-7046	Sequence 7046, Ap
c 580	11	73.3	4191	5	US-09-724-676-32198	Sequence 32198, A	c 653	11	73.3	5741	5	US-09-724-676-7052	Sequence 7052, Ap
c 581	11	73.3	4191	5	US-09-724-676A-32198	Sequence 32198, A	c 654	11	73.3	5741	5	US-09-724-676A-7046	Sequence 7046, Ap
c 582	11	73.3	4194	5	US-09-724-676-2272	Sequence 2272, Ap	c 655	11	73.3	5741	5	US-09-724-676A-7052	Sequence 7052, Ap
c 583	11	73.3	4194	5	US-09-724-676-2273	Sequence 2273, Ap	c 656	11	73.3	5825	5	US-09-724-676-7029	Sequence 7029, Ap
c 584	11	73.3	4194	5	US-09-724-676A-2272	Sequence 2272, Ap	c 657	11	73.3	5825	5	US-09-724-676A-7029	Sequence 7029, Ap
c 585	11	73.3	4194	5	US-09-724-676A-2273	Sequence 2273, Ap	c 658	11	73.3	5861	5	US-09-724-676-7026	Sequence 7026, Ap
c 586	11	73.3	4208	5	US-09-724-676-45541	Sequence 45541, A	c 659	11	73.3	5861	5	US-09-724-676-7033	Sequence 7033, Ap
c 587	11	73.3	4208	5	US-09-724-676A-45541	Sequence 45541, A	c 660	11	73.3	5861	5	US-09-724-676A-7026	Sequence 7026, Ap
c 588	11	73.3	4289	5	US-09-724-676-32184	Sequence 32184, A	c 661	11	73.3	5861	5	US-09-724-676A-7033	Sequence 7033, Ap
c 589	11	73.3	4333	5	US-09-724-676A-32184	Sequence 32184, A	c 662	11	73.3	5867	5	US-09-724-676-7106	Sequence 7106, Ap
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c 592	11	73.3	4342	5	US-09-724-676-23237	Sequence 23237, A	c 665	11	73.3	5903	5	US-09-724-676-7109	Sequence 7109, Ap
c 593	11	73.3	4342	5	US-09-724-676A-23237	Sequence 23237, A	c 666	11	73.3	5903	5	US-09-724-676A-7102	Sequence 7102, Ap
c 594	11	73.3	4345	5	US-09-724-676-23240	Sequence 23240, A	c 667	11	73.3	5903	5	US-09-724-676A-7109	Sequence 7109, Ap
c 595	11	73.3	4345	5	US-09-724-676A-23240	Sequence 23240, A	c 668	11	73.3	6069	6	US-10-240-453-268	Sequence 268, App
c 596	11	73.3	4347	5	US-09-724-676-7039	Sequence 7039, Ap	c 669	11	73.3	6069	6	US-10-240-453-193	Sequence 193, App
c 597	11	73.3	4347	5	US-09-724-676A-7039	Sequence 7039, Ap	c 670	11	73.3	6080	5	US-09-724-676-7037	Sequence 7037, Ap
c 598	11	73.3	4383	5	US-09-724-676-7036	Sequence 7036, Ap	c 671	11	73.3	6080	5	US-09-724-676A-7037	Sequence 7037, Ap
c 599	11	73.3	4383	5	US-09-724-676-7042	Sequence 7042, Ap	c 672	11	73.3	6116	5	US-09-724-676-7034	Sequence 7034, Ap
c 600	11	73.3	4383	5	US-09-724-676A-7036	Sequence 7036, Ap	c 673	11	73.3	6116	5	US-09-724-676-7040	Sequence 7040, Ap
c 601	11	73.3	4383	5	US-09-724-676A-7042	Sequence 7042, Ap	c 674	11	73.3	6116	5	US-09-724-676A-7034	Sequence 7034, Ap
c 602	11	73.3	4384	5	US-09-724-676-23239	Sequence 23239, A	c 675	11	73.3	6116	5	US-09-724-676A-7040	Sequence 7040, Ap
c 603	11	73.3	4384	5	US-09-724-676A-23239	Sequence 23239, A	c 676	11	73.3	6200	5	US-09-724-676-7074	Sequence 7074, Ap
c 604	11	73.3	4396	5	US-09-724-676-32203	Sequence 32203, A	c 677	11	73.3	6200	5	US-09-724-676A-7074	Sequence 7074, Ap
c 605	11	73.3	4396	5	US-09-724-676A-32203	Sequence 32203, A	c 678	11	73.3	6212	6	US-10-240-425-1218	Sequence 1218, Ap
c 606	11	73.3	4440	5	US-09-724-676-32207	Sequence 32207, A	c 679	11	73.3	6236	5	US-09-724-676-7043	Sequence 7043, Ap
c 607	11	73.3	4440	5	US-09-724-676A-32207	Sequence 32207, A	c 680	11	73.3	6236	5	US-09-724-676-7103	Sequence 7103, Ap
c 608	11	73.3	4467	5	US-09-724-676-7092	Sequence 7092, Ap	c 681	11	73.3	6236	5	US-09-724-676A-7043	Sequence 7043, Ap
c 609	11	73.3	4467	5	US-09-724-676A-7092	Sequence 7092, Ap	c 682	11	73.3	6236	5	US-09-724-676A-7103	Sequence 7103, Ap
c 610	11	73.3	4503	5	US-09-724-676-7023	Sequence 7023, Ap	c 683	11	73.3	6566	7	US-60-423-552-60	Sequence 60, Appl



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c 831	10	66.7	496	6	US-10-240-425-15	Sequence 15, App1	c 904	10	66.7	730	5	US-09-513-999C-762	Sequence 762, App
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c 833	10	66.7	500	5	US-09-724-676-40442	Sequence 40442, A	c 906	10	66.7	732	5	US-09-724-676A-6655	Sequence 6655, Ap
c 834	10	66.7	500	5	US-09-724-676A-40442	Sequence 40442, A	c 907	10	66.7	735	5	US-09-134-000C-574	Sequence 574, App
c 835	10	66.7	505	6	US-10-194-163-376	Sequence 376, App	c 908	10	66.7	737	5	US-09-724-676-6669	Sequence 6669, Ap
c 836	10	66.7	509	5	US-09-724-676-38721	Sequence 38721, A	c 909	10	66.7	737	5	US-09-724-676A-6669	Sequence 6669, Ap
c 837	10	66.7	509	5	US-09-724-676A-38721	Sequence 38721, A	c 910	10	66.7	740	5	US-09-724-676-6662	Sequence 6662, Ap
c 838	10	66.7	510	5	US-09-724-676-42133	Sequence 42133, A	c 911	10	66.7	740	5	US-09-724-676A-6662	Sequence 6662, Ap
c 839	10	66.7	510	5	US-09-724-676A-42133	Sequence 42133, A	c 912	10	66.7	745	5	US-09-513-999C-3929	Sequence 3929, Ap
c 840	10	66.7	514	1	PCN-US02-34777-1656	Sequence 1656, Ap	c 913	10	66.7	745	5	US-09-724-676-6680	Sequence 6680, Ap
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c 842	10	66.7	528	6	US-10-240-425-947	Sequence 947, App	c 915	10	66.7	754	5	US-09-724-676-6634	Sequence 6634, Ap
c 843	10	66.7	537	5	US-09-724-676-6682	Sequence 6682, Ap	c 916	10	66.7	763	5	US-09-724-676-6634	Sequence 6634, Ap
c 844	10	66.7	537	5	US-09-724-676A-6682	Sequence 6682, Ap	c 917	10	66.7	763	5	US-09-724-676A-6634	Sequence 6634, Ap
c 845	10	66.7	538	5	US-09-724-676-11024	Sequence 11024, A	c 918	10	66.7	763	5	US-09-724-676A-6636	Sequence 6636, Ap
c 846	10	66.7	538	5	US-09-724-676A-11024	Sequence 11024, A	c 919	10	66.7	766	5	US-09-724-676A-6636	Sequence 6636, Ap
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c 848	10	66.7	563	5	US-09-724-676-40437	Sequence 40437, A	c 921	10	66.7	766	5	US-09-724-676A-6651	Sequence 6651, Ap
c 849	10	66.7	563	5	US-09-724-676A-40437	Sequence 40437, A	c 922	10	66.7	766	5	US-09-724-676A-6653	Sequence 6653, Ap
c 850	10	66.7	569	6	US-10-255-536-235	Sequence 235, App	c 923	10	66.7	768	5	US-09-724-676-6649	Sequence 6649, Ap
c 851	10	66.7	574	6	US-10-203-138A-6731	Sequence 6731, Ap	c 924	10	66.7	768	5	US-09-724-676-6649	Sequence 6649, Ap
c 852	10	66.7	574	6	US-10-203-138A-9954	Sequence 9954, Ap	c 925	10	66.7	768	5	US-09-724-676A-6646	Sequence 6646, Ap
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c 855	10	66.7	580	5	US-09-724-676A-6671	Sequence 6671, Ap	c 928	10	66.7	771	5	US-09-724-676-6644	Sequence 6644, Ap
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c 860	10	66.7	616	5	US-09-724-676-6657	Sequence 6657, Ap	c 933	10	66.7	771	5	US-09-724-676A-6665	Sequence 6665, Ap
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c 863	10	66.7	618	5	US-09-724-676-39073	Sequence 39073, A	c 936	10	66.7	773	5	US-09-724-676A-12360	Sequence 12360, A
c 864	10	66.7	621	5	US-09-724-676A-39073	Sequence 39073, A	c 937	10	66.7	774	5	US-09-724-676-6659	Sequence 6659, Ap
c 865	10	66.7	621	5	US-09-724-676-6670	Sequence 6670, Ap	c 938	10	66.7	774	5	US-09-724-676A-6659	Sequence 6659, Ap
c 866	10	66.7	624	5	US-09-724-676A-6670	Sequence 6670, Ap	c 939	10	66.7	774	5	US-09-724-676A-6661	Sequence 6661, Ap
c 867	10	66.7	624	5	US-09-724-676-6663	Sequence 6663, Ap	c 940	10	66.7	774	6	US-10-092-411A-305	Sequence 305, App
c 868	10	66.7	624	5	US-09-724-676A-6663	Sequence 6663, Ap	c 941	10	66.7	774	6	US-10-092-411A-305	Sequence 305, App
c 869	10	66.7	631	5	US-09-724-676-28472	Sequence 28472, A	c 942	10	66.7	788	5	US-09-724-676-6676	Sequence 6676, Ap
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c 871	10	66.7	653	5	US-09-724-676-6681	Sequence 6681, Ap	c 944	10	66.7	788	5	US-09-724-676A-6676	Sequence 6676, Ap
c 872	10	66.7	653	5	US-09-724-676A-6681	Sequence 6681, Ap	c 945	10	66.7	788	5	US-09-724-676A-6678	Sequence 6678, Ap
c 873	10	66.7	653	6	US-10-145-087A-189	Sequence 189, App	c 946	10	66.7	789	5	US-09-724-676-12369	Sequence 12369, A
c 874	10	66.7	663	6	US-10-143-031A-189	Sequence 189, App	c 947	10	66.7	789	5	US-09-724-676A-12369	Sequence 12369, A
c 875	10	66.7	663	6	US-10-145-092A-189	Sequence 189, App	c 948	10	66.7	796	5	US-09-724-676-6683	Sequence 6683, Ap
c 876	10	66.7	663	6	US-10-162-522A-189	Sequence 189, App	c 949	10	66.7	796	5	US-09-724-676A-6683	Sequence 6683, Ap
c 877	10	66.7	663	6	US-10-165-038A-189	Sequence 189, App	c 950	10	66.7	799	6	US-10-203-138A-7846	Sequence 7846, Ap
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c 885	10	66.7	671	5	US-09-724-676-28476	Sequence 28476, A	c 958	10	66.7	820	5	US-09-513-999C-763	Sequence 763, App
c 886	10	66.7	671	5	US-09-724-676A-28476	Sequence 28476, A	c 959	10	66.7	822	5	US-09-724-676-39084	Sequence 39084, A
c 887	10	66.7	685	6	US-10-264-237-731	Sequence 731, App	c 960	10	66.7	822	5	US-09-724-676A-39084	Sequence 39084, A
c 888	10	66.7	687	5	US-09-724-676-6677	Sequence 6677, Ap	c 961	10	66.7	830	5	US-09-724-676-6637	Sequence 6637, Ap
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c 891	10	66.7	687	5	US-09-724-676A-6679	Sequence 6679, Ap	c 964	10	66.7	833	5	US-09-724-676A-6654	Sequence 6654, Ap
c 892	10	66.7	691	5	US-09-724-676-21190	Sequence 21190, A	c 965	10	66.7	840	5	US-09-724-676-5177	Sequence 5177, Ap
c 893	10	66.7	691	5	US-09-724-676A-21190	Sequence 21190, A	c 966	10	66.7	840	5	US-09-724-676A-5177	Sequence 5177, Ap
c 894	10	66.7	692	6	US-10-240-425-466	Sequence 466, App	c 967	10	66.7	841	5	US-09-724-676-42739	Sequence 42739, A
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c 896	10	66.7	693	5	US-09-724-676A-6656	Sequence 6656, Ap	c 969	10	66.7	843	5	US-09-724-676-5178	Sequence 5178, Ap
c 897	10	66.7	693	5	US-09-724-676-6684	Sequence 6684, Ap	c 970	10	66.7	843	5	US-09-724-676-6615	Sequence 6615, Ap
c 898	10	66.7	695	5	US-09-724-676A-6684	Sequence 6684, Ap	c 971	10	66.7	843	5	US-09-724-676-6632	Sequence 6632, Ap
c 899	10	66.7	696	5	US-09-724-676-6622	Sequence 6622, Ap	c 972	10	66.7	843	5	US-09-724-676A-5178	Sequence 5178, Ap
c 900	10	66.7	696	5	US-09-724-676A-5622	Sequence 6622, Ap	c 973	10	66.7	843	5	US-09-724-676A-6615	Sequence 6615, Ap
c 901	10	66.7	709	5	US-09-513-999C-759	Sequence 759, App	c 974	10	66.7	843	5	US-09-724-676A-6632	Sequence 6632, Ap
c 902	10	66.7	729	5	US-09-724-676-6638	Sequence 6638, Ap	c 975	10	66.7	846	5	US-09-724-676-6617	Sequence 6617, Ap

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c 992 10 66.7 854 5 US-09-724-676-6627 Sequence 6627, Ap  
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c 994 10 66.7 854 5 US-09-724-676A-6625 Sequence 6625, Ap  
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## ALIGNMENTS

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; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 47407  
; LENGTH: 2876  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676-47407

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Db 1422 CCTTCTCGCCCTGTT 1436  
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; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676A  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
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; ORGANISM: Homo sapiens  
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Db 1422 CCTTCTCGCCCTGTT 1436  
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; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 24273  
; LENGTH: 4338  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676-24273

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Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2821 CCTTCTCGCCCTGTT 2807  
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; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676A  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 24273  
; LENGTH: 4338  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676A-24273

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Best Local Similarity 100.0%; Pred. No. 1.7;  
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; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 24268

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; LENGTH: 4848
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-24268

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Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3331 CCTTCTCGCCCTGTT 3317

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; Sequence 24268, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24268
; LENGTH: 4848
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-24268

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
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Db 3331 CCTTCTCGCCCTGTT 3317

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; Sequence 67, Application US/10133937
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,
; TITLE OF INVENTION: DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND
; TITLE OF INVENTION: OTHER BIOLOGICAL STATES
; FILE REFERENCE: 11613.56US01
; CURRENT APPLICATION NUMBER: US/10/133,937
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 99
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US-10-133-937-67

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Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8
US-09-724-676-24272/c
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; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
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; SEQ ID NO 24272
; LENGTH: 5589
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-24272

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Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
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Db 2821 CCTTCTCGCCCTGTT 2807

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; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
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; SEQ ID NO 24272
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US-09-724-676A-24272

Query Match      100.0%; Score 15; DB 5; Length 5589;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15
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Db 2821 CCTTCTCGCCCTGTT 2807

RESULT 10
US-09-724-676-24271/c
; Sequence 24271, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
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; NUMBER OF SEQ ID NOS: 97222
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; SEQ ID NO 24271
; LENGTH: 5642
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-24271

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Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2821 CCTTCTCGCCCTGTT 2807

## RESULT 11

US-09-724-676A-24271/c  
; Sequence 24271, Application US/09724676A  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676A  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 24271  
; LENGTH: 5642  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676A-24271

Query Match 100.0%; Score 15; DB 5; Length 5642;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15

Db 2821 CCTTCTCGCCCTGTT 2807

## RESULT 12

US-09-724-676-24267/c  
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; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 24267  
; LENGTH: 6099  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676-24267

Query Match 100.0%; Score 15; DB 5; Length 6099;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15

Db 3331 CCTTCTCGCCCTGTT 3317

## RESULT 13

US-09-724-676A-24267/c  
; Sequence 24267, Application US/09724676A  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
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; CURRENT APPLICATION NUMBER: US/09/724,676A  
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; NUMBER OF SEQ ID NOS: 97222  
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; LENGTH: 6099  
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; ORGANISM: Homo sapiens  
US-09-724-676A-24267

Query Match 100.0%; Score 15; DB 5; Length 6099;

Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCGCCCTGTT 15

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## RESULT 14

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; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676  
; CURRENT FILING DATE: 2000-11-28  
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; ORGANISM: Homo sapiens  
US-09-724-676-24266

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Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3331 CCTTCTCGCCCTGTT 3317

## RESULT 15

US-09-724-676A-24266/c  
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; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676A  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
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; ORGANISM: Homo sapiens  
US-09-724-676A-24266

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Db 3331 CCTTCTCGCCCTGTT 3317

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

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5	15	100.0	41	1	PCT-US00-35491-6	Sequence 6, Appl
6	15	100.0	41	29	US-09-750-609-5	Sequence 5, Appl
7	15	100.0	41	29	US-09-750-609-6	Sequence 6, Appl
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11	15	100.0	197	36	US-09-960-481-2932	Sequence 2907, Ap
12	15	100.0	248	14	US-09-076-667-2907	Sequence 47840, A
13	15	100.0	248	21	US-09-540-229-47840	Sequence 2907, Ap
14	15	100.0	248	48	US-60-048-002-2907	Sequence 4668, Ap
15	15	100.0	327	24	US-09-637-890-4668	Sequence 2311, Ap
16	15	100.0	327	25	US-09-652-918-2311	Sequence 106084,
17	15	100.0	355	33	US-09-865-439A-106084	Sequence 150004,
18	15	100.0	355	64	US-60-207-458-150004	Sequence 8529, Ap
19	15	100.0	376	22	US-09-552-086-8529	Sequence 3885, Ap
20	15	100.0	393	3	US-07-952-911-3885	Sequence 23661, A
21	15	100.0	393	16	US-09-293-972-23661	



Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGTT 15  
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Db 14 CCTTCTCCCTGTT 28

RESULT 5  
PCT-US00-35491-6/c  
; Sequence 6, Application PC/TUS0035491  
; GENERAL INFORMATION:  
; APPLICANT: Robertson, David  
; APPLICANT: Blakely, Randy D.  
; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND  
; FILE REFERENCE: Attorney Docket No. 1242-27-2-2  
; CURRENT APPLICATION NUMBER: PCT/US00/35491  
; CURRENT FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: 60/175,456  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: 60/173,682  
; PRIOR FILING DATE: 1999-12-29  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 41  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US00-35491-6

Query Match 100.0%; Score 15; DB 1; Length 41;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGTT 15  
|||||

Db 28 CCTTCTCCCTGTT 14

RESULT 6  
US-09-750-609-5  
; Sequence 5, Application US/09750609  
; GENERAL INFORMATION:  
; APPLICANT: Robertson, David  
; APPLICANT: Blakely, Randy D.  
; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND  
; FILE REFERENCE: Attorney Docket No. 1242-27-2-2  
; CURRENT APPLICATION NUMBER: US/09/750,609  
; CURRENT FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: 60/175,456  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: 60/173,682  
; PRIOR FILING DATE: 1999-12-29  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 41  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-750-609-5

Query Match 100.0%; Score 15; DB 29; Length 41;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGTT 15  
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Db 14 CCTTCTCCCTGTT 28

RESULT 7  
US-09-750-609-6/c

; Sequence 6, Application US/09750609  
; GENERAL INFORMATION:  
; APPLICANT: Robertson, David  
; APPLICANT: Blakely, Randy D.  
; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND  
; FILE REFERENCE: Attorney Docket No. 1242-27-2-2  
; CURRENT APPLICATION NUMBER: US/09/750,609  
; CURRENT FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: 60/175,456  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: 60/173,682  
; PRIOR FILING DATE: 1999-12-29  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 41  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-750-609-6

Query Match 100.0%; Score 15; DB 29; Length 41;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGTT 15  
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Db 28 CCTTCTCCCTGTT 14

RESULT 8  
US-60-173-682-5  
; Sequence 5, Application US/60173682  
; GENERAL INFORMATION:  
; APPLICANT: Robertson, David  
; APPLICANT: Blakely, Randy D.  
; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND  
; FILE REFERENCE: Attorney Docket No. 1242-27  
; CURRENT APPLICATION NUMBER: US/60/173,682  
; CURRENT FILING DATE: 1999-12-29  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 41  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-173-682-5

Query Match 100.0%; Score 15; DB 61; Length 41;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGTT 15  
|||||

Db 14 CCTTCTCCCTGTT 28

RESULT 9  
US-60-173-682-6/c  
; Sequence 6, Application US/60173682  
; GENERAL INFORMATION:  
; APPLICANT: Robertson, David  
; APPLICANT: Blakely, Randy D.  
; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND  
; FILE REFERENCE: Attorney Docket No. 1242-27  
; CURRENT APPLICATION NUMBER: US/60/173,682  
; CURRENT FILING DATE: 1999-12-29  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 41

; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-173-682-6

Query Match 100.0%; Score 15; DB 61; Length 41;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGTT 15  
Db 28 CCTTCTCCCTGTT 14  
|||||

RESULT 10  
US-09-306-349-2932  
; Sequence 2932, Application US/09306349  
; GENERAL INFORMATION:  
; APPLICANT: Byrum, Joseph R.  
; APPLICANT: Heck, Gregory R.  
; APPLICANT: La Rosa, Thomas J.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(15367)B  
; CURRENT APPLICATION NUMBER: US/09/306,349  
; CURRENT FILING DATE: 1999-05-07  
; NUMBER OF SEQ ID NOS: 53893  
; SEQ ID NO 2932  
; LENGTH: 197  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: unsure at all n locations  
; OTHER INFORMATION: Clone ID: 701040886H1  
US-09-306-349-2932

Query Match 100.0%; Score 15; DB 17; Length 197;  
Best Local Similarity 100.0%; Pred. No. 3.6e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGTT 15  
Db 3 CCTTCTCCCTGTT 17  
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RESULT 11  
US-09-960-481-2932  
; Sequence 2932, Application US/09960481  
; GENERAL INFORMATION:  
; APPLICANT: Byrum, Joseph R.  
; APPLICANT: Heck, Gregory R.  
; APPLICANT: La Rosa, Thomas J.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(15367)C  
; CURRENT APPLICATION NUMBER: US/09/960,481  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: US 09/306,349  
; PRIOR FILING DATE: 1999-05-10  
; NUMBER OF SEQ ID NOS: 53893  
; SEQ ID NO 2932  
; LENGTH: 197  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1).(197)  
; OTHER INFORMATION: unsure at all n locations  
; OTHER INFORMATION: Clone ID: 701040886H1  
US-09-960-481-2932

Query Match 100.0%; Score 15; DB 36; Length 197;  
Best Local Similarity 100.0%; Pred. No. 3.6e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGTT 15  
Db 3 CCTTCTCCCTGTT 17  
|||||

RESULT 12  
US-09-076-667-2907  
; Sequence 2907, Application US/09076667  
; GENERAL INFORMATION:  
; APPLICANT: Gooding, Douglas H.  
; APPLICANT: Stuve, Laura L.  
; APPLICANT: Stuart, Susan G.  
; APPLICANT: Ito, Laura Y.  
; APPLICANT: Akerblom, Ingrid E.  
; APPLICANT: Delegeane, Angelo M.  
; APPLICANT: Naughton, Rebecca E.  
; APPLICANT: Klingler, Tod M.  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM  
; TITLE OF INVENTION: HUMAN BRAIN  
; NUMBER OF SEQUENCES: 4483  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/076,667  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CERRONE, MICHAEL C.  
; REGISTRATION NUMBER: 39,132  
; REFERENCE/DOCKET NUMBER: PD-0370P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 855-0555  
; TELEFAX: (415) 845-4166  
; INFORMATION FOR SEQ ID NO: 2907:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 248 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; CLONE: 3268389H1  
US-09-076-667-2907

Query Match 100.0%; Score 15; DB 14; Length 248;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGTT 15  
Db 75 CCTTCTCCCTGTT 89  
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RESULT 13  
US-09-540-229-47840  
; Sequence 47840, Application US/09540229  
; GENERAL INFORMATION:  
; APPLICANT: Seilhamer, Jeffrey J.  
; APPLICANT: Delegeane, Angelo M.  
; APPLICANT: Stuart, Susan G.  
; APPLICANT: Stuve, Laura L.  
; APPLICANT: Mullahy, Sara J.

```
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF NERVOUS SYSTEM AND SENSORY ORGANS
; FILE REFERENCE: PD-1033 CIP
; CURRENT APPLICATION NUMBER: US/09/540,229
; CURRENT FILING DATE: 2000-03-31
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 193582
; SOFTWARE: PERL Program
; SEQ ID NO 47840
; LENGTH: 248
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu00535318
; NAME/KEY: unsure
; LOCATION: 211
; OTHER INFORMATION: a, t, c, g, or other
US-09-540-229-47840

Query Match      100.0%; Score 15; DB 21; Length 248;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCTCCCCCTGTT 15
Db 75 CCTCTCCCCCTGTT 89

RESULT 14
US-60-048-002-2907
; Sequence 2907, Application US/60048002
; GENERAL INFORMATION:
; APPLICANT: Gooding, Douglas H.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Akerblom, Ingrid E.
; APPLICANT: Delegeane, Angelo M.
; APPLICANT: Naughton, Rebecca E.
; APPLICANT: Klingler, Tod M.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
; TITLE OF INVENTION: HUMAN BRAIN
; NUMBER OF SEQUENCES: 4483
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/60/048,002
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PD-0370P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 855-0555
; TELEFAX: (415) 845-4166
; INFORMATION FOR SEQ ID NO: 2907:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; MOLECULE TYPE: CDNA
; IMMEDIATE SOURCE:
; CLONE: 3268389H1
US-60-048-002-2907

Query Match      100.0%; Score 15; DB 48; Length 248;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCTCCCCCTGTT 15
Db 75 CCTCTCCCCCTGTT 89

RESULT 15
US-09-637-890-4668/c
; Sequence 4668, Application US/09637890
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Galvin, Katherine A.
; APPLICANT: Culpepper, Janice A.
; APPLICANT: Leiby, Kevin R.
; APPLICANT: Vasicek, Tom
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Villevall, Jean-Luc M. G.
; APPLICANT: Cepada, Mario
; APPLICANT: Kingsbury, Gillian A.
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.1152-001
; CURRENT APPLICATION NUMBER: US/09/637,890
; CURRENT FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 60/147,939
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 10217
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4668
; LENGTH: 327
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-637-890-4668

Query Match      100.0%; Score 15; DB 24; Length 327;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCTCCCCCTGTT 15
Db 168 CCTCTCCCCCTGTT 154

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

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(without alignments)  
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Title: US-09-750-609-10  
Perfect score: 15  
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Searched: 407964 seqs, 359371392 residues

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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- 2: /cgn2.6/ptodata/1/pna/US06\_NEW\_COMB.seq:\*
- 3: /cgn2.6/ptodata/1/pna/US07\_NEW\_COMB.seq:\*
- 4: /cgn2.6/ptodata/1/pna/US08\_NEW\_COMB.seq:\*
- 5: /cgn2.6/ptodata/1/pna/US09\_NEW\_COMB.seq:\*
- 6: /cgn2.6/ptodata/1/pna/US10\_NEW\_COMB.seq:\*
- 7: /cgn2.6/ptodata/1/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15	100.0	352	5	US-09-513-999C-13316
C 2	15	100.0	2520	6	US-10-264-237-1036
C 3	14	93.3	248	5	US-09-620-607B-1245
C 4	14	93.3	908	5	US-09-724-676-38339
C 5	14	93.3	908	5	US-09-724-676A-38339
C 6	14	93.3	1030	5	US-09-724-676-24274
C 7	14	93.3	1030	5	US-09-724-676A-24274
C 8	14	93.3	1509	5	US-09-724-676-2247
C 9	14	93.3	1509	5	US-09-724-676A-2247
C 10	14	93.3	1667	5	US-09-724-676-2234
C 11	14	93.3	1667	5	US-09-724-676A-2234
C 12	14	93.3	1712	5	US-09-724-676-2221
C 13	14	93.3	1712	5	US-09-724-676A-2221
C 14	14	93.3	1755	5	US-09-724-676-2240
C 15	14	93.3	1755	5	US-09-724-676A-2240
C 16	14	93.3	1825	5	US-09-724-676-2246
C 17	14	93.3	1825	5	US-09-724-676A-2246
C 18	14	93.3	1871	5	US-09-724-676-2245
C 19	14	93.3	1871	5	US-09-724-676A-2245
C 20	14	93.3	1913	5	US-09-724-676-2227
C 21	14	93.3	1913	5	US-09-724-676A-2227
C 22	14	93.3	1958	5	US-09-724-676-2214
C 23	14	93.3	1958	5	US-09-724-676A-2214
C 24	14	93.3	1983	5	US-09-724-676-2233
C 25	14	93.3	1983	5	US-09-724-676A-2233
C 26	14	93.3	2028	5	US-09-724-676-2220
C 27	14	93.3	2028	5	US-09-724-676A-2220

C 27	14	93.3	2028	5	US-09-724-676A-2220	Sequence 2220, Ap
C 28	14	93.3	2029	5	US-09-724-676-2232	Sequence 2232, Ap
C 29	14	93.3	2029	5	US-09-724-676A-2232	Sequence 2232, Ap
C 30	14	93.3	2071	5	US-09-724-676-2239	Sequence 2239, Ap
C 31	14	93.3	2071	5	US-09-724-676A-2239	Sequence 2239, Ap
C 32	14	93.3	2072	5	US-09-724-676-2251	Sequence 2251, Ap
C 33	14	93.3	2072	5	US-09-724-676A-2251	Sequence 2251, Ap
C 34	14	93.3	2074	5	US-09-724-676-2218	Sequence 2218, Ap
C 35	14	93.3	2074	5	US-09-724-676A-2218	Sequence 2218, Ap
C 36	14	93.3	2117	5	US-09-724-676-2238	Sequence 2238, Ap
C 37	14	93.3	2117	5	US-09-724-676A-2238	Sequence 2238, Ap
C 38	14	93.3	2229	5	US-09-724-676-2226	Sequence 2226, Ap
C 39	14	93.3	2229	5	US-09-724-676A-2226	Sequence 2226, Ap
C 40	14	93.3	2274	5	US-09-724-676-2213	Sequence 2213, Ap
C 41	14	93.3	2274	5	US-09-724-676A-2213	Sequence 2213, Ap
C 42	14	93.3	2275	5	US-09-724-676-2225	Sequence 2225, Ap
C 43	14	93.3	2275	5	US-09-724-676A-2225	Sequence 2225, Ap
C 44	14	93.3	2320	5	US-09-724-676-2212	Sequence 2212, Ap
C 45	14	93.3	2320	5	US-09-724-676A-2212	Sequence 2212, Ap

ALIGNMENTS

RESULT 1  
US-09-513-999C-13316/C  
; Sequence 13316, Application US/09513999C  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: 59, US2, REG  
; CURRENT APPLICATION NUMBER: US/09/513, 999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 13316  
; LENGTH: 352  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 298  
; OTHER INFORMATION: k-g or t  
; NAME/KEY: misc\_feature  
; LOCATION: 330  
; OTHER INFORMATION: r-a or g  
US-09-513-999C-13316  
Query Match 100.0%; Score 15; DB 5; Length 352;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CTTCTCCCCCTGTT 15  
Db 149 CTTCTCCCCCTGTT 135  
RESULT 2  
US-10-264-237-1036  
; Sequence 1036, Application US/10264237  
; GENERAL INFORMATION:  
; APPLICANT: Birse et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PAL31PI  
; CURRENT APPLICATION NUMBER: US/10/264, 237  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: PCT/US01/16450  
; PRIOR FILING DATE: 2001-05-18

; PRIOR APPLICATION NUMBER: US 60/205,515  
; PRIOR FILING DATE: 2000-05-19  
; NUMBER OF SEQ ID NOS: 2876  
; SOFTWARE: PatentIn Ver. 3.1  
; SEQ ID NO 1036  
; LENGTH: 2520  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (99)-(99)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-10-264-237-1036

Query Match 100.0%; Score 15; DB 6; Length 2520;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGTT 15  
| | | | | | | | | | | | | | | | | | | | | |  
DB 1062 CCTTCTCCCCCTGTT 1076

RESULT 3  
US-09-620-607B-1245/C  
; Sequence 1245, Application US/09620607B  
; GENERAL INFORMATION:  
; APPLICANT: Nehls, Michael  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: Novel Mutated Mammalian Cells and  
; TITLE OF INVENTION: Animals  
; FILE REFERENCE: LEX-0032-USA  
; CURRENT APPLICATION NUMBER: US/09/620,607B  
; CURRENT FILING DATE: 2000-07-20  
; PRIOR APPLICATION NUMBER: US 60/144942  
; PRIOR FILING DATE: 1999-07-20  
; NUMBER OF SEQ ID NOS: 1848  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1245  
; LENGTH: 248  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-620-607B-1245

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DB 88 CTCTCTCCCCCTGTT 75

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US-09-724-676-38339  
; Sequence 38339, Application US/09724676  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 38339  
; LENGTH: 908  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676-38339

Query Match 93.3%; Score 14; DB 5; Length 908;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCTTCTCCCCCTGT 14  
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DB 444 CCTTCTCCCCCTGT 457

RESULT 5  
US-09-724-676A-38339  
; Sequence 38339, Application US/09724676A  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676A  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 38339  
; LENGTH: 908  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676A-38339

Query Match 93.3%; Score 14; DB 5; Length 908;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14  
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DB 444 CCTTCTCCCCCTGT 457

RESULT 6  
US-09-724-676-24274/C  
; Sequence 24274, Application US/09724676  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 24274  
; LENGTH: 1030  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676-24274

Query Match 93.3%; Score 14; DB 5; Length 1030;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14  
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DB 692 CCTTCTCCCCCTGT 679

RESULT 7  
US-09-724-676A-24274/C  
; Sequence 24274, Application US/09724676A  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676A  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 24274  
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; TYPE: DNA  
US-09-724-676A-24274



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; ORGANISM: Homo sapiens
US-09-724-676A-24274

Query Match          93.3%; Score 14; DB 5; Length 1030;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14
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Db 692 CCTTCTCCCCCTGT 679

RESULT 8
US-09-724-676-2247/c
; Sequence 2247, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2247
; LENGTH: 1509
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-2247

Query Match          93.3%; Score 14; DB 5; Length 1509;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14
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Db 831 CCTTCTCCCCCTGT 818

RESULT 9
US-09-724-676A-2247/c
; Sequence 2247, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2247
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-2247

Query Match          93.3%; Score 14; DB 5; Length 1509;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14
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Db 831 CCTTCTCCCCCTGT 818

RESULT 10
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; Sequence 2234, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2234
; LENGTH: 1509
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-2234

Query Match          93.3%; Score 14; DB 5; Length 1509;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14
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Db 831 CCTTCTCCCCCTGT 818

RESULT 11
US-09-724-676A-2234/c
; Sequence 2234, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2234
; LENGTH: 1667
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-2234

Query Match          93.3%; Score 14; DB 5; Length 1667;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14
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Db 989 CCTTCTCCCCCTGT 976

RESULT 12
US-09-724-676-2221/c
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; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2221
; LENGTH: 1712
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-2221

Query Match          93.3%; Score 14; DB 5; Length 1712;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14
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Db 1034 CCTTCTCCCCCTGT 1021

RESULT 13
US-09-724-676A-2221/c
; Sequence 2221, Application US/09724676A
; GENERAL INFORMATION:
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;; TITLE OF INVENTION: Variants of alternative splicing  
;; FILE REFERENCE: 129181.4 Compugen  
;; CURRENT APPLICATION NUMBER: US/09/724,676A  
;; CURRENT FILING DATE: 2000-11-28  
;; NUMBER OF SEQ ID NOS: 97222  
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;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-724-676A-2221

Query Match 93.3%; Score 14; DB 5; Length 1712;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14  
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Db 1034 CCTTCTCCCCCTGT 1021

RESULT 14  
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; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
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; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676-2240

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Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
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Db 831 CCTTCTCCCCCTGT 818

RESULT 15  
US-09-724-676A-2240/c  
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; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676A  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2240  
; LENGTH: 1755  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676A-2240

Query Match 93.3%; Score 14; DB 5; Length 1755;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14  
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Db 831 CCTTCTCCCCCTGT 818

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c	32	15	100.0	435	22	US-09-560-875A-9898	Sequence 9898, Ap		105	15	100.0	15857	39	US-10-080-129-1704	Sequence 1704, Ap
c	33	15	100.0	445	30	US-09-785-276A-50356	Sequence 50356, A		106	15	100.0	15857	40	US-10-105-299-15118	Sequence 15118, A
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	35	15	100.0	452	34	US-09-906-555-10936	Sequence 10936, A		108	15	100.0	133311	65	US-60-212-664-230	Sequence 230, App
	36	15	100.0	456	20	US-09-534-846B-25592	Sequence 25592, A		109	15	100.0	391912	69	US-60-258-251-25	Sequence 25, Appl
	37	15	100.0	463	29	US-09-726-806-1928	Sequence 1928, Ap		110	14	93.3	51	79	US-60-353-987-723033	Sequence 723033, A
	38	15	100.0	467	25	US-09-654-617-15997	Sequence 15997, A		111	14	93.3	25	71	US-60-278-258-17443	Sequence 186, App
	39	15	100.0	467	27	US-09-684-016-15997	Sequence 15997, A		112	14	93.3	202	8	US-08-438-571A-186	Sequence 7766, Ap
c	40	15	100.0	474	24	US-09-634-306B-64600	Sequence 64600, A		113	14	93.3	220	23	US-09-606-977-7766	Sequence 7766, Ap
c	41	15	100.0	474	38	US-10-027-632-64600	Sequence 64600, A		114	14	93.3	241	69	US-60-253-456-5758	Sequence 5758, Ap
	42	15	100.0	492	81	US-60-377-240-8398	Sequence 8398, Ap		115	14	93.3	251	22	US-09-572-409-13665	Sequence 13665, A
	43	15	100.0	509	1	PCT-US01-08631-1856	Sequence 1856, Ap		116	14	93.3	252	13	US-08-999-861-2887	Sequence 2887, Ap
	44	15	100.0	549	1	US-09-652-918-998	Sequence 998, App		117	14	93.3	252	46	US-60-028-852-286	Sequence 286, App
c	45	15	100.0	607	26	US-09-663-784-184	Sequence 184, App		118	14	93.3	264	21	US-09-540-212A-51596	Sequence 51596, A
c	46	15	100.0	676	24	US-09-634-306B-308408	Sequence 308408, A		119	14	93.3	269	12	US-08-823-271-1772	Sequence 1772, Ap
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	48	15	100.0	676	38	US-10-027-632-97105	Sequence 97105, A		121	14	93.3	272	21	US-09-540-766-55791	Sequence 55791, A
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c 178	14	93.3	477	38	US-10-027-632-63180	Sequence 63180, A	c 251	14	93.3	2624	28	US-09-702-134-18044	Sequence 18044, A
c 179	14	93.3	477	38	US-10-027-632-310263	Sequence 310263,	c 252	14	93.3	2624	31	US-09-815-264-77331	Sequence 77331, A
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c 187	14	93.3	491	38	US-10-027-632-287701	Sequence 287701,	c 260	14	93.3	2658	29	US-09-726-807-3209	Sequence 3209, Ap
c 188	14	93.3	496	34	US-09-920-953-8229	Sequence 8229, Ap	c 261	14	93.3	2740	80	US-09-629-469A-10998	Sequence 74, Appl
c 189	14	93.3	497	6	US-08-276-163B-7505	Sequence 7505, Ap	c 262	14	93.3	2775	24	US-09-629-469A-10998	Sequence 10998, A
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c 191	14	93.3	497	6	US-08-276-163B-7505	Sequence 7505, Ap	c 264	14	93.3	2953	24	US-09-634-306B-112395	Sequence 112395,
c 192	14	93.3	509	25	US-09-840-145-7505	Sequence 7505, Ap	c 265	14	93.3	2953	38	US-10-027-632-112395	Sequence 112395,
c 193	14	93.3	509	25	US-09-649-161-7119	Sequence 7119, Ap	c 266	14	93.3	2977	29	US-09-758-455-99	Sequence 99, Appl
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c 195	14	93.3	561	25	US-09-644-873-6239	Sequence 6239, Ap	c 268	14	93.3	3250	80	US-09-360-207-40578	Sequence 40578, A
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c 197	14	93.3	574	38	US-10-029-386-12679	Sequence 12679, A	c 270	14	93.3	3308	24	US-09-620-392-24732	Sequence 24732, A
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c 317	14	93.3	13169	28	US-09-702-134-25267	Sequence 25267, A	390	13	86.7	209	1	PCT-US01-00663-24656	Sequence 24656, A
c 318	14	93.3	13169	31	US-09-815-264-64690	Sequence 64690, A	391	13	86.7	209	33	US-09-864-761-23954	Sequence 23954, A
c 319	14	93.3	13169	24	US-09-620-392-39822	Sequence 39822, A	392	13	86.7	209	41	US-10-182-993-23954	Sequence 18503, A
c 320	14	93.3	13670	24	PCT-US01-01334-12825	Sequence 12825, A	393	13	86.7	209	41	US-10-182-997-17058	Sequence 17058, A
c 321	14	93.3	16877	1	PCT-US01-01338-3349	Sequence 3349, App	394	13	86.7	209	42	US-10-203-134-24588	Sequence 24588, A
c 322	14	93.3	16877	30	US-09-764-874-12825	Sequence 12825, A	395	13	86.7	209	42	US-10-203-135-23512	Sequence 23512, A
c 323	14	93.3	16877	30	US-09-764-877-3349	Sequence 3349, App	396	13	86.7	209	42	US-10-203-136-24667	Sequence 24667, A
c 324	14	93.3	16877	39	US-10-092-400-12825	Sequence 12825, A	397	13	86.7	209	42	US-10-203-137-24656	Sequence 24656, A
c 325	14	93.3	16877	42	US-10-242-515-3349	Sequence 3349, App	398	13	86.7	209	42	US-10-203-139-23708	Sequence 23708, A
c 326	14	93.3	17278	24	US-09-620-392-50417	Sequence 50417, A	399	13	86.7	209	42	US-10-203-139-23708	Sequence 23708, A
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c 328	14	93.3	18651	31	US-09-815-264-74799	Sequence 74799, A	401	13	86.7	210	18	US-09-504-629A-616	Sequence 616, App
c 329	14	93.3	18676	68	US-60-248-505-428	Sequence 428, App	402	13	86.7	210	19	US-09-519-444-616	Sequence 616, App
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c 335	14	93.3	24371	31	US-09-815-264-64612	Sequence 64612, A	408	13	86.7	210	34	US-10-025-380-616	Sequence 616, App
c 336	14	93.3	25578	24	US-09-620-392-11061	Sequence 11061, A	409	13	86.7	215	25	US-09-654-617-41822	Sequence 41822, A
c 337	14	93.3	25580	28	US-09-702-134-5224	Sequence 5224, App	410	13	86.7	215	27	US-09-684-016-41822	Sequence 41822, A
c 338	14	93.3	25580	31	US-09-815-264-64882	Sequence 64882, A	411	13	86.7	216	21	US-09-540-208-58170	Sequence 58170, A
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c 343	14	93.3	32152	30	US-09-760-485-1024	Sequence 1024, App	416	13	86.7	220	17	US-09-304-517A-18599	Sequence 18599, A
c 344	14	93.3	32152	42	US-10-216-436-1024	Sequence 1024, App	417	13	86.7	220	17	US-09-371-146A-18599	Sequence 18599, A
c 345	14	93.3	32152	42	US-10-216-583-1928	Sequence 1928, App	418	13	86.7	220	25	US-09-654-617-31157	Sequence 31157, A
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c 356	14	93.3	61710	39	US-10-092-399-38594	Sequence 479, App	429	13	86.7	238	33	US-08-901-902-320	Sequence 320, App
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c 358	14	93.3	79257	35	US-09-948-933-517	Sequence 8350, App	431	13	86.7	240	20	US-09-623-379-320	Sequence 320, App
c 359	14	93.3	135259	1	PCT-US02-25766-8350	Sequence 145, App	432	13	86.7	240	46	US-60-253-653-11281	Sequence 11281, A
c 360	14	93.3	157897	68	US-60-243-468-145	Sequence 145, App	433	13	86.7	243	69	US-08-865-594-4898	Sequence 4898, App
c 361	14	93.3	157897	49	US-09-404-520-32861	Sequence 32861, A	434	13	86.7	245	12	US-60-253-653-11281	Sequence 11281, A
c 362	13	86.7	49	18	US-09-755-374A-25269	Sequence 25269, A	435	13	86.7	245	21	US-09-540-229-84487	Sequence 84487, A
c 363	13	86.7	51	29	US-09-755-374A-25270	Sequence 25270, A	436	13	86.7	246	20	US-60-253-653-26828	Sequence 26828, A
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c 370	13	86.7	115	13	US-08-992-868-4324	Sequence 4324, App	443	13	86.7	251	20	US-60-025-467-1314	Sequence 1314, App
c 371	13	86.7	115	20	US-09-535-896-15613	Sequence 15613, A	444	13	86.7	256	17	US-09-306-349-10394	Sequence 10394, A
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c 374	13	86.7	157	25	US-09-684-016-339478	Sequence 339478, A	447	13	86.7	261	27	US-09-688-848-2168	Sequence 2168, App
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c 376	13	86.7	157	12	US-08-824-029-1943	Sequence 1943, App	449	13	86.7	263	69	US-60-253-653-18301	Sequence 18301, A
c 377	13	86.7	157	12	US-09-535-896-15597	Sequence 15597, A	450	13	86.7	263	69	US-08-943-978-2326	Sequence 2326, App
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c 468	13	86.7	273	20	US-09-535-896-15584	Sequence 15584, A	c 541	13	86.7	337	17	US-09-332-782-11470	Sequence 11470, A
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c 470	13	86.7	273	34	US-09-912-292-18493	Sequence 18493, A	543	13	86.7	337	17	US-09-362-510A-32072	Sequence 32072, A
c 471	13	86.7	276	20	US-09-534-840-3044	Sequence 3044, Ap	c 544	13	86.7	337	19	US-09-515-694-11470	Sequence 11470, A
c 472	13	86.7	276	20	US-09-535-896-1824	Sequence 1824, Ap	545	13	86.7	337	29	US-09-724-750-7131	Sequence 7131, Ap
c 473	13	86.7	281	21	US-09-540-222-155393	Sequence 155393, A	c 546	13	86.7	337	33	US-09-867-701-10110	Sequence 10110, A
c 474	13	86.7	281	58	US-60-141-232-1591	Sequence 1591, Ap	547	13	86.7	337	33	US-09-904-013-32072	Sequence 32072, A
c 475	13	86.7	283	20	US-09-534-840-3041	Sequence 3041, Ap	548	13	86.7	337	61	US-60-171-431-7131	Sequence 7131, Ap
c 476	13	86.7	283	21	US-09-540-768-56324	Sequence 56324, A	c 549	13	86.7	337	64	US-60-207-484-10110	Sequence 10110, A
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c 479	13	86.7	285	64	US-60-207-484-4769	Sequence 4769, Ap	c 552	13	86.7	340	14	US-09-076-897B-1595	Sequence 1595, Ap
c 480	13	86.7	286	14	US-09-070-695A-2154	Sequence 2154, Ap	c 553	13	86.7	340	14	US-09-076-897C-1595	Sequence 1595, Ap
c 481	13	86.7	286	20	US-09-534-858-4461	Sequence 4461, Ap	c 554	13	86.7	340	63	US-60-197-872-25027	Sequence 25027, A
c 482	13	86.7	286	20	US-09-535-896-15618	Sequence 15618, A	555	13	86.7	342	29	US-09-724-750-4861	Sequence 4861, Ap
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c 487	13	86.7	292	29	US-09-724-750-9042	Sequence 9042, Ap	560	13	86.7	344	6	US-08-221-623A-305	Sequence 305, App
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c 490	13	86.7	294	21	US-09-540-212A-58952	Sequence 58952, A	563	13	86.7	344	14	US-09-076-897-1504	Sequence 1504, Ap
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c 492	13	86.7	297	29	US-09-724-750-715	Sequence 49890, A	565	13	86.7	344	14	US-09-076-897B-1504	Sequence 1504, Ap
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c 520	13	86.7	322	63	US-60-197-873-33738	Sequence 33738, A	c 593	13	86.7	365	17	US-09-362-510-29944	Sequence 29944, A
c 521	13	86.7	324	18	US-09-436-762A-31898	Sequence 31898, A	c 594	13	86.7	365	19	US-09-362-510A-29944	Sequence 29944, A
c 522	13	86.7	324	19	US-09-521-640-136599	Sequence 136599, A	c 595	13	86.7	365	17	US-09-521-640-237689	Sequence 237689, A
c 523	13	86.7	325	8	US-08-401-791A-14322	Sequence 14322, A	596	13	86.7	365	34	US-09-904-013-29944	Sequence 29944, A
c 524	13	86.7	325	8	US-08-401-791B-14322	Sequence 14322, A	c 597	13	86.7	365	58	US-60-140-769-32438	Sequence 32438, A
c 525	13	86.7	327	28	US-09-710-281-3084	Sequence 3084, Ap	c 598	13	86.7	366	25	US-09-654-617-369258	Sequence 369258, A
c 526	13	86.7	329	32	US-09-834-366-51421	Sequence 51421, A	c 599	13	86.7	366	27	US-09-684-016-369258	Sequence 369258, A
c 527	13	86.7	329	63	US-60-197-873-51421	Sequence 51421, A	c 600	13	86.7	369	24	US-09-637-086A-43691	Sequence 43691, A
c 528	13	86.7	330	18	US-09-489-036-25995	Sequence 25995, A	c 601	13	86.7	369	24	US-09-637-086B-43691	Sequence 43691, A
c 529	13	86.7	330	35	US-09-943-143-25995	Sequence 25995, A	c 602	13	86.7	369	25	US-09-654-617-227387	Sequence 227387, A
c 530	13	86.7	335	16	US-09-205-070-42231	Sequence 42231, A	c 603	13	86.7	369	27	US-09-684-016-227387	Sequence 227387, A
c 531	13	86.7	335	17	US-09-321-214-20037	Sequence 20037, A	c 604	13	86.7	371	32	US-09-849-526A-14850	Sequence 14850, A
c 532	13	86.7	335	17	US-09-340-623-42231	Sequence 42231, A	c 605	13	86.7	371	64	US-60-202-214-14605	Sequence 14605, A



c 606	13	86.7	372	19	US-09-519-705-748	Sequence 748, App	679	13	86.7	401	1	PCT-US01-03800A-115	Sequence 115, App
c 607	13	86.7	372	19	US-09-519-705-1257	Sequence 1257, App	680	13	86.7	401	16	US-09-293-972-30063	Sequence 30063, A
c 608	13	86.7	372	22	US-09-574-454-748	Sequence 748, App	681	13	86.7	401	16	US-09-496-914A-1464	Sequence 1464, Ap
c 609	13	86.7	372	22	US-09-574-454-1257	Sequence 1257, App	682	13	86.7	401	22	US-09-560-875A-1464	Sequence 1464, Ap
c 610	13	86.7	372	42	US-10-221-279-739	Sequence 739, App	683	13	86.7	401	34	US-09-904-939-30063	Sequence 30063, A
c 611	13	86.7	372	42	US-10-221-279-1241	Sequence 1241, App	c 684	13	86.7	403	23	US-09-606-977-54854	Sequence 54854, A
c 612	13	86.7	373	1	PCT-US01-01354-1599	Sequence 1599, App	685	13	86.7	404	25	US-09-606-977-3241	Sequence 3241, Ap
c 613	13	86.7	373	30	US-09-764-905-1599	Sequence 1599, App	686	13	86.7	405	16	US-09-644-871-33009	Sequence 33009, A
c 614	13	86.7	373	39	US-10-092-399-1599	Sequence 1599, App	687	13	86.7	405	16	US-09-235-076-33009	Sequence 33009, A
c 615	13	86.7	373	41	US-10-155-881-12327	Sequence 12327, App	688	13	86.7	405	17	US-09-277-227-414	Sequence 414, App
c 616	13	86.7	373	63	US-60-197-872-43332	Sequence 43332, A	689	13	86.7	405	29	US-09-332-782-33009	Sequence 33009, A
c 617	13	86.7	374	23	US-09-606-977-35488	Sequence 35488, A	690	13	86.7	405	34	US-09-737-223-33009	Sequence 33009, A
c 618	13	86.7	374	31	US-09-824-559-7669	Sequence 7669, App	691	13	86.7	406	34	US-09-909-627-414	Sequence 414, App
c 619	13	86.7	375	5	US-08-196-363-10397	Sequence 10397, A	692	13	86.7	406	35	US-09-918-995-33009	Sequence 33009, A
c 620	13	86.7	375	5	US-08-196-363-10397	Sequence 10397, A	693	13	86.7	406	35	US-09-918-995-33009	Sequence 33009, A
c 621	13	86.7	375	5	US-08-196-363-10397	Sequence 10397, A	694	13	86.7	406	35	US-09-933-524A-93096	Sequence 93096, A
c 622	13	86.7	375	32	US-09-859-490-10397	Sequence 10397, A	695	13	86.7	406	35	US-09-933-524A-93096	Sequence 93096, A
c 623	13	86.7	375	32	US-09-859-490-10397	Sequence 10397, A	696	13	86.7	406	35	US-09-933-524A-93096	Sequence 93096, A
c 624	13	86.7	378	23	US-09-606-977-43452	Sequence 43452, A	697	13	86.7	408	14	US-09-076-897A-5037	Sequence 5037, Ap
c 625	13	86.7	379	23	US-09-606-977-43452	Sequence 43452, A	698	13	86.7	408	14	US-09-076-897B-5037	Sequence 5037, Ap
c 626	13	86.7	379	23	US-09-606-977-43452	Sequence 43452, A	699	13	86.7	408	14	US-09-076-897C-5037	Sequence 5037, Ap
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c 628	13	86.7	379	22	US-09-521-640-43101	Sequence 13068, A	701	13	86.7	408	16	US-09-293-972-20833	Sequence 20833, A
c 629	13	86.7	381	1	PCT-US01-08631-119	Sequence 119, App	c 702	13	86.7	408	17	US-09-362-510-49143	Sequence 49143, A
c 630	13	86.7	381	11	US-08-790-774-1258	Sequence 1258, App	703	13	86.7	408	17	US-09-362-510-49143	Sequence 49143, A
c 631	13	86.7	382	35	US-09-528-409-77283	Sequence 77283, A	704	13	86.7	408	17	US-09-362-510-49143	Sequence 49143, A
c 632	13	86.7	382	35	US-09-528-409-77283	Sequence 77283, A	705	13	86.7	409	17	US-09-362-510-49143	Sequence 49143, A
c 633	13	86.7	382	35	US-09-528-409-77283	Sequence 77283, A	706	13	86.7	409	17	US-09-362-510-49143	Sequence 49143, A
c 634	13	86.7	383	1	PCT-US02-25766-2100	Sequence 2100, App	707	13	86.7	409	25	US-09-521-640-282947	Sequence 282947, A
c 635	13	86.7	383	16	US-09-271-122-928	Sequence 928, App	708	13	86.7	409	25	US-09-521-640-282947	Sequence 282947, A
c 636	13	86.7	383	28	US-09-713-841-928	Sequence 928, App	709	13	86.7	409	25	US-09-521-640-282947	Sequence 282947, A
c 637	13	86.7	383	34	US-09-880-107-1077	Sequence 1077, App	c 710	13	86.7	410	19	US-09-521-640-143677	Sequence 143677, A
c 638	13	86.7	383	34	US-09-927-875-928	Sequence 928, App	711	13	86.7	411	19	US-09-521-640-143677	Sequence 143677, A
c 639	13	86.7	383	34	US-09-927-875-928	Sequence 928, App	712	13	86.7	411	19	US-09-521-640-143677	Sequence 143677, A
c 640	13	86.7	383	34	US-09-927-875-928	Sequence 928, App	713	13	86.7	411	19	US-09-521-640-143677	Sequence 143677, A
c 641	13	86.7	383	34	US-09-927-875-928	Sequence 928, App	714	13	86.7	411	19	US-09-521-640-143677	Sequence 143677, A
c 642	13	86.7	385	26	US-09-654-617-161559	Sequence 161559, A	715	13	86.7	417	35	US-09-528-409-91880	Sequence 91880, A
c 643	13	86.7	385	26	US-09-654-617-161559	Sequence 161559, A	716	13	86.7	417	35	US-09-528-409-91880	Sequence 91880, A
c 644	13	86.7	385	26	US-09-654-617-161559	Sequence 161559, A	717	13	86.7	417	35	US-09-528-409-91880	Sequence 91880, A
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c 648	13	86.7	385	26	US-09-654-617-161559	Sequence 161559, A	721	13	86.7	417	35	US-09-528-409-91880	Sequence 91880, A
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c 653	13	86.7	385	26	US-09-654-617-161559	Sequence 161559, A	726	13	86.7	417	35	US-09-528-409-91880	Sequence 91880, A
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c 655	13	86.7	385	26	US-09-654-617-161559	Sequence 161559, A	728	13	86.7	417	35	US-09-528-409-91880	Sequence 91880, A
c 656	13	86.7	385	26	US-09-654-617-161559	Sequence 161559, A	729	13	86.7	417	35	US-09-528-409-91880	Sequence 91880, A
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c 660	13	86.7	385	26	US-09-654-617-161559	Sequence 161559, A	733	13	86.7	417	35	US-09-528-409-91880	Sequence 91880, A
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c 663	13	86.7	385	26	US-09-654-617-161559	Sequence 161559, A	c 736	13	86.7	417	35	US-09-528-409-91880	Sequence 91880, A
c 664	13	86.7	385	26	US-09-654-617-161559	Sequence 161559, A	737	13	86.7	417	35	US-09-528-409-91880	Sequence 91880, A
c 665	13	86.7	385	26	US-09-654-617-161559	Sequence 161559, A	738	13	86.7	417	35	US-09-528-409-91880	Sequence 91880, A
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c 667	13	86.7	385	26	US-09-654-617-161559	Sequence 161559, A	740	13	86.7	417	35	US-09-528-409-91880	Sequence 91880, A
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c 676	13	86.7	385	26	US-09-654-617-161559	Sequence 161559, A	749	13	86.7	417	35	US-09-528-409-91880	Sequence 91880, A
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c 678	13	86.7	385	26	US-09-654-617-161559	Sequence 161559, A	751	13	86.7	417	35	US-09-528-409-91880	Sequence 91880, A



C 752	13	86.7	425	23	US-09-606-977-29398	Sequence 29398, A	C 825	13	86.7	448	58	US-60-145-146-2015	Sequence 2015, Ap
C 753	13	86.7	426	23	US-09-606-977-49896	Sequence 49896, A	826	13	86.7	448	63	US-60-196-710-3094	Sequence 3094, Ap
C 754	13	86.7	427	17	US-09-306-350A-40222	Sequence 40222, A	827	13	86.7	448	63	US-60-196-718-2876	Sequence 2876, Ap
C 755	13	86.7	427	18	US-09-406-292A-2530	Sequence 2530, Ap	C 828	13	86.7	448	63	US-60-197-872-16931	Sequence 16931, A
C 756	13	86.7	427	19	US-09-521-640-201607	Sequence 201607, A	C 829	13	86.7	449	1	PCT-US01-11993-68	Sequence 68, Appl
C 757	13	86.7	427	34	US-09-909-629-40222	Sequence 40222, A	C 830	13	86.7	449	16	US-09-287-618-31910	Sequence 31910, A
C 758	13	86.7	427	58	US-60-140-769-23038	Sequence 23038, A	831	13	86.7	449	18	US-09-404-284-1048	Sequence 1048, Ap
C 759	13	86.7	429	17	US-09-362-510-13847	Sequence 13847, A	832	13	86.7	449	19	US-09-524-038-1048	Sequence 1048, Ap
C 760	13	86.7	429	17	US-09-362-510A-13847	Sequence 13847, A	833	13	86.7	449	23	US-09-606-977-46916	Sequence 46916, A
C 761	13	86.7	429	34	US-09-904-013-13847	Sequence 13847, A	834	13	86.7	449	38	US-10-011-154-1048	Sequence 1048, Ap
C 762	13	86.7	429	64	US-60-207-458-40267	Sequence 40267, A	835	13	86.7	450	38	US-09-528-409-69973	Sequence 69973, A
C 763	13	86.7	430	23	US-09-606-977-74253	Sequence 74253, A	836	13	86.7	450	39	US-09-866-555-18498	Sequence 18498, A
C 764	13	86.7	431	17	US-09-399-720-20580	Sequence 20580, A	837	13	86.7	450	35	US-09-933-524-69973	Sequence 69973, A
C 765	13	86.7	431	18	US-09-465-877-1424	Sequence 1424, Ap	838	13	86.7	450	35	US-09-933-524A-69973	Sequence 69973, A
C 766	13	86.7	431	19	US-09-528-409-94313	Sequence 94313, A	839	13	86.7	452	16	US-09-248-797-14	Sequence 14, Appl
C 767	13	86.7	431	34	US-09-906-555-1424	Sequence 1424, Ap	840	13	86.7	452	34	US-09-925-564-14	Sequence 14, Appl
C 768	13	86.7	431	34	US-09-921-378-20580	Sequence 20580, A	C 841	13	86.7	453	23	US-09-606-977-70688	Sequence 70688, A
C 769	13	86.7	431	35	US-09-933-524-94313	Sequence 94313, A	C 842	13	86.7	455	16	US-09-293-972-7980	Sequence 7980, Ap
C 770	13	86.7	431	35	US-09-933-524A-94313	Sequence 94313, A	C 843	13	86.7	455	34	US-09-904-939-7980	Sequence 7980, Ap
C 771	13	86.7	432	33	US-09-865-439A-40023	Sequence 40023, A	C 844	13	86.7	456	31	US-09-813-206-607	Sequence 607, App
C 772	13	86.7	432	64	US-60-207-458-84297	Sequence 84297, A	C 845	13	86.7	456	31	US-09-813-206-607	Sequence 607, App
C 773	13	86.7	433	17	US-09-394-745-44218	Sequence 44218, A	C 846	13	86.7	456	32	US-09-846-038-542	Sequence 542, App
C 774	13	86.7	433	17	US-09-394-745-44218	Sequence 44218, A	C 846	13	86.7	459	18	US-09-431-517-2061	Sequence 2061, App
C 775	13	86.7	433	19	US-09-521-640-22616	Sequence 22616, A	C 847	13	86.7	459	19	US-09-528-409-40813	Sequence 40813, A
C 776	13	86.7	433	19	US-09-528-409-91852	Sequence 91852, A	C 848	13	86.7	459	35	US-09-933-524A-40813	Sequence 40813, A
C 777	13	86.7	433	21	US-09-540-229-110265	Sequence 110265, A	C 849	13	86.7	459	35	US-09-933-524A-40813	Sequence 40813, A
C 778	13	86.7	433	22	US-09-552-087-9239	Sequence 9239, Ap	C 850	13	86.7	459	38	US-10-020-338-24328	Sequence 24328, A
C 779	13	86.7	433	22	US-09-552-087B-9239	Sequence 9239, Ap	C 851	13	86.7	459	60	US-60-169-400-1212	Sequence 1212, Ap
C 780	13	86.7	433	22	US-09-565-306-67833	Sequence 67833, A	C 852	13	86.7	461	61	US-60-172-375-2315	Sequence 2315, Ap
C 781	13	86.7	433	35	US-09-933-524-91852	Sequence 91852, A	C 853	13	86.7	462	18	US-09-417-507-6373	Sequence 6373, Ap
C 782	13	86.7	433	35	US-09-933-524A-91852	Sequence 91852, A	C 854	13	86.7	462	33	US-09-865-419A-46335	Sequence 46335, A
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C 784	13	86.7	435	1	PCT-US01-01354-23077	Sequence 23077, A	C 856	13	86.7	464	23	US-09-606-977-51575	Sequence 51575, A
C 785	13	86.7	435	1	PCT-US01-01354-23078	Sequence 23078, A	C 857	13	86.7	464	23	US-09-606-977-51575	Sequence 51575, A
C 786	13	86.7	435	1	PCT-US01-01354-23079	Sequence 23079, A	C 858	13	86.7	464	64	US-60-207-458-56025	Sequence 56025, A
C 787	13	86.7	435	30	US-09-764-905-23077	Sequence 23077, A	C 859	13	86.7	465	63	US-60-196-710-2461	Sequence 2461, Ap
C 788	13	86.7	435	30	US-09-764-905-23078	Sequence 23078, A	C 859	13	86.7	465	63	US-60-196-710-2461	Sequence 2461, Ap
C 789	13	86.7	435	30	US-09-764-905-23079	Sequence 23079, A	C 860	13	86.7	466	23	US-09-606-977-45237	Sequence 45237, A
C 790	13	86.7	435	39	US-10-092-399-23077	Sequence 23077, A	C 861	13	86.7	467	1	PCT-US01-01324-4721	Sequence 4721, Ap
C 791	13	86.7	435	39	US-10-092-399-23078	Sequence 23078, A	C 862	13	86.7	467	1	PCT-US01-01353-733	Sequence 733, App
C 792	13	86.7	435	39	US-10-092-399-23079	Sequence 23079, A	C 863	13	86.7	467	19	US-09-521-640-150963	Sequence 150963
C 793	13	86.7	435	61	US-60-172-362-3870	Sequence 3870, Ap	C 864	13	86.7	467	39	US-10-079-979-4721	Sequence 4721, Ap
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## ALIGNMENTS

## RESULT 1

PCr-US00-35491-10  
; Sequence 10, Application PCrTUS0035491  
; GENERAL INFORMATION:  
; APPLICANT: Robertson, David  
; APPLICANT: Blakely, Randy D.  
; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND  
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO  
; FILE REFERENCE: Attorney Docket No. 1242-27 PCT  
; CURRENT FILING DATE: 2000-12-28  
; CURRENT FILING DATE: 2000-12-28  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR FILING DATE: 60/175,456  
; PRIOR FILING DATE: 1999-12-29  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCr-US00-35491-10

Query Match 100.0%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CCTTCTCCCTCTGTT 15

## RESULT 2

US-09-750-609-10  
; Sequence 10, Application US/09750609  
; GENERAL INFORMATION:  
; APPLICANT: Robertson, David  
; APPLICANT: Blakely, Randy D.

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; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
; FILE REFERENCE: Attorney Docket No. 1242-27-2-2
; CURRENT APPLICATION NUMBER: US/09/750,609
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 60/175,456
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/173,682
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-750-609-10

Query Match      100.0%; Score 15; DB 29; Length 15;
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; Sequence 10, Application US/60173682
; GENERAL INFORMATION:
; APPLICANT: Robertson, David
; APPLICANT: Blakely, Randy D.
; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
; FILE REFERENCE: Attorney Docket No. 1242-27
; CURRENT APPLICATION NUMBER: US/60/173,682
; CURRENT FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-173-682-10

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; Sequence 5, Application PC/TUS0035491
; GENERAL INFORMATION:
; APPLICANT: Robertson, David
; APPLICANT: Blakely, Randy D.
; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
; FILE REFERENCE: Attorney Docket No. 1242-27 PCT
; CURRENT APPLICATION NUMBER: PCT/US00/35491
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 60/175,456
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/173,682
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 40
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US-09-750-609-5

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Best Local Similarity 100.0%; Pred. No. 2.9e+02;
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RESULT 5
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; Sequence 6, Application PC/TUS0035491
; GENERAL INFORMATION:
; APPLICANT: Robertson, David
; APPLICANT: Blakely, Randy D.
; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
; FILE REFERENCE: Attorney Docket No. 1242-27 PCT
; CURRENT APPLICATION NUMBER: PCT/US00/35491
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 60/175,456
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/173,682
; PRIOR FILING DATE: 1999-12-29
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PCT-US00-35491-6

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; Sequence 5, Application US/09750609
; GENERAL INFORMATION:
; APPLICANT: Robertson, David
; APPLICANT: Blakely, Randy D.
; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
; FILE REFERENCE: Attorney Docket No. 1242-27-2
; CURRENT APPLICATION NUMBER: US/09/750,609
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 60/175,456
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/173,682
; PRIOR FILING DATE: 1999-12-29
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US-09-750-609-5

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PCT-US00-35491-5

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RESULT 5
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; Sequence 6, Application PC/TUS0035491
; GENERAL INFORMATION:
; APPLICANT: Robertson, David
; APPLICANT: Blakely, Randy D.
; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
; FILE REFERENCE: Attorney Docket No. 1242-27 PCT
; CURRENT APPLICATION NUMBER: PCT/US00/35491
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 60/175,456
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/173,682
; PRIOR FILING DATE: 1999-12-29
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PCT-US00-35491-6

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RESULT 6
US-09-750-609-5
; Sequence 5, Application US/09750609
; GENERAL INFORMATION:
; APPLICANT: Robertson, David
; APPLICANT: Blakely, Randy D.
; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
; FILE REFERENCE: Attorney Docket No. 1242-27-2
; CURRENT APPLICATION NUMBER: US/09/750,609
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 60/175,456
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/173,682
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-750-609-5

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Thu Dec 12 08:30:30 2002

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; CURRENT APPLICATION NUMBER: US/60/173,682
; CURRENT FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-173-682-6

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; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15367)B
; CURRENT APPLICATION NUMBER: US/09/306,349
; CURRENT FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 53893
; SEQ ID NO 2932
; LENGTH: 197
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 701040886H1
US-09-306-349-2932

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; Sequence 2932, Application US/09960481
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15367)C
; CURRENT APPLICATION NUMBER: US/09/960,481
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 09/306,349
; PRIOR FILING DATE: 1999-05-10
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; CURRENT APPLICATION NUMBER: US/60/173,682
; CURRENT FILING DATE: 1999-12-29
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; LENGTH: 41
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; ORGANISM: Homo sapiens
US-60-173-682-6

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8
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; Sequence 5, Application US/60173682
; GENERAL INFORMATION:
; APPLICANT: Robertson, David
; APPLICANT: Blakely, Randy D.
; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
; FILE REFERENCE: Attorney Docket No. 1242-27
; CURRENT APPLICATION NUMBER: US/60/173,682
; CURRENT FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-173-682-5

Query Match 100.0%; Score 15; DB 61; Length 41;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
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RESULT 9
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; Sequence 6, Application US/60173682
; GENERAL INFORMATION:
; APPLICANT: Robertson, David
; APPLICANT: Blakely, Randy D.
; TITLE OF INVENTION: GENETIC MUTATION UNDERLYING ORTHOSTATIC INTOLERANCE AND
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS RELATING THERETO
; FILE REFERENCE: Attorney Docket No. 1242-27
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: Sequence 47840, Application US/09540229

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; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; IMMEDIATE SOURCE:
; CLONE: 3268389H1
; US-60-048-002-2907
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; Sequence 4668, Application US/09637890
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Galvin, Katherine
; APPLICANT: Culpepper, Janice A.
; APPLICANT: Leiby, Kevin R.
; APPLICANT: Vasicek, Tom
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Villeval, Jean-Luc M. G.
; APPLICANT: Cepada, Mario
; APPLICANT: Kingsbury, Gillian A.
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.1152-001
; CURRENT APPLICATION NUMBER: US/09/637,890
; CURRENT FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 60/147,939
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 10217
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4668
; LENGTH: 327
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-637-890-4668
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: December 11, 2002, 17:10:08 : Search time 88.5 Seconds  
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Title: US-09-750-609-10  
Perfect score: 15  
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Searched: 407964 seqs, 359371392 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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c 155	14	93.3	6230	5	US-09-724-676A-2193	Sequence 2193, Ap	c 228	12	80.0	70383	6	US-10-283-247-3	Sequence 3, Appl1
c 156	14	93.3	6232	5	US-09-724-676-2160	Sequence 2160, Ap	c 229	12	80.0	70383	6	US-10-283-247-3	Sequence 3, Appl1
c 157	14	93.3	6232	5	US-09-724-676A-2160	Sequence 2160, Ap	c 230	12	80.0	70383	6	US-10-283-247-3	Sequence 3, Appl1
c 158	14	93.3	6275	5	US-09-724-676-2180	Sequence 2180, Ap	c 231	12	80.0	70383	6	US-10-283-247-3	Sequence 3, Appl1
c 159	14	93.3	6275	5	US-09-724-676A-2180	Sequence 2180, Ap	c 232	12	80.0	70383	6	US-10-283-247-3	Sequence 3, Appl1
c 160	14	93.3	6279	5	US-09-724-676-2199	Sequence 2199, Ap	c 233	12	80.0	70383	6	US-10-283-247-3	Sequence 3, Appl1
c 161	14	93.3	6279	5	US-09-724-676A-2199	Sequence 2199, Ap	c 234	12	80.0	70383	6	US-10-283-247-3	Sequence 3, Appl1
c 162	14	93.3	6324	5	US-09-724-676-2185	Sequence 2185, Ap	c 235	12	80.0	70383	6	US-10-283-247-3	Sequence 3, Appl1
c 163	14	93.3	6324	5	US-09-724-676A-2185	Sequence 2185, Ap	c 236	12	80.0	70383	6	US-10-283-247-3	Sequence 3, Appl1
c 164	14	93.3	6370	5	US-09-724-676-2164	Sequence 2164, Ap	c 237	12	80.0	70383	6	US-10-283-247-3	Sequence 3, Appl1
c 165	14	93.3	6370	5	US-09-724-676A-2164	Sequence 2164, Ap	c 238	12	80.0	70383	6	US-10-283-247-3	Sequence 3, Appl1
c 166	14	93.3	6433	5	US-09-724-676-2167	Sequence 2167, Ap	c 239	12	80.0	70383	6	US-10-283-247-3	Sequence 3, Appl1
c 167	14	93.3	6433	5	US-09-724-676A-2167	Sequence 2167, Ap	c 240	12	80.0	70383	6	US-10-283-247-3	Sequence 3, Appl1
c 168	14	93.3	6478	5	US-09-724-676A-2241	Sequence 2241, Ap	c 241	12	80.0	70383	6	US-10-283-247-3	Sequence 3, Appl1
c 169	14	93.3	6478	5	US-09-724-676A-2241	Sequence 2241, Ap	c 242	12	80.0	70383	6	US-10-283-247-3	Sequence 3, Appl1
c 170	14	93.3	6482	5	US-09-724-676A-2172	Sequence 2172, Ap	c 243	12	80.0	70383	6	US-10-283-247-3	Sequence 3, Appl1
c 171	14	93.3	6482	5	US-09-724-676A-2172	Sequence 2172, Ap	c 244	12	80.0	70383	6	US-10-283-247-3	Sequence 3, Appl1
c 172	14	93.3	6525	5	US-09-724-676-2192	Sequence 2192, Ap	c 245	12	80.0	70383	6	US-10-283-247-3	Sequence 3, Appl1

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c 246	12	80.0	2057	6	US-10-366-829-15	Sequence 15, Appl	319	12	80.0	3496	5	US-09-724-676A-31329	Sequence 31329, A
247	12	80.0	2230	5	US-09-724-676-16240	Sequence 16240, A	320	12	80.0	3512	5	US-09-724-676-44419	Sequence 44419, A
248	12	80.0	2230	5	US-09-724-676A-16240	Sequence 16240, A	321	12	80.0	3512	5	US-09-724-676A-44419	Sequence 44419, A
249	12	80.0	2245	5	US-09-724-676-16242	Sequence 16242, A	322	12	80.0	3592	5	US-09-724-676-13824	Sequence 13824, A
250	12	80.0	2245	5	US-09-724-676A-16242	Sequence 16242, A	323	12	80.0	3592	5	US-09-724-676A-13824	Sequence 13824, A
251	12	80.0	2349	5	US-09-724-676-16241	Sequence 16241, A	324	12	80.0	3617	5	US-09-724-676-44417	Sequence 44417, A
252	12	80.0	2349	5	US-09-724-676A-16241	Sequence 16241, A	325	12	80.0	3617	5	US-09-724-676A-44417	Sequence 44417, A
c 253	12	80.0	2354	6	US-10-194-163-275	Sequence 275, App	326	12	80.0	3702	5	US-09-724-676-31302	Sequence 31302, A
254	12	80.0	2380	5	US-09-724-676-31338	Sequence 31338, A	327	12	80.0	3702	5	US-09-724-676A-31302	Sequence 31302, A
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c 256	12	80.0	2574	5	US-09-724-676-40184	Sequence 40184, A	329	12	80.0	3711	5	US-09-724-676A-40182	Sequence 40182, A
c 257	12	80.0	2574	5	US-09-724-676A-40184	Sequence 40184, A	330	12	80.0	3749	5	US-09-724-676-40179	Sequence 40179, A
c 258	12	80.0	2577	5	US-09-724-676-40177	Sequence 40177, A	331	12	80.0	3749	5	US-09-724-676A-40179	Sequence 40179, A
c 259	12	80.0	2577	5	US-09-724-676A-40177	Sequence 40177, A	332	12	80.0	3779	5	US-09-724-676-31298	Sequence 31298, A
c 260	12	80.0	2612	5	US-09-724-676-40181	Sequence 40181, A	333	12	80.0	3779	5	US-09-724-676A-31298	Sequence 31298, A
c 261	12	80.0	2612	5	US-09-724-676A-40181	Sequence 40181, A	334	12	80.0	3816	5	US-09-724-676-40170	Sequence 40170, A
c 262	12	80.0	2679	5	US-09-724-676-40172	Sequence 40172, A	335	12	80.0	3816	5	US-09-724-676A-40170	Sequence 40170, A
c 263	12	80.0	2679	5	US-09-724-676A-40172	Sequence 40172, A	336	12	80.0	3838	5	US-09-724-676-25355	Sequence 25355, A
c 264	12	80.0	2682	5	US-09-724-676-40165	Sequence 40165, A	337	12	80.0	3838	5	US-09-724-676A-25355	Sequence 25355, A
c 265	12	80.0	2682	5	US-09-724-676A-40165	Sequence 40165, A	338	12	80.0	3839	5	US-09-724-676-40183	Sequence 40183, A
c 266	12	80.0	2717	5	US-09-724-676-40169	Sequence 40169, A	339	12	80.0	3839	5	US-09-724-676A-40183	Sequence 40183, A
c 267	12	80.0	2717	5	US-09-724-676A-40169	Sequence 40169, A	340	12	80.0	3854	5	US-09-724-676-40166	Sequence 40166, A
c 268	12	80.0	2733	5	US-09-724-676-40166	Sequence 40166, A	341	12	80.0	3854	5	US-09-724-676A-40166	Sequence 40166, A
c 269	12	80.0	2736	5	US-09-724-676A-40160	Sequence 40160, A	342	12	80.0	3870	5	US-09-724-676-40158	Sequence 40158, A
c 270	12	80.0	2736	5	US-09-724-676A-40154	Sequence 40154, A	343	12	80.0	3870	5	US-09-724-676A-40158	Sequence 40158, A
c 271	12	80.0	2736	5	US-09-724-676A-40154	Sequence 40154, A	344	12	80.0	3877	5	US-09-724-676-40180	Sequence 40180, A
c 272	12	80.0	2741	5	US-09-724-676-16219	Sequence 16219, A	345	12	80.0	3877	5	US-09-724-676A-40180	Sequence 40180, A
c 273	12	80.0	2741	5	US-09-724-676A-16219	Sequence 16219, A	346	12	80.0	3882	5	US-09-724-676-31313	Sequence 31313, A
c 274	12	80.0	2754	5	US-09-724-676-40176	Sequence 40176, A	347	12	80.0	3882	5	US-09-724-676A-31313	Sequence 31313, A
c 275	12	80.0	2754	5	US-09-724-676A-40176	Sequence 40176, A	348	12	80.0	3891	5	US-09-724-676-40174	Sequence 40174, A
c 276	12	80.0	2764	5	US-09-724-676-16224	Sequence 16224, A	349	12	80.0	3891	5	US-09-724-676A-40174	Sequence 40174, A
c 277	12	80.0	2764	5	US-09-724-676A-16224	Sequence 16224, A	350	12	80.0	3908	5	US-09-724-676-40155	Sequence 40155, A
c 278	12	80.0	2771	5	US-09-724-676-40157	Sequence 40157, A	351	12	80.0	3908	5	US-09-724-676A-40155	Sequence 40155, A
c 279	12	80.0	2771	5	US-09-724-676A-40157	Sequence 40157, A	352	12	80.0	3927	1	PCT-US02-04915-228	Sequence 228, App
c 280	12	80.0	2779	5	US-09-724-676-40173	Sequence 40173, A	353	12	80.0	3944	5	US-09-724-676-40171	Sequence 40171, A
c 281	12	80.0	2791	5	US-09-724-676-40173	Sequence 40173, A	354	12	80.0	3944	5	US-09-724-676A-40171	Sequence 40171, A
c 282	12	80.0	2791	5	US-09-724-676-16221	Sequence 16221, A	355	12	80.0	3959	5	US-09-724-676-31309	Sequence 31309, A
c 283	12	80.0	2807	5	US-09-724-676A-16221	Sequence 16221, A	356	12	80.0	3959	5	US-09-724-676A-31309	Sequence 31309, A
c 284	12	80.0	2807	5	US-09-979-603A-1	Sequence 1, Appl	357	12	80.0	3982	5	US-09-724-676-40168	Sequence 40168, A
c 285	12	80.0	2807	5	US-09-979-603-1	Sequence 1, Appl	358	12	80.0	3982	5	US-09-724-676A-40168	Sequence 40168, A
c 286	12	80.0	2841	5	US-09-724-676-40197	Sequence 40197, A	359	12	80.0	3996	5	US-09-724-676-40162	Sequence 40162, A
c 287	12	80.0	2841	5	US-09-724-676A-40197	Sequence 40197, A	360	12	80.0	3996	5	US-09-724-676A-40162	Sequence 40162, A
c 288	12	80.0	2859	5	US-09-724-676-40164	Sequence 40164, A	361	12	80.0	3998	5	US-09-724-676-40159	Sequence 40159, A
c 289	12	80.0	2859	5	US-09-724-676A-40164	Sequence 40164, A	362	12	80.0	3998	5	US-09-724-676A-40159	Sequence 40159, A
c 290	12	80.0	2876	5	US-09-724-676-40230	Sequence 40230, A	363	12	80.0	4013	5	US-09-724-676-40208	Sequence 40208, A
c 291	12	80.0	2876	5	US-09-724-676A-40230	Sequence 40230, A	364	12	80.0	4013	5	US-09-724-676A-40208	Sequence 40208, A
c 292	12	80.0	2884	5	US-09-724-676-40161	Sequence 40161, A	365	12	80.0	4019	5	US-09-724-676-40175	Sequence 40175, A
c 293	12	80.0	2884	5	US-09-724-676A-40161	Sequence 40161, A	366	12	80.0	4019	5	US-09-724-676A-40175	Sequence 40175, A
c 294	12	80.0	2913	5	US-09-724-676-40153	Sequence 40153, A	367	12	80.0	4026	5	US-09-724-676-31322	Sequence 31322, A
c 295	12	80.0	2913	5	US-09-724-676A-40153	Sequence 40153, A	368	12	80.0	4026	5	US-09-724-676A-31322	Sequence 31322, A
c 296	12	80.0	2938	5	US-09-724-676-40150	Sequence 40150, A	369	12	80.0	4036	5	US-09-724-676-40156	Sequence 40156, A
c 297	12	80.0	2938	5	US-09-724-676A-40150	Sequence 40150, A	370	12	80.0	4036	5	US-09-724-676A-40156	Sequence 40156, A
c 298	12	80.0	3018	5	US-09-724-676-40189	Sequence 40189, A	371	12	80.0	4044	5	US-09-724-676-25346	Sequence 25346, A
c 299	12	80.0	3018	5	US-09-724-676A-40189	Sequence 40189, A	372	12	80.0	4044	5	US-09-724-676A-25346	Sequence 25346, A
c 300	12	80.0	3027	5	US-09-724-676-31336	Sequence 31336, A	373	12	80.0	4050	5	US-09-724-676-40151	Sequence 40151, A
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c 304	12	80.0	3239	5	US-09-724-676-31323	Sequence 31323, A	377	12	80.0	4124	5	US-09-724-676-40163	Sequence 40163, A
c 305	12	80.0	3239	5	US-09-724-676A-31323	Sequence 31323, A	378	12	80.0	4124	5	US-09-724-676A-40163	Sequence 40163, A
c 306	12	80.0	3266	5	US-09-724-676-34792	Sequence 34792, A	379	12	80.0	4141	5	US-09-724-676-40219	Sequence 40219, A
c 307	12	80.0	3266	5	US-09-724-676A-34792	Sequence 34792, A	380	12	80.0	4141	5	US-09-724-676A-40219	Sequence 40219, A
c 308	12	80.0	3316	5	US-09-724-676-31319	Sequence 31319, A	381	12	80.0	4155	5	US-09-724-676-40167	Sequence 40167, A
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c 310	12	80.0	3350	5	US-09-724-676-34791	Sequence 34791, A	383	12	80.0	4178	5	US-09-724-676-40152	Sequence 40152, A
c 311	12	80.0	3350	5	US-09-724-676A-34791	Sequence 34791, A	384	12	80.0	4178	5	US-09-724-676A-40152	Sequence 40152, A
c 312	12	80.0	3374	5	US-09-724-676-44420	Sequence 44420, A	385	12	80.0	4204	5	US-09-724-676-12933	Sequence 12933, A
c 313	12	80.0	3374	5	US-09-724-676A-44420	Sequence 44420, A	386	12	80.0	4204	5	US-09-724-676A-12933	Sequence 12933, A
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c 316	12	80.0	3479	5	US-09-724-676-44418	Sequence 44418, A	389	12	80.0	4258	5	US-09-724-676-12931	Sequence 12931, A
c 317	12	80.0	3479	5	US-09-724-676A-44418	Sequence 44418, A	390	12	80.0	4258	5	US-09-724-676A-12931	Sequence 12931, A
c 318	12	80.0	3496	5	US-09-724-676-31329	Sequence 31329, A	391	12	80.0	4265	5	US-09-724-676-12937	Sequence 12937, A



c 538	12	80.0	6167	6	US-10-240-453-46	Sequence 46, Appl	c 611	11	73.3	208	5	US-09-513-999C-12545	Sequence 12545, A
c 539	12	80.0	6252	5	US-09-724-676-25358	Sequence 25358, A	612	11	73.3	209	6	US-10-203-138A-9916	Sequence 9916, Ap
c 540	12	80.0	6252	5	US-09-724-676A-25358	Sequence 25358, A	613	11	73.3	216	5	US-09-513-999C-16728	Sequence 16728, A
c 541	12	80.0	6257	5	US-09-724-676-25357	Sequence 25357, A	614	11	73.3	229	6	US-10-266-131-828	Sequence 828, App
c 542	12	80.0	6257	5	US-09-724-676A-25357	Sequence 25357, A	615	11	73.3	229	1	PCT-US02-36628-26	Sequence 26, Appl
c 543	12	80.0	6403	5	US-09-724-676-12763	Sequence 12763, A	616	11	73.3	258	5	US-09-513-999C-29796	Sequence 29796, A
c 544	12	80.0	6403	5	US-09-724-676A-12763	Sequence 12763, A	617	11	73.3	261	1	PCT-US02-34777-405	Sequence 405, App
c 545	12	80.0	6430	5	US-09-724-676-25356	Sequence 25356, A	618	11	73.3	261	6	US-10-283-017-405	Sequence 405, App
c 546	12	80.0	6430	5	US-09-724-676A-25356	Sequence 25356, A	619	11	73.3	263	5	US-09-513-999C-2281	Sequence 2281, Ap
c 547	12	80.0	7647	5	US-09-724-676-31283	Sequence 31283, A	620	11	73.3	270	5	US-09-513-999C-984	Sequence 984, App
c 548	12	80.0	7647	5	US-09-724-676A-31283	Sequence 31283, A	621	11	73.3	276	5	US-09-513-999C-28905	Sequence 28905, A
c 549	12	80.0	7724	5	US-09-724-676-31279	Sequence 31279, A	622	11	73.3	277	5	US-09-513-999C-27150	Sequence 27150, A
c 550	12	80.0	7724	5	US-09-724-676A-31279	Sequence 31279, A	623	11	73.3	283	5	US-09-513-999C-28528	Sequence 28528, A
c 551	12	80.0	7802	6	US-10-240-453-58	Sequence 58, Appl	624	11	73.3	296	6	US-10-240-425-1393	Sequence 1393, Ap
c 552	12	80.0	7827	5	US-09-724-676-31292	Sequence 31292, A	625	11	73.3	328	5	US-09-513-999C-33809	Sequence 33809, A
c 553	12	80.0	7827	5	US-09-724-676A-31292	Sequence 31292, A	626	11	73.3	343	5	US-09-513-999C-25726	Sequence 25726, A
c 554	12	80.0	7904	5	US-09-724-676-31288	Sequence 31288, A	627	11	73.3	347	5	US-09-513-999C-2258	Sequence 2258, Ap
c 555	12	80.0	7904	5	US-09-724-676A-31288	Sequence 31288, A	628	11	73.3	355	6	US-10-060-069-13	Sequence 13, Appl
c 556	12	80.0	8434	5	US-09-724-676-31282	Sequence 31282, A	629	11	73.3	356	6	US-09-606-397A-55	Sequence 55, Appl
c 557	12	80.0	8434	5	US-09-724-676A-31282	Sequence 31282, A	630	11	73.3	369	6	US-10-266-131-2738	Sequence 2738, Ap
c 558	12	80.0	8511	5	US-09-724-676-31278	Sequence 31278, A	631	11	73.3	374	5	US-09-513-999C-8247	Sequence 8247, Ap
c 559	12	80.0	8511	5	US-09-724-676A-31278	Sequence 31278, A	632	11	73.3	383	5	US-09-513-999C-20772	Sequence 20772, A
c 560	12	80.0	8614	5	US-09-724-676-31291	Sequence 31291, A	633	11	73.3	389	5	US-09-513-999C-33847	Sequence 33847, A
c 561	12	80.0	8614	5	US-09-724-676A-31291	Sequence 31291, A	634	11	73.3	419	6	US-10-203-138A-310	Sequence 310, App
c 562	12	80.0	8691	5	US-09-724-676-31287	Sequence 31287, A	635	11	73.3	426	6	US-10-203-138A-4803	Sequence 4803, Ap
c 563	12	80.0	8691	5	US-09-724-676A-31287	Sequence 31287, A	636	11	73.3	428	5	US-09-513-999C-1494	Sequence 1494, Ap
c 564	12	80.0	9081	5	US-09-724-676-31280	Sequence 31280, A	637	11	73.3	439	5	US-09-513-999C-27925	Sequence 27925, A
c 565	12	80.0	9081	5	US-09-724-676A-31280	Sequence 31280, A	638	11	73.3	445	6	US-10-203-138A-4972	Sequence 4972, Ap
c 566	12	80.0	9105	5	US-09-724-676-31281	Sequence 31281, A	639	11	73.3	454	5	US-09-724-676-29158	Sequence 29158, A
c 567	12	80.0	9105	5	US-09-724-676A-31281	Sequence 31281, A	640	11	73.3	454	5	US-09-724-676A-29158	Sequence 29158, A
c 568	12	80.0	9158	5	US-09-724-676-31340	Sequence 31340, A	641	11	73.3	456	6	US-10-203-138A-600	Sequence 600, App
c 569	12	80.0	9158	5	US-09-724-676A-31340	Sequence 31340, A	642	11	73.3	456	6	US-10-203-138A-2571	Sequence 2571, Ap
c 570	12	80.0	9182	5	US-09-724-676-31277	Sequence 31277, A	643	11	73.3	463	6	US-10-203-138A-2604	Sequence 2604, Ap
c 571	12	80.0	9182	5	US-09-724-676A-31277	Sequence 31277, A	644	11	73.3	468	6	US-10-280-864-3	Sequence 3, Appl
c 572	12	80.0	9261	5	US-09-724-676-31289	Sequence 31289, A	645	11	73.3	475	5	US-09-724-676-7925	Sequence 7925, Ap
c 573	12	80.0	9261	5	US-09-724-676A-31289	Sequence 31289, A	646	11	73.3	475	5	US-09-724-676A-7925	Sequence 7925, Ap
c 574	12	80.0	9285	5	US-09-724-676-31290	Sequence 31290, A	647	11	73.3	475	6	US-10-203-138A-1393	Sequence 1393, Ap
c 575	12	80.0	9285	5	US-09-724-676A-31290	Sequence 31290, A	648	11	73.3	478	6	US-10-203-138A-2011	Sequence 2011, Ap
c 576	12	80.0	9338	5	US-09-724-676-31285	Sequence 31285, A	649	11	73.3	479	6	US-10-203-138A-10296	Sequence 10296, A
c 577	12	80.0	9338	5	US-09-724-676A-31285	Sequence 31285, A	650	11	73.3	481	6	US-10-203-138A-1169	Sequence 1169, Ap
c 578	12	80.0	9362	5	US-09-724-676-31286	Sequence 31286, A	651	11	73.3	485	6	US-10-203-138A-3241	Sequence 3241, Ap
c 579	12	80.0	9362	5	US-09-724-676A-31286	Sequence 31286, A	652	11	73.3	488	6	US-10-203-138A-5762	Sequence 5762, Ap
c 580	12	80.0	11330	1	PCT-US02-32727-39	Sequence 39, Appl	653	11	73.3	493	6	US-10-203-138A-7703	Sequence 7703, Ap
c 581	12	80.0	11330	6	US-10-057-498-39	Sequence 39, Appl	654	11	73.3	502	5	US-09-724-676-14559	Sequence 14559, A
c 582	12	80.0	14127	5	US-09-724-676-33734	Sequence 33734, A	655	11	73.3	502	5	US-09-724-676A-14559	Sequence 14559, A
c 583	12	80.0	14127	5	US-09-724-676A-33734	Sequence 33734, A	656	11	73.3	504	5	US-09-724-676A-14559	Sequence 14559, A
c 584	12	80.0	14800	5	US-09-724-676-33732	Sequence 33732, A	657	11	73.3	504	5	US-09-724-676-7920	Sequence 7920, Ap
c 585	12	80.0	14800	5	US-09-724-676A-33732	Sequence 33732, A	658	11	73.3	504	5	US-09-724-676A-7920	Sequence 7920, Ap
c 586	12	80.0	14835	5	US-09-724-676-33733	Sequence 33733, A	659	11	73.3	546	6	PCT-US02-34777-936	Sequence 936, App
c 587	12	80.0	14835	5	US-09-724-676A-33733	Sequence 33733, A	660	11	73.3	547	6	US-10-283-017-936	Sequence 936, App
c 588	12	80.0	15645	6	US-10-085-198-111	Sequence 111, App	661	11	73.3	570	6	US-10-152-319A-248	Sequence 248, App
c 589	12	80.0	18073	5	US-09-728-552-12	Sequence 12, Appl	662	11	73.3	605	5	US-10-266-131-182	Sequence 182, App
c 590	12	80.0	45450	1	PCT-US02-32700-7	Sequence 7, Appl	663	11	73.3	605	5	US-09-724-676-3673	Sequence 3673, Ap
c 591	12	80.0	45450	6	US-10-271-416-7	Sequence 7, Appl	664	11	73.3	605	5	US-09-724-676A-3673	Sequence 3673, Ap
c 592	12	80.0	53500	6	US-10-267-255-76	Sequence 76, Appl	665	11	73.3	625	6	US-10-203-138A-8372	Sequence 8372, Ap
c 593	12	80.0	133760	6	US-10-240-425-1101	Sequence 1101, Ap	666	11	73.3	628	5	US-09-724-676-14557	Sequence 14557, A
c 594	12	80.0	207433	6	US-10-277-216-5	Sequence 5, Appl	667	11	73.3	636	5	US-09-724-676A-14557	Sequence 14557, A
c 595	12	80.0	659158	6	US-09-771-208A-20	Sequence 20, Appl	668	11	73.3	636	5	US-09-724-676-26486	Sequence 26486, A
c 596	11	73.3	19	6	US-10-293-338-7137	Sequence 7137, Ap	669	11	73.3	638	5	US-09-724-676A-26486	Sequence 26486, A
c 597	11	73.3	81	5	US-09-513-999C-23685	Sequence 23685, A	670	11	73.3	638	5	US-09-724-676A-14544	Sequence 14544, A
c 598	11	73.3	87	5	US-09-513-999C-23553	Sequence 23553, A	671	11	73.3	659	5	US-09-724-676-42343	Sequence 42343, A
c 599	11	73.3	93	5	US-09-513-999C-33619	Sequence 33619, A	672	11	73.3	659	5	US-09-724-676A-42343	Sequence 42343, A
c 600	11	73.3	118	5	US-09-513-999C-33625	Sequence 33625, A	673	11	73.3	673	6	US-10-152-319A-1340	Sequence 1340, Ap
c 601	11	73.3	121	6	US-10-209-787-349	Sequence 349, App	674	11	73.3	687	1	PCT-US02-32432-43	Sequence 43, Appl
c 602	11	73.3	121	6	US-10-209-787-350	Sequence 350, App	675	11	73.3	693	5	US-09-724-676-29604	Sequence 29604, A
c 603	11	73.3	130	5	US-09-513-999C-24744	Sequence 24744, A	676	11	73.3	693	5	US-09-724-676A-29604	Sequence 29604, A
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c 605	11	73.3	150	5	US-09-513-999C-26415	Sequence 26415, A	678	11	73.3	711	5	US-09-724-676-14556	Sequence 14556, A
c 606	11	73.3	153	6	US-10-203-138A-7944	Sequence 7944, Ap	679	11	73.3	711	5	US-09-724-676A-14556	Sequence 14556, A
c 607	11	73.3	161	5	US-09-513-999C-16217	Sequence 16217, A	680	11	73.3	744	5	US-09-620-607B-644	Sequence 644, App
c 608	11	73.3	164	6	US-10-266-131-1686	Sequence 1686, Ap	681	11	73.3	744	5	US-09-724-676-7068	Sequence 7068, Ap
c 609	11	73.3	171	6	US-10-203-138A-7128	Sequence 7128, Ap	682	11	73.3	744	5	US-09-724-676A-7068	Sequence 7068, Ap
c 610	11	73.3	180	6	US-10-203-138A-5496	Sequence 5496, Ap	683	11	73.3	758	5	US-09-724-676-6144	Sequence 6144, Ap

c 684	11	73.3	758	5	US-09-724-676A-6144	Sequence 6144, Ap	757	11	73.3	999	5	US-09-724-676A-14541	Sequence 14541, A
c 685	11	73.3	776	5	US-09-724-676-14543	Sequence 14543, A	758	11	73.3	1001	5	US-09-724-676-14515	Sequence 14515, A
c 686	11	73.3	776	5	US-09-724-676A-14543	Sequence 14543, A	759	11	73.3	1001	5	US-09-724-676A-14515	Sequence 14515, A
c 687	11	73.3	780	5	US-09-724-676-7066	Sequence 7066, Ap	c 760	11	73.3	1006	5	US-09-724-676-17582	Sequence 17582, A
c 688	11	73.3	780	5	US-09-724-676-7071	Sequence 7071, Ap	c 761	11	73.3	1006	5	US-09-724-676A-17582	Sequence 17582, A
c 689	11	73.3	780	5	US-09-724-676A-7066	Sequence 7066, Ap	c 762	11	73.3	1010	5	US-09-724-676A-3680	Sequence 3680, Ap
c 690	11	73.3	780	5	US-09-724-676A-7071	Sequence 7071, Ap	c 763	11	73.3	1010	5	US-09-724-676A-14517	Sequence 14517, A
c 691	11	73.3	794	5	US-09-724-676-14519	Sequence 14519, A	c 764	11	73.3	1017	5	US-09-724-676-14517	Sequence 14517, A
c 692	11	73.3	794	5	US-09-724-676A-14519	Sequence 14519, A	c 765	11	73.3	1017	5	US-09-724-676-24664	Sequence 24664, A
c 693	11	73.3	803	5	US-09-724-676-14558	Sequence 14558, A	c 766	11	73.3	1017	5	US-09-724-676A-14517	Sequence 14517, A
c 694	11	73.3	803	5	US-09-724-676A-14558	Sequence 14558, A	c 767	11	73.3	1017	5	US-09-724-676A-24664	Sequence 24664, A
c 695	11	73.3	815	5	US-09-724-676-14548	Sequence 14548, A	c 768	11	73.3	1020	5	US-09-724-676-14530	Sequence 14530, A
c 696	11	73.3	815	5	US-09-724-676A-14548	Sequence 14548, A	c 769	11	73.3	1020	5	US-09-724-676A-14530	Sequence 14530, A
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c 698	11	73.3	827	5	US-09-724-676-35661	Sequence 35661, A	c 771	11	73.3	1024	5	US-09-724-676-18519	Sequence 18519, A
c 699	11	73.3	827	5	US-09-724-676A-35661	Sequence 35661, A	c 772	11	73.3	1024	5	US-09-724-676A-18519	Sequence 18519, A
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c 701	11	73.3	837	5	US-09-724-676A-13422	Sequence 13422, A	c 774	11	73.3	1025	5	US-09-724-676A-47370	Sequence 47370, A
c 702	11	73.3	843	5	US-09-724-676-18517	Sequence 18517, A	c 775	11	73.3	1026	5	US-09-724-676-26461	Sequence 26461, A
c 703	11	73.3	843	5	US-09-724-676A-18517	Sequence 18517, A	c 776	11	73.3	1026	5	US-09-724-676-26467	Sequence 26467, A
c 704	11	73.3	843	6	US-10-264-237-415	Sequence 415, App	c 777	11	73.3	1026	5	US-09-724-676-26470	Sequence 26470, A
c 705	11	73.3	844	5	US-09-724-676-14555	Sequence 14555, A	c 778	11	73.3	1026	5	US-09-724-676A-26461	Sequence 26461, A
c 706	11	73.3	844	5	US-09-724-676A-14555	Sequence 14555, A	c 779	11	73.3	1026	5	US-09-724-676A-26467	Sequence 26467, A
c 707	11	73.3	850	5	US-09-724-676-38090	Sequence 38090, A	c 780	11	73.3	1026	5	US-09-724-676A-26470	Sequence 26470, A
c 708	11	73.3	850	5	US-09-724-676A-38090	Sequence 38090, A	c 781	11	73.3	1026	5	US-09-724-676-18522	Sequence 18522, A
c 709	11	73.3	852	5	US-09-724-676-18520	Sequence 18520, A	c 782	11	73.3	1027	5	US-09-724-676A-18522	Sequence 18522, A
c 710	11	73.3	852	5	US-09-724-676A-18520	Sequence 18520, A	c 783	11	73.3	1027	5	US-09-724-676-20036	Sequence 20036, A
c 711	11	73.3	853	5	US-09-724-676-3674	Sequence 3674, Ap	c 784	11	73.3	1042	5	US-09-724-676A-20036	Sequence 20036, A
c 712	11	73.3	853	5	US-09-724-676A-3674	Sequence 3674, Ap	c 785	11	73.3	1042	5	PCT-US02-32721-184	Sequence 184, App
c 713	11	73.3	861	5	US-09-724-676-25950	Sequence 25950, A	c 786	11	73.3	1050	6	US-10-057-498-184	Sequence 184, App
c 714	11	73.3	861	5	US-09-724-676A-25950	Sequence 25950, A	c 787	11	73.3	1050	6	US-09-724-676-26473	Sequence 26473, A
c 715	11	73.3	865	5	US-09-724-676-14535	Sequence 14535, A	c 788	11	73.3	1065	5	US-09-724-676-26476	Sequence 26476, A
c 716	11	73.3	865	5	US-09-724-676A-14535	Sequence 14535, A	c 789	11	73.3	1065	5	US-09-724-676-26480	Sequence 26480, A
c 717	11	73.3	880	5	US-09-724-676A-14535	Sequence 14535, A	c 790	11	73.3	1065	5	US-09-724-676-26483	Sequence 26483, A
c 718	11	73.3	887	5	US-09-724-676-14531	Sequence 14531, A	c 791	11	73.3	1065	5	US-09-724-676-26483	Sequence 26483, A
c 719	11	73.3	887	5	US-09-724-676A-2574	Sequence 2574, Ap	c 792	11	73.3	1065	5	US-09-724-676A-26473	Sequence 26473, A
c 720	11	73.3	887	5	US-09-724-676A-14531	Sequence 14531, A	c 793	11	73.3	1065	5	US-09-724-676A-26476	Sequence 26476, A
c 721	11	73.3	894	5	US-09-724-676-34780	Sequence 34780, A	c 794	11	73.3	1065	5	US-09-724-676A-26480	Sequence 26480, A
c 722	11	73.3	894	5	US-09-724-676A-34780	Sequence 34780, A	c 795	11	73.3	1065	5	US-09-724-676A-26483	Sequence 26483, A
c 723	11	73.3	898	5	US-09-724-676-14511	Sequence 14511, A	c 796	11	73.3	1066	5	US-09-724-676-25805	Sequence 25805, A
c 724	11	73.3	898	5	US-09-724-676A-14511	Sequence 14511, A	c 797	11	73.3	1066	5	US-09-724-676A-25805	Sequence 25805, A
c 725	11	73.3	909	5	US-09-724-676-14542	Sequence 14542, A	c 798	11	73.3	1066	5	US-09-724-676A-25805	Sequence 25805, A
c 726	11	73.3	909	5	US-09-724-676A-14542	Sequence 14542, A	c 799	11	73.3	1078	5	US-09-724-676A-6496	Sequence 6496, Ap
c 727	11	73.3	912	6	US-10-264-237-649	Sequence 649, App	c 800	11	73.3	1078	5	US-09-724-676A-6496	Sequence 6496, Ap
c 728	11	73.3	918	5	US-09-724-676-14552	Sequence 14552, A	c 801	11	73.3	1089	5	US-09-724-676A-24656	Sequence 24656, A
c 729	11	73.3	918	5	US-09-724-676A-14552	Sequence 14552, A	c 802	11	73.3	1089	5	US-09-724-676A-24656	Sequence 24656, A
c 730	11	73.3	922	6	US-10-264-237-1006	Sequence 1006, Ap	c 803	11	73.3	1094	5	US-09-724-676A-14527	Sequence 14527, A
c 731	11	73.3	927	5	US-09-724-676-14518	Sequence 14518, A	c 804	11	73.3	1094	5	US-09-724-676A-14527	Sequence 14527, A
c 732	11	73.3	927	5	US-09-724-676A-14518	Sequence 14518, A	c 805	11	73.3	1101	5	US-09-724-676A-20035	Sequence 20035, A
c 733	11	73.3	932	5	US-09-724-676-25213	Sequence 25213, A	c 806	11	73.3	1101	5	US-09-724-676A-20035	Sequence 20035, A
c 734	11	73.3	932	5	US-09-724-676A-25213	Sequence 25213, A	c 807	11	73.3	1105	5	US-09-724-676-17921	Sequence 17921, A
c 735	11	73.3	933	6	US-10-278-173-43	Sequence 43, Appl	c 808	11	73.3	1105	5	US-09-724-676A-17921	Sequence 17921, A
c 736	11	73.3	934	5	US-09-724-676-14554	Sequence 14554, A	c 809	11	73.3	1110	5	US-09-724-676A-14529	Sequence 14529, A
c 737	11	73.3	934	5	US-09-724-676A-14554	Sequence 14554, A	c 810	11	73.3	1110	5	US-09-724-676A-14529	Sequence 14529, A
c 738	11	73.3	936	5	US-09-724-676-34773	Sequence 34773, A	c 811	11	73.3	1110	5	US-09-724-676A-24663	Sequence 24663, A
c 739	11	73.3	936	5	US-09-724-676A-34773	Sequence 34773, A	c 812	11	73.3	1110	5	US-09-724-676A-24663	Sequence 24663, A
c 740	11	73.3	961	5	US-09-724-676-18523	Sequence 18523, A	c 813	11	73.3	1127	5	US-09-724-676A-47371	Sequence 47371, A
c 741	11	73.3	961	5	US-09-724-676A-18523	Sequence 18523, A	c 814	11	73.3	1127	5	US-09-724-676A-47371	Sequence 47371, A
c 742	11	73.3	970	5	US-09-724-676-18514	Sequence 18514, A	c 815	11	73.3	1134	5	US-09-724-676A-42342	Sequence 42342, A
c 743	11	73.3	970	5	US-09-724-676A-18514	Sequence 18514, A	c 816	11	73.3	1134	5	US-09-724-676A-42342	Sequence 42342, A
c 744	11	73.3	983	5	US-09-724-676-14539	Sequence 14539, A	c 817	11	73.3	1142	5	US-09-724-676A-18513	Sequence 18513, A
c 745	11	73.3	983	5	US-09-724-676A-14539	Sequence 14539, A	c 818	11	73.3	1142	5	US-09-724-676A-18513	Sequence 18513, A
c 746	11	73.3	991	5	US-09-724-676-14523	Sequence 14523, A	c 819	11	73.3	1145	5	US-09-724-676-18516	Sequence 18516, A
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c 748	11	73.3	996	5	US-09-724-676-26447	Sequence 26447, A	c 821	11	73.3	1161	1	PCT-US02-32432-42	Sequence 42, Appl
c 749	11	73.3	996	5	US-09-724-676-26447	Sequence 26447, A	c 822	11	73.3	1161	6	US-10-152-319A-1903	Sequence 1903, Ap
c 750	11	73.3	996	5	US-09-724-676-26454	Sequence 26454, A	c 823	11	73.3	1182	5	US-09-724-676-24655	Sequence 24655, A
c 751	11	73.3	996	5	US-09-724-676-26454	Sequence 26454, A	c 824	11	73.3	1182	5	US-09-724-676A-24655	Sequence 24655, A
c 752	11	73.3	996	5	US-09-724-676A-26444	Sequence 26444, A	c 825	11	73.3	1185	5	US-09-724-676A-24655	Sequence 24655, A
c 753	11	73.3	996	5	US-09-724-676A-26444	Sequence 26444, A	c 826	11	73.3	1185	5	US-09-724-676A-42340	Sequence 42340, A
c 754	11	73.3	996	5	US-09-724-676A-26451	Sequence 26451, A	c 827	11	73.3	1186	5	US-09-724-676A-42340	Sequence 42340, A
c 755	11	73.3	996	5	US-09-724-676A-26451	Sequence 26451, A	c 828	11	73.3	1186	5	US-09-724-676-2535	Sequence 2535, Ap
c 756	11	73.3	999	5	US-09-724-676-14541	Sequence 14541, A	c 829	11	73.3	1187	5	US-09-724-676A-1672	Sequence 1672, Ap

c 830	11	73.3	1187	5	US-09-724-676A-1672	Sequence 1672, Ap	903	11	73.3	1332	6	US-10-137-872A-443	Sequence 443, App
c 831	11	73.3	1190	5	US-09-724-676-18518	Sequence 18518, A	904	11	73.3	1332	6	US-10-137-873A-443	Sequence 443, App
c 832	11	73.3	1191	5	US-09-724-676A-18518	Sequence 18518, A	905	11	73.3	1332	6	US-10-125-921A-443	Sequence 443, App
c 833	11	73.3	1193	5	US-09-724-676-18521	Sequence 18521, A	906	11	73.3	1332	6	US-10-125-928A-443	Sequence 443, App
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## ALIGNMENTS

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RESULT 1
US-09-513-999C-13316/c
; Sequence 13316, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.052.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 13316
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 298
; OTHER INFORMATION: k=g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 330
; OTHER INFORMATION: r=a or g
; US-09-513-999C-13316
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Best Local Similarity 100.0%; Pred. No. 7.7;
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DB 149 CCTTCTCCCTGTT 135
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US-10-264-237-1036
; Sequence 1036, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
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; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
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; LENGTH: 2520
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
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; US-10-264-237-1036
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RESULT 3
US-09-620-607B-1245/c
; Sequence 1245, Application US/09620607B
; GENERAL INFORMATION:
; APPLICANT: Nehls, Michael
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Mutated Mammalian Cells and
; FILE REFERENCE: LEX-0032-USA
; CURRENT APPLICATION NUMBER: US/09/620,607B
; CURRENT FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/144942
; PRIOR FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 1848
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1245
; LENGTH: 248
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-620-607B-1245
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Best Local Similarity 100.0%; Pred. No. 28;
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RESULT 4
US-09-724-676-38339
; Sequence 38339, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Comugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Comugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38339
; LENGTH: 908
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; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676-38339

Query Match 93.3%; Score 14; DB 5; Length 908;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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## RESULT 5

US-09-724-676A-38339  
; Sequence 38339, Application US/09724676A

; GENERAL INFORMATION:

; APPLICANT: Compugen LTD

; TITLE OF INVENTION: Variants of alternative splicing

; FILE REFERENCE: 129181.4 Compugen

; CURRENT APPLICATION NUMBER: US/09/724,676A

; CURRENT FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 97222

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 38339

; LENGTH: 908

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-724-676A-38339

Query Match 93.3%; Score 14; DB 5; Length 908;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 444 CCTTCTCCCCCTGT 457

## RESULT 6

US-09-724-676-24274/c

; Sequence 24274, Application US/09724676

; GENERAL INFORMATION:

; APPLICANT: Compugen LTD

; TITLE OF INVENTION: Variants of alternative splicing

; FILE REFERENCE: 129181.4 Compugen

; CURRENT APPLICATION NUMBER: US/09/724,676

; CURRENT FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 97222

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 24274

; LENGTH: 1030

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-724-676-24274

Query Match 93.3%; Score 14; DB 5; Length 1030;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCCCTGT 14  
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Db 692 CCTTCTCCCCCTGT 679

## RESULT 7

US-09-724-676A-24274/c

; Sequence 24274, Application US/09724676A

; GENERAL INFORMATION:

; APPLICANT: Compugen LTD

; TITLE OF INVENTION: Variants of alternative splicing

; FILE REFERENCE: 129181.4 Compugen

; CURRENT APPLICATION NUMBER: US/09/724,676A

; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 24274

; LENGTH: 1030

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-724-676A-24274

Query Match 93.3%; Score 14; DB 5; Length 1030;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 692 CCTTCTCCCCCTGT 679

## RESULT 8

US-09-724-676-2247/c

; Sequence 2247, Application US/09724676

; GENERAL INFORMATION:

; APPLICANT: Compugen LTD

; TITLE OF INVENTION: Variants of alternative splicing

; FILE REFERENCE: 129181.4 Compugen

; CURRENT APPLICATION NUMBER: US/09/724,676

; CURRENT FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 97222

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2247

; LENGTH: 1509

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-724-676-2247

Query Match 93.3%; Score 14; DB 5; Length 1509;  
Best Local Similarity 100.0%; Pred. No. 26;  
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QY 1 CCTTCTCCCCCTGT 14  
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Db 831 CCTTCTCCCCCTGT 818

## RESULT 9

US-09-724-676A-2247/c

; Sequence 2247, Application US/09724676A

; GENERAL INFORMATION:

; APPLICANT: Compugen LTD

; TITLE OF INVENTION: Variants of alternative splicing

; FILE REFERENCE: 129181.4 Compugen

; CURRENT APPLICATION NUMBER: US/09/724,676A

; CURRENT FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 97222

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2247

; LENGTH: 1509

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-724-676A-2247

Query Match 93.3%; Score 14; DB 5; Length 1509;  
Best Local Similarity 100.0%; Pred. No. 26;  
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Db 831 CCTTCTCCCCCTGT 818

## RESULT 10

US-09-724-676-2234/c

; Sequence 2234, Application US/09724676



; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2234  
; LENGTH: 1667  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676-2234

Query Match 93.3%; Score 14; DB 5; Length 1667;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGT 14  
Db 989 CCTTCTCCCCCTGT 976

RESULT 11  
US-09-724-676A-2234/c  
; Sequence 2234, Application US/09724676A  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676A  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2234  
; LENGTH: 1667  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676A-2234

Query Match 93.3%; Score 14; DB 5; Length 1667;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGT 14  
Db 989 CCTTCTCCCCCTGT 976

RESULT 12  
US-09-724-676-2221/c  
; Sequence 2221, Application US/09724676  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2221  
; LENGTH: 1712  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676-2221

Query Match 93.3%; Score 14; DB 5; Length 1712;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGT 14  
Db 1034 CCTTCTCCCCCTGT 1021

RESULT 13  
US-09-724-676A-2221/c  
; Sequence 2221, Application US/09724676A  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676A  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2221  
; LENGTH: 1712  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676A-2221

Query Match 93.3%; Score 14; DB 5; Length 1712;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGT 14  
Db 1034 CCTTCTCCCCCTGT 1021

RESULT 14  
US-09-724-676-2240/c  
; Sequence 2240, Application US/09724676  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2240  
; LENGTH: 1755  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676-2240

Query Match 93.3%; Score 14; DB 5; Length 1755;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTCTCCCCCTGT 14  
Db 831 CCTTCTCCCCCTGT 818

RESULT 15  
US-09-724-676A-2240/c  
; Sequence 2240, Application US/09724676A  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676A  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2240  
; LENGTH: 1755  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676A-2240

Query Match 93.3%; Score 14; DB 5; Length 1755;  
Best Local Similarity 100.0%; Pred. No. 26;

Qy 1 CCTTCTCCCCCTGT 14  
Db 1034 CCTTCTCCCCCTGT 1021



Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCTTCTCCGCCCTGT 14  
Db 831 CCTTCTCCGCCCTGT 818

Search completed: December 11, 2002, 20:30:16  
Job time : 97.5 secs

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